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(54) Title: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR ANALYSIS OF GENE EXPRESSION IN HUMAN HELA CELLS OR OTHER HUMAN CERVICAL EPITHELIAL CELLS

(57) Abstract: A single exon nucleic acid microarray comprising a plurality of single exon nucleic acid probes for measuring gene expression in a sample derived from human HeLa cells is described. Also described are single exon nucleic acid probes expressed in the HeLa cells and their use in methods for detecting gene expression.

HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL  
FOR ANALYSIS OF GENE EXPRESSION IN HUMAN HELA CELLS OR  
OTHER HUMAN CERVICAL EPITHELIAL CELLS

5 CROSS REFERENCE TO RELATED APPLICATIONS

The present application is a continuation-in-part of U.S.  
patent application serial nos. 09/632,366, filed August 3,  
2000 and 09/608,408, filed June 30, 2000; claims the  
10 benefit under 35 U.S.C. s 119(e) of U.S. provisional patent  
application serial nos. 60/236,359, filed September 27,  
2000, 60/234,687, filed September 21, 2000, 60/207,456,  
filed May 26, 2000, and 60/180,312, filed February 4, 2000;  
and further claims the benefit under 35 U.S.C. s 119(a) of  
15 UK patent application no. 0024263.6, filed October 4, 2000,  
the disclosures of which are incorporated herein by  
reference in their entireties.

REFERENCE TO SEQUENCE LISTING AND INCORPORATION BY  
20 REFERENCE THEREOF

The present application includes a Sequence Listing in  
electronic format, filed pursuant to PCT Administrative  
Instructions 801 - 806 on a single CD-R disc, in  
25 triplicate, containing a file named pto\_HELA.txt, created  
24 January 2001, having 18,781,468 bytes. The Sequence  
Listing contained in said file on said disc is incorporated  
herein by reference in its entirety.

30 Field of the Invention

The present invention relates to genome-derived  
single exon microarrays useful for verifying the expression  
of regions of genomic DNA predicted to encode protein. In  
35 particular, the present invention relates to unique genome-



derived single exon nucleic acid probes expressed in human HeLa cells and single exon nucleic acid microarrays that include such probes.

5 Background of the Invention

For almost two decades following the invention of general techniques for nucleic acid sequencing, Sanger et al., *Proc. Natl. Acad. Sci. USA* 70(4):1209-13 (1973); Gilbert et al., *Proc. Natl. Acad. Sci. USA* 70(12):3581-4  
10 (1973), these techniques were used principally as tools to further the understanding of proteins - known or suspected - about which a basic foundation of biological knowledge had already been built. In many cases, the cloning effort that preceded sequence identification had  
15 been both informed and directed by that antecedent biological understanding.

For example, the cloning of the T cell receptor for antigen was predicated upon its known or suspected cell type-specific expression, by its suspected membrane  
20 association, and by the predicted assembly of its gene via T cell-specific somatic recombination. Subsequent sequencing efforts at once confirmed and extended understanding of this family of proteins. Hedrick et al., *Nature* 308(5955):153-8 (1984).

25 More recently, however, the development of high throughput sequencing methods and devices, in concert with large public and private undertakings to sequence the human and other genomes, has altered this investigational paradigm: today, sequence information often precedes  
30 understanding of the basic biology of the encoded protein product.

One of the approaches to large-scale sequencing is predicated upon the proposition that expressed sequences - that is, those accessible through isolation of  
35 mRNA - are of greatest initial interest. This "expressed

sequence tag" ("EST") approach has already yielded vast amounts of sequence data (see for example Adams et al., *Science* 252:1651 (1991); Williamson, *Drug Discov. Today* 4:115 (1999)). For nucleic acids sequenced by this  
5 approach, often the only biological information that is known a priori with any certainty is the likelihood of biologic expression itself. By virtue of the species and tissue from which the mRNA had originally been obtained, most such sequences are also annotated with the identity of  
10 the species and at least one tissue in which expression appears likely.

More recently, the pace of genomic sequencing has accelerated dramatically. When genomic DNA serves as the initial substrate for sequencing efforts, expression cannot  
15 be presumed; often the only a priori biological information about the sequence includes the species and chromosome (and perhaps chromosomal map location) of origin.

With the ever-accelerating pace of sequence accumulation by directed, EST, and genomic sequencing  
20 approaches – and in particular, with the accumulation of sequence information from multiple genera, from multiple species within genera, and from multiple individuals within a species – there is an increasing need for methods that rapidly and effectively permit the functions of nucleic  
25 sequences to be elucidated. And as such functional information accumulates, there is a further need for methods of storing such functional information in meaningful and useful relationship to the sequence itself; that is, there is an increasing need for means and  
30 apparatus for annotating raw sequence data with known or predicted functional information.

Although the increase in the pace of genomic sequencing is due in large part to technological changes in sequencing strategies and instrumentation, Service, *Science*  
35 280:995 (1998); Pennisi, *Science* 283: 1822-1823 (1999),

there is an important functional motivation as well.

While it was understood that the EST approach would rarely be able to yield sequence information about the noncoding portions of the genome, it now also appears  
5 the EST approach is capable of capturing only a fraction of a genome's actual expression complexity.

For example, when the *C. elegans* genome was fully sequenced, gene prediction algorithms identified over 19,000 potential genes, of which only 7,000 had been found  
10 by EST sequencing. *C. elegans* Sequencing Consortium, *Science* 282:2012 (1998). Analogously, the recently completed sequence of chromosome 2 of *Arabidopsis* predicts over 4000 genes, Lin et al., *Nature*, 402:761 (1999), of which only about 6% had previously been identified via EST  
15 sequencing efforts. Although the human genome has the greatest depth of EST coverage, it is still woefully short of surrendering all of its genes. One recent estimate suggests that the human genome contains more than 146,000 genes, which would at this point leave greater than half of  
20 the genes undiscovered. It is now predicted that many genes, perhaps 20 to 50%, will only be found by genomic sequencing.

There is, therefore, a need for methods that permit the functional regions of genomic sequence – and  
25 most importantly, but not exclusively, regions that function to encode genes – to be identified.

Much of the coding sequence of the human genome is not homologous to known genes, making detection of open reading frames ("ORFs") and predictions of gene function  
30 difficult. Computational methods exist for predicting coding regions in eukaryotic genomes. Gene prediction programs such as GRAIL and GRAIL II, Uberbacher et al., *Proc. Natl. Acad. Sci. USA* 88(24):11261-5 (1991); Xu et al., *Genet. Eng.* 16:241-53 (1994); Uberbacher et al.,  
35 *Methods Enzymol.* 266:259-81 (1996); GENEFINDER, Solovyev et

al., *Nucl. Acids. Res.* 22:5156-63 (1994); Solovyev et al.,  
*Ismb* 5:294-302 (1997); and GENESCAN, Burge et al., *J. Mol.*  
*Biol.* 268:78-94 (1997), predict many putative genes without  
known homology or function. Such programs are known,  
5 however, to give high false positive rates. Burset et al.,  
*Genomics* 34:353-367 (1996). Using a consensus obtained by  
a plurality of such programs is known to increase the  
reliability of calling exons from genomic sequence.  
Ansari-Lari et al., *Genome Res.* 8(1):29-40 (1998)

10 Identification of functional genes from genomic  
data remains, however, an imperfect art. For example, in  
reporting the full sequence of human chromosome 21, the  
Chromosome 21 Mapping and Sequencing Consortium reports  
that prior bioinformatic estimates of human gene number may  
15 need to be revised substantially downwards. *Nature*  
405:311-199 (2000); Reeves, *Nature* 405:283-284 (2000).

Thus, there is a need for methods and apparatus  
that permit the functions of the regions identified  
bioinformatically - and specifically, that permit the  
20 expression of regions predicted to encode protein - readily  
to be confirmed experimentally.

Recently, the development of nucleic acid  
microarrays has made possible the automated and highly  
parallel measurement of gene expression. Reviewed in  
25 Schena (ed.), DNA Microarrays : A Practical Approach  
(Practical Approach Series), Oxford University Press (1999)  
(ISBN: 0199637768); *Nature Genet.* 21(1)(suppl):1 - 60  
(1999); Schena (ed.), Microarray Biochip: Tools and  
Technology, Eaton Publishing Company/BioTechniques Books  
30 Division (2000) (ISBN: 1881299376).

It is common for microarrays to be derived from  
cDNA/EST libraries, either from those previously described  
in the literature, such as those from the I.M.A.G.E.  
consortium, Lennon et al., *Genomics* 33(1):151-2 (1996), or  
35 from the construction of "problem specific" libraries

targeted at a particular biological question, R.S. Thomas  
et al., *Cancer Res.* (in press). Such microarrays by  
definition can measure expression only of those genes found  
in EST libraries, and thus have not been useful as probes  
5 for genes discovered solely by genomic sequencing.

The utility of using whole genome nucleic acid  
microarrays to answer certain biological questions has been  
demonstrated for the yeast *Saccharomyces cerevisiae*. De  
Risi et al., *Science* 278:680 (1997). The vast majority of  
10 yeast nuclear genes, approximately 95% however, are single  
exon genes, i.e., lack introns, Lopez et al., *RNA* 5:1135-  
1137 (1999); Goffeau et al., *Science* 274:563-67 (1996),  
permitting coding regions more readily to be identified.  
Whole genome nucleic acid microarrays have not generally  
15 been used to probe gene expression from more complex  
eukaryotic genomes, and in particular from those averaging  
more than one intron per gene.

#### Summary of the Invention

20

The present invention solves these and other  
problems in the art by providing methods and apparatus for  
predicting, confirming, and displaying functional  
information derived from genomic sequence. The present  
25 invention also provides apparatus for verifying the  
expression of putative genes identified within genomic  
sequence.

In particular, the invention provides novel  
genome-derived single exon nucleic acid microarrays useful  
30 for verifying the expression of putative genes identified  
within genomic sequence.

The present invention also provides compositions  
and kits for the ready production of nucleic acids  
identical in sequence to, or substantially identical in  
35 sequence to, probes on the genome-derived single exon

microarrays of the present invention.

Accordingly, in a first aspect of the invention, there is provided a spatially-addressable set of single exon nucleic acid probes for measuring gene expression in a sample derived from human HeLa cells or other human cervical epithelial cells, comprising a plurality of single exon nucleic acid probes according to any one of the nucleotide sequences set out in SEQ ID NOS: 1 - 9,290 or a complementary sequence, or a portion of such a sequence.

By plurality is meant at least two, suitably at least 20, most suitably at least 100, preferably at least 1000 and, most preferably, upto 5000.

In one embodiment of the first aspect, each of said plurality of probes is separately and addressably amplifiable.

In an alternative embodiment, each of said plurality of probes is separately and addressably isolatable from said plurality.

In a preferred embodiment, each of said plurality of probes is amplifiable using at least one common primer. Preferably, each of said plurality of probes is amplifiable using a first and a second common primer.

In yet another embodiment, said set of single exon nucleic acid probes comprises between 50 - 20,000 probes, for example, 50 - 5000.

Suitably, said set of single exon nucleic acid probes comprises at least 50 - 1000 discrete single exon nucleic acid probes having a sequence as set out in any of SEQ ID NOS.: 1 - 18,392 or a complimentary sequence, or a portion of such a sequence.

Preferably, the average length of the single exon nucleic acid probes is between 200 and 500 bp. It is preferred that the average length should be at least 200bp, suitably at least 250bp, most suitably at least 300bp, preferably at least 400bp and, most preferably, 500 bp.

In another embodiment, the single exon nucleic acid probes lack prokaryotic and bacteriophage vector sequence. It is preferred that at least 50%, suitably at least 60%, most suitably at least 70%, preferably at least 5 75%, more preferably at least 80, 85, 90, 95 or 99% of said single exon nucleic acid probes lack prokaryotic and bacteriophage vector sequence.

In another preferred embodiment, said single exon nucleic acid lack homopolymeric stretches of A or T. It is 10 preferred that at least 50%, suitably at least 60%, most suitably at least 70%, preferably at least 75%, more preferably at least 80, 85, 90, 95 or 99% of said single exon nucleic acid probes lack homopolymeric stretches of A or T.

15 Preferably, a spatially-addressable set of single exon nucleic acid probes in accordance with the first aspect of the invention is addressably disposed upon a substrate.

Suitable substrates include a filter membrane 20 which may, preferably, be nitrocellulose or nylon. The nylon may preferably, be positively-charged. Other suitable substrates include glass, amorphous silicon, crystalline silicon, and plastic. Further suitable materials include polymethylacrylic, polyethylene, polypropylene, 25 polyacrylate, polymethylmethacrylate, polyvinylchloride, polytetrafluoroethylene, polystyrene, polycarbonate, polyacetal, polysulfone, celluloseacetate, cellulosenitrate, nitrocellulose, and mixtures thereof.

In a second aspect of the invention, there is 30 provided a microarray comprising a spatially addressable set of single exon nucleic acid probes in accordance with the first aspect of the invention.

In one embodiment, a genome-derived single-exon microarray is packaged together with such an ordered set of 35 amplifiable probes corresponding to the probes, or one or

more subsets of probes, thereon. In alternative embodiments, the ordered set of amplifiable probes is packaged separately from the genome-derived single exon microarray.

5 In another aspect, the invention provides genome-derived single exon nucleic acid probes useful for gene expression analysis, and particularly for gene expression analysis by microarray. In particular embodiments of this aspect, the present invention provides human single-exon  
10 probes that include specifically-hybridizable fragments of SEQ ID Nos. 9,291 - 18,392, wherein the fragment hybridizes at high stringency to an expressed human gene. In particular embodiments, the invention provides single exon probes comprising SEQ ID Nos. 1 - 9,290.

15 Accordingly, in a third aspect of the invention, there is provided a single exon nucleic acid probe for measuring human gene expression in a sample derived from human HeLa cells or other human cervical epithelial cells which is a nucleic acid molecule comprising a nucleotide  
20 sequence as set out in any of SEQ ID NOs.: 1 - 9,290 or a complementary sequence or a fragment thereof wherein said probe hybridizes at high stringency to a nucleic acid expressed in the human HeLa cells or other human cervical epithelial cells.

25 In one embodiment, a single exon nucleic acid probe in accordance with the third aspect comprises a nucleotide sequence as set out in any of SEQ ID NOs.: 9,291 - 18,392 or a complementary sequence or a fragment thereof.

In a fourth aspect of the invention, there is  
30 provided a single exon nucleic acid probe for measuring human gene expression in a sample derived from human HeLa cells or other human cervical epithelial cells which is a nucleic acid molecule having a sequence encoding a peptide comprising a peptide sequence as set out in any of SEQ ID  
35 NOs.: 18,393 - 26,941 or a complementary sequence or a



fragment thereof wherein said probe hybridizes at high stringency to a nucleic acid expressed in the human HeLa cells or other human cervical epithelial cells.

Preferably, a single exon nucleic acid probe in accordance with the third or fourth aspects of the invention comprises between at least 15 and 50 contiguous nucleotides of said SEQ ID NO:. It is preferred that the single exon nucleic acid probe comprises at least 15, suitably at least 20, more suitably at least 25 or preferably at least 50 contiguous nucleotides of said SEQ ID NO:.

In another preferred embodiment, a single exon nucleic acid probe in accordance with the third or fourth aspects of the invention is between 3kb and 25kb in length. It is preferred that said probe is no more than 3kb, suitably no more than 5kb, more suitably no more than 10kb, preferably 15kb, more preferably 20kb or, most preferably, no more than 20kb in length.

Preferably, a single exon nucleic acid probe in accordance with either the fifth or sixth aspect of the invention is DNA, preferably single-stranded DNA, RNA or PNA.

In another embodiment of either the third or fourth aspect of the invention, a single exon nucleic acid probe is detectably labeled. Suitable detectable labels include a radionuclide, a fluorescent label or a first member of a specific binding pair. Suitable fluorescent labels include dyes such as cyanine dyes, preferably Cy3 and Cy5 although other suitable dyes will be known to those skilled in the art.

In a particularly preferred embodiment, a single exon nucleic acid probe in accordance with either the third or fourth aspect of the invention lacks prokaryotic and bacteriophage vector sequence. In yet another embodiment, a single exon nucleic acid probe in accordance with either

the third or fourth aspect of the invention lacks homopolymeric stretches of A or T.

In a fifth aspect of the invention, there is provided an amplifiable nucleic acid composition,

5 comprising:

the single exon nucleic acid probe in accordance with either of the third or fourth aspects of the invention; and at least one nucleic acid primer;

wherein said at least one primer is sufficient to  
10 prime enzymatic amplification of said probe.

In an sixth aspect of the invention, there is provided a method of measuring gene expression in a sample derived from human HeLa cells or other human cervical epithelial cells, comprising:

15 contacting the single exon microarray in accordance with the second aspect of the invention, with a first collection of detectably labeled nucleic acids, said first collection of nucleic acids derived from mRNA of human HeLa cells or other human cervical epithelial cells;  
20 and then

measuring the label detectably bound to each probe of said microarray.

In a seventh aspect of the invention, there is provided a method of identifying exons in a eukaryotic  
25 genome, comprising:

algorithmically predicting at least one exon from genomic sequence of said eukaryote; and then

detecting specific hybridization of detectably labeled nucleic acids to a single exon probe,

30 wherein said detectably labeled nucleic acids are derived from mRNA from the HeLa cells or other human cervical epithelial cells of said eukaryote, said probe is a single exon probe having a fragment identical in sequence to, or complementary in sequence to, said predicted exon,  
35 said probe is included within a single exon microarray in

accordance with the first aspect of the invention, and said fragment is selectively hybridizable at high stringency.

In a eighth aspect of the invention, there is provided a method of assigning exons to a single gene,

5 comprising:

identifying a plurality of exons from genomic sequence in accordance with the seventh aspect of the invention; and then

10 measuring the expression of each of said exons in a plurality of tissues and/or cell types using hybridization to single exon microarrays having a probe with said exon,

wherein a common pattern of expression of said exons in said plurality of tissues and/or cell types  
15 indicates that the exons should be assigned to a single gene.

In an ninth aspect of the invention, there is provided a nucleic acid sequence as set out in any of SEQ ID NOS: 1 - 18,392 wherein said sequence encodes a peptide.

20 In a tenth aspect of the invention, there is provided a peptide encoded by a sequence comprising a sequence as set out in any of SEQ ID NOS: 9,291 - 18,392, or a complementary sequence or coding portion thereof.

In a preferred embodiment, a peptide may be  
25 encoded by a sequence comprising a sequence set out in any of SEQ ID NOS.: 1 -9,290.

In a further aspect, the invention provides peptides comprising an amino acid sequence translated from the DNA fragments, said amino acid sequences comprising SEQ  
30 ID NOS.: 18,393 - 26,941.

Accordingly in a eleventh aspect of the invention there is provided a peptide comprising a sequence as set out in any of SEQ ID NOS: 18,393 - 26,941, or fragment thereof.

35 In another aspect, the invention provides means

for displaying annotated sequence, and in particular, for displaying sequence annotated according to the methods and apparatus of the present invention. Further, such display can be used as a preferred graphical user interface for  
5 electronic search, query, and analysis of such annotated sequence.

### Detailed Description of the Invention

10

#### Definitions

As used herein, the term "microarray" and phrase "nucleic acid microarray" refer to a substrate-bound collection of plural nucleic acids, hybridization to each  
15 of the plurality of bound nucleic acids being separately detectable. The substrate can be solid or porous, planar or non-planar, unitary or distributed.

As so defined, the term "microarray" and phrase "nucleic acid microarray" include all the devices so called  
20 in Schena (ed.), DNA Microarrays: A Practical Approach (Practical Approach Series), Oxford University Press (1999) (ISBN: 0199637768); *Nature Genet.* 21(1)(suppl):1 - 60 (1999); and Schena (ed.), Microarray Biochip: Tools and Technology, Eaton Publishing Company/BioTechniques Books  
25 Division (2000) (ISBN: 1881299376). As so defined, the term "microarray" and phrase "nucleic acid microarray" further include substrate-bound collections of plural nucleic acids in which the nucleic acids are distributably disposed on a plurality of beads, rather than on a unitary  
30 planar substrate, as is described, *inter alia*, in Brenner et al., *Proc. Natl. Acad. Sci. USA* 97(4):166501670 (2000); in such case, the term "microarray" and phrase "nucleic acid microarray" refer to the plurality of beads in aggregate.

35 As used herein with respect to a nucleic acid

microarray, the term "probe" refers to the nucleic acid that is, or is intended to be, bound to the substrate; in such context, the term "target" thus refers to nucleic acid intended to be bound thereto by Watson-Crick

5 complementarity. As used herein with respect to solution phase hybridization, the term "probe" refers to the nucleic acid of known sequence that is detectably labeled.

As used herein, the expression "probe comprising SEQ ID NO.", and variants thereof, intends a nucleic acid  
10 probe, at least a portion of which probe has either (i) the sequence directly as given in the referenced SEQ ID NO., or (ii) a sequence complementary to the sequence as given in the referenced SEQ ID NO., the choice as between sequence directly as given and complement thereof dictated by the  
15 requirement that the probe hybridize to mRNA.

As used herein, the term "open reading frame" and the equivalent acronym "ORF" refer to that portion of an exon that can be translated in its entirety into a sequence of contiguous amino acids i.e. a nucleic acid sequence  
20 that, in at least one reading frame, does not possess stop codons; the term does not require that the ORF encode the entirety of a natural protein.

As used herein, the term "amplicon" refers to a PCR product amplified from human genomic DNA, containing  
25 the predicted exon.

As used herein the term "exon" refers to the consensus prediction of the various exon and gene predicting algorithms i.e. a nucleic acid sequence bioinformatically predicted to encode a portion of a  
30 natural protein.

As used herein, the term "peptide" refers to a sequence of amino acids. The sequences referred to as PEPTIDE SEQ ID NOS.: are the predicted peptide sequences that would be translated from one of the exons, or a  
35 portion thereof set out in exon SEQ ID NOS.: The codons

encoding the peptide are wholly contained within the exon.

As used herein, a "portions" of a defined nucleotide sequence or sequences can be and, preferably, are fragments unique to that sequence or to one or a  
5 combination of those sequences. A fragment unique to a nucleic acid molecule is one that is a signature for the larger nucleic acid molecule.

As used herein, the phrase "expression of a probe" and its linguistic variants means that the ORF  
10 present within the probe, or its complement, is present within a target mRNA.

As used herein, "stringent conditions" refers to parameters well known to those skilled in the art. When a nucleic acid molecule is said to be hybridisable to another  
15 of a given sequence under "stringent conditions" it is meant that it is homologous to the given sequence.

As used herein, the phrase "specific binding pair" intends a pair of molecules that bind to one another with high specificity. Binding pairs are said to exhibit  
20 specific binding when they exhibit avidity of at least  $10^7$ , preferably at least  $10^8$ , more preferably at least  $10^9$  liters/mole. Nonlimiting examples of specific binding pairs are: antibody and antigen; biotin and avidin; and biotin and streptavidin.

As used herein with respect to the visual display  
25 of annotated genomic sequence, the term "rectangle" means any geometric shape that has at least a first and a second border, wherein the first and second borders each are capable of mapping uniquely to a point of another visual  
30 object of the display.

As used herein, a "Mondrian" means a visual display in which a single genomic sequence is annotated with predicted and experimentally confirmed functional information.

35

Brief Description of the Drawings

The present invention is further illustrated with  
5 reference to the following non-limiting figures and  
examples in which:

FIG. 1 illustrates a process for predicting  
functional regions from genomic sequence, confirming the  
functional activity of such regions experimentally, and  
10 associating and displaying the data so obtained in  
meaningful and useful relationship to the original sequence  
data;

FIG. 2 further elaborates that portion of the  
process schematized in FIG. 1 for predicting functional  
15 regions from genomic sequence;

FIG. 3 illustrates a Mondrian visual display;

FIG. 4 presents a Mondrian showing a hypothetical  
annotated genomic sequence;

FIG. 5 is a histogram showing the distribution of  
20 ORF length and PCR products as obtained, with ORF length  
shown in black and PCR product length shown in dotted  
lines;

FIG. 6 is a histogram showing the distribution,  
among exons predicted according to the methods described,  
25 of expression as measured using simultaneous two color  
hybridization to a genome-derived single exon microarray.  
The graph shows the number of sequence-verified products  
that were either not expressed ("0"), expressed in one or  
more but not all tested tissues ("1" - "9"), or expressed  
30 in all tissues tested ("10");

FIG. 7 is a pictorial representation of the  
expression of verified sequences that showed expression  
with signal intensity greater than 3 in at least one  
tissue, with: FIG. 7A showing the expression as measured by  
35 microarray hybridization in each of the 10 measured

tissues, and the expression as measured "bioinformatically" by query of EST, NR and SwissProt databases; with FIG. 7B showing the legend for display of physical expression (ratio) in FIG. 7A; and with FIG. 7C showing the legend for scoring EST hits as depicted in FIG. 7A;

FIG. 8 shows a comparison of normalized CY3 signal intensity for arrayed sequences that were identical to sequences in existing EST, NR and SwissProt databases or that were dissimilar (unknown), where black denotes the signal intensity for all sequence-verified products with a BLAST Expect ("E") value of greater than  $1e-30$  ( $1 \times 10^{-30}$ ) ("unknown") and a dotted line denotes sequence-verified spots with a BLAST expect ("E") value of less than  $1e-30$  ( $1 \times 10^{-30}$ ) ("known");

FIG. 9 presents a Mondrian of BAC AC008172 (bases 25,000 to 130,000), containing the carbamyl phosphate synthetase gene (AF154830.1); and

FIG. 10 is a Mondrian of BAC A049839.

20

Methods and Apparatus for Predicting, Confirming, Annotating, and Displaying Functional Regions From Genomic Sequence Data

FIG. 1 is a flow chart illustrating in broad outline a process for predicting functional regions from genomic sequence, confirming and characterizing the functional activity of such regions experimentally, and then associating and displaying the information so obtained in meaningful and useful relationship to the original sequence data.

The initial input into process 10 of the present invention is drawn from one or more databases containing genomic sequence data. Because genomic sequence is usually obtained from subgenomic fragments, the sequence



data typically will be stored in a series of records corresponding to these subgenomic sequenced fragments. Some fragments will have been catenated to form larger contiguous sequences ("contigs"); others will not. A  
5 finite percentage of sequence data in the database will typically be erroneous, consisting *inter alia* of vector sequence, sequence created from aberrant cloning events, sequence of artificial polylinkers, and sequence that was erroneously read.

10 Each sequence record in database 100 will minimally contain as annotation a unique sequence identifier (accession number), and will typically be annotated further to identify the date of accession, species of origin, and depositor. Because database 100 can  
15 contain nongenomic sequence, each sequence will typically be annotated further to permit query for genomic sequence. Chromosomal origin, optionally with map location, can also be present. Data can be, and over time increasingly will be, further annotated with additional information, in part  
20 through use of the present invention, as described below. Annotation can be present within the data records, in information external to database 100 and linked to the records thereto, or through a combination of the two.

Databases useful as genomic sequence database 100  
25 in the present invention include GenBank, and particularly include several divisions thereof, including the htgs(draft), NT (nucleotide, command line), and NR (nonredundant) divisions. GenBank is produced by the National Institutes of Health and is maintained by the  
30 National Center for Biotechnology Information (NCBI). Databases of genomic sequence from species other than human, such as mouse, rat, Arabidopsis, *C. elegans*, *C. brigssii*, *Drosophila*, zebra fish, and other higher eukaryotic organisms will also prove useful as genomic  
35 sequence database 100.

Genomic sequence obtained by query of genomic sequence database 100 is then input into one or more processes 200 for identification of regions therein that are predicted to have a biological function as specified by the user. Such functions include, but are not limited to, encoding protein, regulating transcription, regulating message transport after transcription into mRNA, regulating message splicing after transcription into mRNA, of regulating message degradation after transcription into mRNA, and the like. Other functions include directing somatic recombination events, contributing to chromosomal stability or movement, contributing to allelic exclusion or X chromosome inactivation, and the like.

The particular genomic sequence to be input into process 200 will depend upon the function for which relevant sequence is to be identified as well as upon the approach chosen for such identification. Process step 200 can be iterated to identify different functions within a given genomic region. In such case, the input often will be different for the several iterations.

Sequences predicted to have the requisite function by process 200 are then input into process 300, where a subset of the input sequences suitable for experimental confirmation is identified. Experimental confirmation can involve physical and/or bioinformatic assay. Where the subsequent experimental assay is bioinformatic, rather than physical, there are fewer constraints on the sequences that can be tested, and in this latter case therefore process 300 can output the entirety of the input sequence.

The subset of sequences output from process 300 is then used in process 400 for experimental verification and characterization of the function predicted in process 200, which experimental verification can, and often will, include both physical and bioinformatic assay.

Process 500 annotates the sequence data with the functional information obtained in the physical and/or bioinformatic assays of process 400. Such annotation can be done using any technique that usefully relates the functional information to the sequence, as, for example, by incorporating the functional data into the sequence data record itself, by linking records in a hierarchical or relational database, by linking to external databases, by a combination thereof, or by other means well known within the database arts. The data can even be submitted for incorporation into databases maintained by others, such as GenBank, which is maintained by NCBI.

As further noted in FIG. 1, additional annotation can be input into process 500 from external sources 600.

The annotated data is then displayed in process 800, either before, concomitantly with, or after optional storage 700 on nontransient media, such as magnetic disk, optical disc, magnetooptical disk, flash memory, or the like.

FIG. 1 shows that the experimental data output from process 400 can be used in each preceding step of process 10: e.g., facilitating identification of functional sequences in process 200, facilitating identification of an experimentally suitable subset thereof in process 300, and facilitating creation of physical and/or informational substrates for, and performance of subsequent assay, of functional sequences in process 400.

Information from each step can be passed directly to the succeeding process, or stored in permanent or interim form prior to passage to the succeeding process. Often, data will be stored after each, or at least a plurality, of such process steps. Any or all process steps can be automated.

FIG. 2 further elaborates the prediction of functional sequence within genomic sequence according to

process 200.

Genomic sequence database 100 is first queried 20 for genomic sequence.

The sequence required to be returned by query 20  
5 will depend, in the first instance, upon the function to be identified.

For example, genomic sequences that function to encode protein can be identified *inter alia* using gene prediction approaches, comparative sequence analysis  
10 approaches, or combinations of the two. In gene prediction analysis, sequence from one genome is input into process 200 where at least one, preferably a plurality, of algorithmic methods are applied to identify putative coding regions. In comparative sequence analysis, by contrast,  
15 corresponding, e.g., syntenic, sequence from a plurality of sources, typically a plurality of species, is input into process 200, where at least one, possibly a plurality, of algorithmic methods are applied to compare the sequences and identify regions of least variability.

20 The exact content of query 20 will also depend upon the database queried. For example, if the database contains both genomic and nongenomic sequence, perhaps derived from multiple species, and the function to be determined is protein coding regions in human genomic  
25 sequence, the query will accordingly require that the sequence returned be genomic and derived from humans.

Query 20 can also incorporate criteria that compel return of sequence that meets operative requirements of the subsequent analytical method. Alternatively, or in  
30 addition, such operative criteria can be enforced in subsequent preprocess step 24.

For example, if the function sought to be identified is protein coding, query 20 can incorporate criteria that return from genomic sequence database 100  
35 only those sequences present within contigs sufficiently

long as to have obviated substantial fragmentation of any given exon among a plurality of separate sequence fragments.

Such criteria can, for example, consist of a  
5 required minimal individual genomic sequence fragment length, such as 10 kb, more typically 20 kb, 30 kb, 40kb, and preferably 50 kb or more, as well as an optional further or alternative requirement that sequence from any given clone, such as a bacterial artificial chromosome  
10 ("BAC"), be presented in no more than a finite maximal number of fragments, such as no more than 20 separate pieces, more typically no more than 15 fragments, even more typically no more than about 10 - 12 fragments.

Results using the present invention have shown  
15 that genomic sequence from bacterial artificial chromosomes (BACs) is sufficient for gene prediction analysis according to the present invention if the sequence is at least 50 kb in length, and if additionally the sequence from any given BAC is presented in fewer than 15, and preferably fewer  
20 than 10, fragments. Accordingly, query 20 can incorporate a requirement that data accessioned from BAC sequencing be in fewer than 15, preferably fewer than 10, fragments.

An additional criterion that can be incorporated into the query can be the date, or range of dates, of  
25 sequence accession. Although the process has been described above as if genomic sequence database 100 were static, it is of course understood that the genomic sequence databases need not be static, and indeed are typically updated on a frequent, even hourly, basis. Thus,  
30 as further described in Examples 1 and 2, *infra*, it is possible to query the database for newly added sequence, either newly added after an absolute date, or newly added relative to a prior analysis performed using the methods and apparatus of the present invention. In this way, the  
35 process herein described can incorporate a dynamic,

temporal component.

One utility of such temporal limitation is to identify, from newly accessioned genomic sequence, the presence of novel genes, particularly those not previously identified by EST sequencing (or other sequencing efforts that are similarly based upon gene expression). As further described in Example 1, such an approach has shown that newly accessioned human genomic sequence, when analyzed for sequences that function to encode protein, readily identifies genes that are novel over those in existing EST and other expression databases. This makes the methods of the present invention extremely powerful gene discovery tools. And as would be appreciated, such gene discovery can be performed using genomic sequence from species other than human.

If query 20 incorporates multiple criteria, such as above-described, the multiple criteria can be performed as a series of separate queries or as a single query, depending in part upon the query language, the complexity of the query, and other considerations well known in the database arts.

If query 20 returns no genomic sequence meeting the query criteria, the negative result can be reported by process 22, and process 200 (and indeed, entire process 10) ended 23, as shown. Alternatively, or in addition to report and termination of the initial inquiry, a new query 20 can be generated that takes into account the initial negative result.

When query 20 returns sequence meeting the query criteria, the returned sequence is then passed to optional preprocessing 24, suitable and specific for the desired analytical approach and the particular analytical methods thereof to be used in process 25.

Preprocessing 24 can include processes suitable for many approaches and methods thereof, as well as

processes specifically suited for the intended subsequent analysis.

Preprocessing 24 suitable for most approaches and methods will include elimination of sequence irrelevant to, or that would interfere with, the subsequent analysis. Such sequence includes repetitive sequence, such as Alu repeats and LINE elements, vector sequence, artificial sequence, such as artificial polylinkers, and the like. Such removal can readily be performed by identification and subsequent masking of the undesired sequence.

Identification can be effected by comparing the genomic sequence returned by query 20 with public or private databases containing known repetitive sequence, vector sequence, artificial sequence, and other artifactual sequence. Such comparison can readily be done using programs well known in the art, such as CROSS\_MATCH, or by proprietary sequence comparison programs the engineering of which is well within the skill in the art.

Alternatively, or in addition, undesirable, including artifactual, sequence can be identified algorithmically without comparison to external databases and thereafter removed. For example, synthetic polylinker sequence can be identified by an algorithm that identifies a significantly higher than average density of known restriction sites. As another example, vector sequence can be identified by algorithms that identify nucleotide or codon usage at variance with that of the bulk of the genomic sequence.

Once identified, undesired sequence can be removed. Removal can usefully be done by masking the undesired sequence as, for example, by converting the specific nucleotide references to one that is unrecognized by the subsequent bioinformatic algorithms, such as "X". Alternatively, but at present less preferred, the undesired sequence can be excised from the returned genomic sequence,

leaving gaps.

Preprocessing 24 can further include selection from among duplicative sequences of that one sequence of highest quality. Higher quality can be measured as a lower percentage of, fewest number of, or least densely clustered occurrence of ambiguous nucleotides, defined as those nucleotides that are identified in the genomic sequence using symbols indicating ambiguity. Higher quality can also or alternatively be valued by presence in the longest contig.

Preprocessing 24 can, and often will, also include formatting of the data as specifically appropriate for passage to the analytical algorithms of process 25. Such formatting can and typically will include, *inter alia*, addition of a unique sequence identifier, either derived from the original accession number in genomic sequence database 100, or newly applied, and can further include additional annotation. Formatting can include conversion from one to another sequence listing standard, such as conversion to or from FASTA or the like, depending upon the input expected by the subsequent process.

Preprocessing, which can be optional depending upon the function desired to be identified and the informational requirements of the methods for effecting such identification, is followed by sequence processing 25, where sequences with the desired function are identified within the genomic sequence.

As mentioned above, such functions can include, but are not limited to, encoding protein, regulating transcription, regulating message transport after transcription into mRNA, regulating message splicing after transcription, of regulating message degradation, and the like. Other functions include directing somatic recombination events, contributing to chromosomal stability or movement, contributing to allelic exclusion or X



chromosome inactivation, or the like.

The methods of the present invention are particularly useful for gene discovery, that is, for identifying, from genomic sequence, regions that function  
5 to encode genes, and in a particularly useful embodiment, for identifying regions that function to encode genes not hitherto identified by expression-based or directed cloning and sequencing. In conjunction with verification using the novel single exon microarrays of the present invention, as  
10 further described below, the methods herein described become powerful gene discovery tools.

Accordingly, in a preferred embodiment of the present invention, process 25 is used to identify putative coding regions. Two preferred approaches in process 25 for  
15 identifying sequence that encodes putative genes are gene prediction and comparative sequence analysis.

Gene prediction can be performed using any of a number of algorithmic methods, embodied in one or more software programs, that identify open reading frames (ORFs)  
20 using a variety of heuristics, such as GRAIL, DICTION, and GENEFINDER. Comparative sequence analysis similarly can be performed using any of a variety of known programs that identify regions with lower sequence variability.

As further described in Example 1, below, gene  
25 finding software programs yield a range of results. For the newly accessioned human genomic sequence input in Example 1, for example, GRAIL identified the greatest percentage of genomic sequence as putative coding region, 2% of the data analyzed; GENEFINDER was second, calling 1%;  
30 and DICTION yielded the least putative coding region, with 0.8% of genomic sequence called as coding region.

Increased reliability can be obtained when consensus is required among several such methods. Although discussed herein particularly with respect to exon calling,  
35 consensus among methods will in general increase

reliability of predicting other functions as well.

Thus, as indicated by query 26, sequence processing 25, optionally with preprocessing 24, can be repeated with a different method, with consensus among such  
5 iterations determined and reported in process 27.

Process 27 compares the several outputs for a given input genomic sequence and identifies consensus among the separately reported results. The consensus itself, as well as the sequence meeting that consensus, is then stored  
10 in process 29a, displayed in process 29b, and/or output to process 300 for subsequent identification of a subset thereof suitable for assay.

Multiple levels of consensus can be calculated and reported by process 27. For example, as further  
15 described in Example 1, *infra*, process 27 can report consensus as between all specific pairs of methods of gene prediction, as consensus among any one or more of the pairs of methods of gene prediction, or as among all of the gene prediction algorithms used. Thus, in Example 1, process 27  
20 reported that GRAIL and GENEFINDER programs agreed on 0.7% of genomic sequence, that GRAIL and DICTION agreed on 0.5% of genomic sequence, and that the three programs together agreed on 0.25% of the data analyzed. Put another way, 0.25% of the genomic sequence was identified by all three  
25 of the programs as containing putative coding region.

Furthermore, consensus can be required among different approaches to identifying a chosen function.

For example, if the function desired to be identified is coding of protein sequence, and a first used  
30 approach to exon calling is gene prediction, the process can be repeated on the same input sequence, or subset thereof, with another approach, such as comparative sequence analysis. In such a case, where comparative sequence analysis follows gene prediction, the comparison  
35 can be performed not only on genomic nucleic acid sequence,

but additionally or alternatively can be performed on the predicted amino acid sequence translated from the ORFs prior identified by the gene prediction approach.

Although shown as an iterative process, the  
5 multiple analyses required to achieve consensus can be done in series, in parallel, or some combination thereof.

Predicted functional sequence, optionally representing a consensus among a plurality of methods and approaches for determination thereof, is passed to process  
10 300 for identification of a subset thereof for functional assay.

In the preferred embodiment of the methods of the present invention, wherein the function sought to be identified is protein coding, process 300 is used to  
15 identify a subset thereof suitable for experimental verification by physical and/or bioinformatic approaches.

For example, putative ORFs identified in process 200 can be classified, or binned, bioinformatically into putative genes. This binning can be based *inter alia* upon  
20 consideration of the average number of exons/gene in the species chosen for analysis, upon density of exons that have been called on the genomic sequence, and other empirical rules. Thereafter, one or more among the gene-specific ORFs can be chosen for subsequent use in gene  
25 expression assay.

Where such subsequent gene expression assay uses amplified nucleic acid, considerations such as desired amplicon length, primer synthesis requirements, putative exon length, sequence GC content, existence of possible  
30 secondary structure, and the like can be used to identify and select those ORFs that appear most likely successfully to amplify. Where subsequent gene expression assay relies upon nucleic acid hybridization, whether or not using amplified product, further considerations involving  
35 hybridization stringency can be applied to identify that

subset of sequences that will most readily permit sequence-specific discrimination at a chosen hybridization and wash stringency. One particular such consideration is avoidance of putative exons that span repetitive sequence; such  
5 sequence can hybridize spuriously to nonspecific message, reducing specific signal in the hybridization.

For bioinformatic assay, there are fewer constraints on the sequences that can be tested experimentally, and in this latter case therefore process  
10 300 can output the entirety of the input sequence.

The subset of sequences identified by process 300 as suitable for use in assay is then used in process 400 to create the physical and/or informational substrate for experimental verification of the predictions made in  
15 process 200, and thereafter to assay those substrates.

As mentioned, the methods of the present invention are particularly useful for identifying potential coding regions within genomic sequence. In a preferred embodiment of process 400, therefore, the expression of the  
20 sequences predicted to encode protein is verified. The combination of the predictive and experimental methods provides a powerful gene discovery engine.

Thus, in another aspect, the present invention provides methods and apparatus for verifying the expression  
25 of putative genes identified within genomic sequence. In particular, the invention provides a novel method of verifying gene expression in which expression of predicted ORFs is measured and confirmed using a novel type of nucleic acid microarray, the genome-derived single exon  
30 nucleic acid microarrays of the present invention.

Putative ORFs as predicted by a consensus of gene calling, particularly gene prediction, algorithms in process 200, and as further identified as suitable by process 300, are amplified from genomic DNA using the  
35 polymerase chain reaction (PCR). Although PCR is

conveniently used, other amplification approaches can also be used.

Amplification schemes can be designed to capture the entirety of each predicted ORF in an amplicon with  
5 minimal additional (that is, intronic or intergenic) sequence. Because ORFs predicted from human genomic sequence using the methods of the present invention differ in length, such an approach results in amplicons of varying length.

10 However, most predicted ORFs are shorter than 500 bp in length, and although amplicons of at least about 100 or 200 base pairs can be immobilized as probes on nucleic acid microarrays, early experimental results using the methods of the present invention have suggested that longer  
15 amplicons, at least about 400 or 500 base pairs, are more effective. Furthermore, certain advantages derive from application to the microarray of amplicons of defined size.

Therefore, amplification schemes can alternatively, and preferably, be designed to amplify  
20 regions of defined size, preferably at least about 300, 400 or 500 bp, centered about each predicted ORF. Such an approach results in a population of amplicons of limited size diversity, but that typically contain intronic and/or intergenic nucleic acid in addition to putative ORF.

25 Conversely, somewhat fewer than 10% of ORFs predicted from human genomic sequence according to the methods of the present invention exceed 500 bp in length. Portions of such extended ORFs, preferably at least about 300, 400 or 500 bp in length, can be amplified. However, it  
30 has been discovered that the percentage success at amplifying pieces of such ORFs is low, and that such putative exons are more effectively amplified when larger fragments, at least about 1000 or 1500 bp, and even as large as 2000 bp are amplified.

35 The putative ORFs selected in process 300 are

thus input into one or more primer design programs, such as PRIMER3 (available online for use at <http://www-genome.wi.mit.edu/cgi-bin/primer/> ), with a goal of amplifying at least about 500 base pairs of genomic sequence centered within or about ORFs predicted to be no more than about 500 bp, or at least about 1000 - 1500 bp of genomic sequence for ORFs predicted to exceed 500 bp in length, and the primers synthesized by standard techniques. Primers with the requisite sequences can be purchased commercially or synthesized by standard techniques.

Conveniently, a first predetermined sequence can be added commonly to the ORF-specific 5' primer and a second, typically different, predetermined sequence commonly added to each 3' ORF-unique primer. This serves to immortalize the amplicon, that is, serves to permit further amplification of any amplicon using a single set of primers complementary respectively to the common 5' and common 3' sequence elements. The presence of these "universal" priming sequences further facilitates later sequence verification, providing a sequence common to all amplicons at which to prime sequencing reactions. The common 5' and 3' sequences further serve to add a cloning site should any of the ORFs warrant further study.

Such predetermined sequence is usefully at least about 10, 12 or 15 nt in length, and usually does not exceed about 25 nt in length. The "universal" priming sequences used in the examples presented *infra* were each 16 nt long.

The genomic DNA to be used as substrate for amplification will come from the eukaryotic species from which the genomic sequence data had originally been obtained, or a closely related species, and can conveniently be prepared by well known techniques from somatic or germline tissue or cultured cells of the organism. See, e.g., Short Protocols in Molecular Biology

: A Compendium of Methods from Current Protocols in  
Molecular Biology, Ausubel et al. (eds.), 4<sup>th</sup> edition  
(April 1999), John Wiley & Sons (ISBN: 047132938X) and  
Maniatis et al., Molecular Cloning : A Laboratory Manual,  
5 2<sup>nd</sup> edition (December 1989), Cold Spring Harbor Laboratory  
Press (ISBN: 0879693096). Many such prepared genomic DNAs  
are available commercially, with the human genomic DNAs  
additionally having certification of donor informed  
consent.

10           Although the intronic and intergenic material  
flanking putative coding regions in the amplicons could  
potentially interfere with hybridizations during microarray  
experiments, we have found, surprisingly, that differential  
expression ratios are not significantly affected. Rather,  
15 the predominant effect of exon size is to alter the  
absolute signal intensity, rather than its ratio. Equally  
surprising, the art had suggested that single exon probes  
would not provide sufficient signal intensity for high  
stringency hybridization analyses; we find that such probes  
20 not only provide adequate signal, but have substantial  
advantages, as herein described.

          After partial purification, as by size exclusion  
spin column, with or without confirmation as to amplicon  
quality as by gel electrophoresis, each amplicon (single  
25 exon probe) is disposed in an array upon a support  
substrate.

          Methods for creating microarrays by deposition  
and fixation of nucleic acids onto support substrates are  
well known in the art (Reviewed by Schena et al., see  
30 above).

          Typically, the support substrate will be glass,  
although other materials, such as amorphous or crystalline  
silicon or plastics. Such plastics include  
polymethylacrylic, polyethylene, polypropylene,  
35 polyacrylate, polymethylmethacrylate, polyvinylchloride,

polytetrafluoroethylene, polystyrene, polycarbonate, polyacetal, polysulfone, celluloseacetate, cellulosenitrate, nitrocellulose, or mixtures thereof, can also be used. Typically, the support will be rectangular, 5 although other shapes, particularly circular disks and even spheres, present certain advantages. Particularly advantageous alternatives to glass slides as support substrates for array of nucleic acids are optical discs, as described in WO 98/12559.

10 The amplified nucleic acids can be attached covalently to a surface of the support substrate or, more typically, applied to a derivatized surface in a chaotropic agent that facilitates denaturation and adherence by presumed noncovalent interactions, or some combination 15 thereof.

Robotic spotting devices useful for arraying nucleic acids on support substrates can be constructed using public domain specifications (The MGuide, version 2.0, <http://cmgm.stanford.edu/pbrown/mguide/index.html>), or 20 can conveniently be purchased from commercial sources (MicroArray GenII Spotter and MicroArray GenIII Spotter, Molecular Dynamics, Inc., Sunnyvale, CA). Spotting can also be effected by printing methods, including those using ink jet technology.

25 As is well known in the art, microarrays typically also contain immobilized control nucleic acids. For controls useful in providing measurements of background signal for the genome-derived single exon microarrays of the present invention, a plurality of *E. coli* genes can 30 readily be used. As further described in Example 1, 16 or 32 *E. coli* genes suffice to provide a robust measure of background noise in such microarrays.

As is well known in the art, the amplified product disposed in arrays on a support substrate to create 35 a nucleic acid microarray can consist entirely of natural



nucleotides linked by phosphodiester bonds, or alternatively can include either nonnative nucleotides, alternative internucleotide linkages, or both, so long as complementary binding can be obtained in the hybridization.

- 5 If enzymatic amplification is used to produce the immobilized probes, the amplifying enzyme will impose certain further constraints upon the types of nucleic acid analogs that can be generated.

Although particularly described herein as using  
10 high density microarrays constructed on planar substrates, the methods of the present invention for confirming the expression of ORFs predicted from genomic sequence can use any of the known types of microarrays, as herein defined, including lower density planar arrays, and microarrays on  
15 nonplanar, nonunitary, distributed substrates.

For example, gene expression can be confirmed using hybridization to lower density arrays, such as those constructed on membranes, such as nitrocellulose, nylon, and positively-charged derivatized nylon membranes.

- 20 Further, gene expression can also be confirmed using nonplanar, bead-based microarrays such as are described in Brenner et al., *Proc. Natl. Acad. Sci. USA* 97(4):166501670 (2000); U.S. Patent No. 6,057,107; and U.S. Patent No. 5,736,330. In theory, a packed collection of such beads  
25 provides in aggregate a higher density of nucleic acid probe than can be achieved with spotting or lithography techniques on a single planar substrate.

Planar microarrays on solid substrates, however, provide certain useful advantages, including high  
30 throughput and compatibility with existing readers. For example, each standard microscope slide can include at least 1000, typically at least 2000, preferably 5000 and upto 10,000 - 50,000 or more nucleic acid probes of discrete sequence. The number of sequences deposited will  
35 depend on their required application.

Each putative gene can be represented in the array by a single predicted ORF. Alternatively, genes can be represented by more than one predicted ORF. For purposes of measuring differential splicing, more than one  
5 predicted ORF will be provided for a putative gene. And as is well known in the art, each probe of defined sequence, representing a single predicted ORF, can be deposited in a plurality of locations on a single microarray to provide redundancy of signal.

10 The genome-derived single exon microarrays described above differ in several fundamental and advantageous ways from microarrays presently used in the gene expression art, including (1) those created by deposition of mRNA-derived nucleic acids, (2) those created  
15 by *in situ* synthesis of oligonucleotide probes, and (3) those constructed from yeast genomic DNA.

Most nucleic acid microarrays that are in use for study of eukaryotic gene expression have as immobilized probes nucleic acids that are derived - either directly or  
20 indirectly - from expressed message. As discussed above, it is common, for example, for such microarrays to be derived from cDNA/EST libraries, either from those previously described in the literature, see Lennon *et al.*,  
or from the *de novo* construction of "problem specific"  
25 libraries targeted at a particular biological question, R.S. Thomas *et al.*, *Cancer Res.* (in press). Such microarrays are herein collectively denominated "EST microarrays".

Such EST microarrays by definition can measure  
30 expression only of those genes found in EST libraries, shown herein to represent only a fraction of expressed genes. Furthermore, such libraries - and thus microarrays based thereupon - are biased by the tissue or cell type of message origin, by the expression levels of the respective  
35 genes within the tissues, and by the ability of the message

successfully to have been reverse-transcribed and cloned.

Thus, as further discussed in Example 1, the methods of the present invention enable sequences that do not appear in EST or other expression databases to be  
5 determined - subsequently arrayed for expression measurements could not, therefore, have been represented as probes on an EST microarray. And as further demonstrated in the examples, *infra*, the remaining population of genes identified from genomic sequence by the methods of the  
10 present invention - that is, the one third of sequences that had previously been accessioned in EST or other expression databases - are biased toward genes with higher expression levels.

Representation of a message in an EST and/or cDNA  
15 library depends upon the successful reverse transcription, optionally but typically with subsequent successful cloning, of the message. This introduces substantial bias into the population of probes available for arraying in EST microarrays.

20 In contrast, neither reverse transcription nor cloning is required to produce the probes arrayed on the genome-derived single exon microarrays of the present invention. And although the ultimate deposition of a probe on the genome-derived single exon microarray of the present  
25 invention depends upon a successful amplification from genomic material, *a priori* knowledge of the sequence of the desired amplicon affords greater opportunity to recover any given probe sequence recalcitrant to amplification than is afforded by the requirement for successful reverse  
30 transcription and cloning of unknown message in EST approaches.

Thus, the genome-derived single exon microarrays of the present invention present a far greater diversity of probes for measuring gene expression, with far less bias,  
35 than do EST microarrays presently used in the art.

As a further consequence of their ultimate origin from expressed message, the probes in EST microarrays often contain poly-A (or complementary poly-T) stretches derived from the poly-A tail of mature mRNA. These homopolymeric  
5 stretches contribute to cross-hybridization, that is, to a spurious signal occasioned by hybridization to the homopolymeric tail of a labeled cDNA that lacks sequence homology to the gene-specific portion of the probe.

In contrast, the probes arrayed in the genome-  
10 derived single exon microarrays of the present invention lack homopolymeric stretches derived from message polyadenylation, and thus can provide more specific signal. Typically, at least about 50, 60 or 75% of the probes on the genome-derived single exon microarrays of the present  
15 invention lack homopolymeric regions consisting of A or T, where a homopolymeric region is defined for purposes herein as stretches of 25 or more, typically 30 or more, identical nucleotides.

A further distinction, which also affects the  
20 specificity of hybridization, is occasioned by the typical derivation of EST microarray probes from cloned material. Because much of the probe material disposed as probes on EST microarrays is excised or amplified from plasmid, phage, or phagemid vectors, EST microarrays typically  
25 include a fair amount of vector sequence, more so when the probes are amplified, rather than excised, from the vector.

In contrast, the vast majority of probes in the genome-derived single exon microarrays of the present invention contain no prokaryotic or bacteriophage vector  
30 sequence, having been amplified directly or indirectly from genomic DNA. Typically, therefore, at least about 50, 60, 70 or 80% or more of individual exon-including probes disposed on a genome-derived single exon microarray of the present invention lack vector sequence, and particularly  
35 lack sequences drawn from plasmids and bacteriophage.

Preferably, at least about 85, 90 or more than 90% of exon-including probes in the genome-derived single exon microarray of the present invention lack vector sequence. With attention to removal of vector sequences through  
5 preprocessing 24, percentages of vector-free exon-including probes can be as high as 95 - 99%. The substantial absence of vector sequence from the genome-derived single exon microarrays of the present invention results in greater specificity during hybridization, since spurious cross-  
10 hybridization to a probe vector sequence is reduced.

As a further consequence of excision or amplification of probes from vectors in construction of EST microarrays, the probes arrayed thereon often contain artificial sequence, derived from vector polylinker  
15 multiple cloning sites, at both 5' and 3' ends. The probes disposed upon the genome-derived single exon microarrays need have no such artificial sequence appended thereto.

As mentioned above, however, the ORF-specific primers used to amplify putative ORFs can include  
20 artificial sequences, typically 5' to the ORF-specific primer sequence, useful for "universal" (that is, independent of ORF sequence) priming of subsequent amplification or sequencing reactions. When such "universal" 5' and/or 3' priming sequences are appended to  
25 the amplification primers, the probes disposed upon the genome-derived single exon microarray will include artificial sequence similar to that found in EST microarrays. However, the genome-derived single exon microarray of the present invention can be made without  
30 such sequences, and if so constructed, presents an even smaller amount of nonspecific sequence that would contribute to nonspecific hybridization.

Yet another consequence of typical use of cloned material as probes in EST microarrays is that such  
35 microarrays contain probes that result from cloning

artifacts, such as chimeric molecules containing coding region of two separate genes. Derived from genomic material, typically not thereafter cloned, the probes of the genome-derived single exon microarrays of the present invention lack such cloning artifacts, and thus provide greater specificity of signal in gene expression measurements.

A further consequence of the cloned origin of probes on many EST microarrays is that the individual probes often have disparate sizes, which can cause the optimal hybridization stringency to vary among probes on a single microarray. In contrast, as discussed above, the probes arrayed on the genome-derived single exon microarrays of the present invention can readily be designed to have a narrow distribution in sizes, with the range of probe sizes no greater than about 10% of the average size, typically no greater than about 5% of the average probe size.

Because of their origin from fully- or partially-spliced message, probes disposed upon EST arrays will often include multiple exons. The percentage of such exon-spanning probes in an EST microarray can be calculated, on average, based upon the predicted number of exons/gene for the given species and the average length of the immobilized probes. For human genes, the near-complete sequence of human chromosome 22, Dunham et al., *Nature* 402(6761):489-95 (1999), predicts that human genes average 5.5 exons/gene. Even with probes of 200 - 500 bp, the vast majority of human EST microarray probes include more than one exon.

In contrast, by virtue of their origin from algorithmically identified ORFs in genomic sequence, the probes in the genome-derived single exon microarrays of the present invention can consist of individual exons. Thus, in contrast to EST microarrays, at least about 50, 60, 70, 75, 80, 85, 95 or 99% of probes deposited in the genome-

derived microarray of the present invention consist of, or include, no more than one predicted ORF.

This provides the ability, not readily achieved using EST microarrays, to use the genome-derived single  
5 exon microarrays of the present invention to measure tissue-specific expression of individual exons, which in turn allows differential splicing events to be detected and characterized, and in particular, allows the correlation of differential splicing to tissue-specific expression  
10 patterns.

Furthermore, the exons that are represented in EST microarrays are often biased toward the 3' or 5' end of their respective genes, since sequencing strategies used for EST identification are so biased. In contrast, no such  
15 3' or 5' bias necessarily inheres in the selection of exons for disposition on the genome-derived single exon microarrays of the present invention.

Conversely, the probes provided on the genome-derived single exon microarrays of the present invention  
20 typically, but need not necessarily, include intronic and/or intergenic sequence that is absent from EST microarrays, which are derived from mature mRNA. Typically, at least about 50, 60, 70, 80 or 90% of the exon-including probes on the genome-derived single exon  
25 microarrays of the present invention include sequence drawn from noncoding regions. As discussed above, the additional presence of noncoding region does not significantly interfere with measurement of gene expression, and provides the additional opportunity to assay prespliced RNA, and  
30 thus measure such phenomena such as nuclear export control.

The genome-derived single exon microarrays of the present invention are also quite different from *in situ* synthesis microarrays, where probe size is severely constrained by inadequacies in the photolithographic  
35 synthesis process.

Typically, probes arrayed on *in situ* synthesis microarrays are limited to a maximum of about 25 bp. As a well known consequence, hybridization to such chips must be performed at low stringency. In order, therefore, to  
5 achieve unambiguous sequence-specific hybridization results, the *in situ* synthesis microarray requires substantial redundancy, with concomitant programmed arraying for each probe of probe analogues with altered (*i.e.*, mismatched) sequence.

10 In contrast, the longer probe length of the genome-derived single exon microarrays of the present invention allows much higher stringency hybridization and wash. Typically, therefore, exon-including probes on the genome-derived single exon microarrays of the present  
15 invention average at least about 100, 200, 300, 400 or 500 bp in length. By obviating the need for substantial probe redundancy, this approach permits a higher density of probes for discrete exons or genes to be arrayed on the microarrays of the present invention than can be achieved  
20 for *in situ* synthesis microarrays.

A further distinction is that the probes in *in situ* synthesis microarrays typically are covalently linked to the substrate surface. In contrast, the probes disposed on the genome-derived microarray of the present invention  
25 typically are, but need not necessarily be, bound noncovalently to the substrate.

Furthermore, the short probe size on *in situ* microarrays causes large percentage differences in the melting temperature of probes hybridized to their  
30 complementary target sequence, and thus causes large percentage differences in the theoretically optimum stringency across the array as a whole.

In contrast, the larger probe size in the microarrays of the present invention create lower  
35 percentage differences in melting temperature across the



range of arrayed probes.

A further significant advantage of the microarrays of the present invention over *in situ* synthesized arrays is that the quality of each individual probe can be confirmed before deposition. In contrast, the quality of probes cannot be assessed on a probe-by-probe basis for the *in situ* synthesized microarrays presently being used.

The genome-derived single exon microarrays of the present invention are also distinguished over, and present substantial benefits over, the genome-derived microarrays from lower eukaryotes such as yeast. Lashkari et al., *Proc. Natl. Acad. Sci. USA* 94:13057-13062 (1997).

Only about 220 - 250 of the 6100 or so nuclear genes in *Saccharomyces cerevisiae* - that is, only about 4 - 5% - have standard, spliceosomal, introns, Lopez et al., *Nucl. Acids Res.* 28:85-86 (2000); Spingola et al., *RNA* 5(2):221-34 (1999). Furthermore, the entire yeast genome has already been sequenced. These two facts permit the ready amplification and disposition of single-ORF amplicons on such microarray without the requirement for antecedent use of gene prediction and/or comparative sequence analyses.

Thus, a significant aspect of the present invention is the ability to identify and to confirm expression of predicted coding regions in genomic sequence drawn from eukaryotic organisms that have a higher percentage of genes having introns than do yeast such as *Saccharomyces cerevisiae*, particularly in genomic sequence drawn from eukaryotes in which at least about 10, 20 or 50% of protein-encoding genes have introns. In preferred embodiments, the methods and apparatus of the present invention are used to identify and confirm expression of novel genes from genomic sequence of eukaryotes in which the average number of introns per gene is at least about

one, two or three or more.

After the physical substrate is prepared, experimental verification of predicted function is performed.

5 In a preferred embodiment of the present invention, where the function sought to be identified in genomic sequence is protein coding, experimental verification is performed by measuring expression of the putative ORFs, typically through nucleic acid hybridization  
10 experiments, and in particularly preferred embodiments, through hybridization to genome-derived single exon microarrays prepared as above- described.

Expression is conveniently measured and expressed for each probe in the microarray as a ratio of the  
15 expression measured concurrently in a plurality of mRNA sources, according to techniques well known in the microarray art, Reviewed in Schena et al., and as further described in Example 2, below. The mRNA source for the reference against which specific expression is measured can  
20 be drawn from a homogeneous mRNA source, such as a single cultured cell-type, or alternatively can be heterogeneous, as from a pool of mRNA derived from multiple tissues and/or cell types, as further described in Example 2, *infra*.

mRNA can be prepared by standard techniques, see  
25 Ausubel et al. and Maniatis et al., or purchased commercially. The mRNA is then typically reverse-transcribed in the presence of labeled nucleotides: the index source (that in which expression is desired to be measured) is reverse transcribed in the presence of  
30 nucleotides labeled with a first label, typically a fluorophore (fluorochrome; fluor; fluorescent dye); the reference source is reverse transcribed in the presence of a second label, typically a fluorophore, typically fluorometrically-distinguishable from the first label. As  
35 further described in Example 2, *infra*, Cy3 and Cy5 dyes

prove particularly useful in these methods. After partial purification of the index and reference targets, hybridization to the probe array is conducted according to standard techniques, typically under a coverslip.

5           After wash, microarrays are conveniently scanned using a commercial microarray scanning device, such as a Gen3 Scanner (Molecular Dynamics, Sunnyvale, CA). Data on expression is then passed, with or without interim storage, to process 500, where the results for each probe are  
10 related to the original sequence.

Often, hybridization of target material to the genome-derived single exon microarray will identify certain of the probes thereon as of particular interest. Thus, it is often desirable that the user be able readily to obtain  
15 sufficient quantities of an individual probe, either for subsequent arrayed deposition upon an additional support substrate, often as part of a microarray having a plurality of probes so identified, or alternatively or additionally as a solitary solid-phase or solution-phase probe, for  
20 further use.

Thus, in another aspect, the present invention provides compositions and kits for the ready production of nucleic acids identical in sequence to, or substantially identical in sequence to, probes on the genome-derived  
25 single exon microarrays of the present invention.

In this aspect, a small quantity of each probe is disposed, typically without attachment to substrate, in a spatially-addressable ordered set, typically one per well of a microtiter dish. Although a 96 well microtiter plate  
30 can be used, greater efficiency is obtained using higher density arrays, such as are provided by microtiter plates having 384, 864, 1536, 3456, 6144, or 9600 wells, and although microtiter plates having physical depressions (wells) are conveniently used, any device that permits  
35 addressable withdrawal of reagent from fluidly-

noncommunicating areas can be used.

In this aspect of the invention, therefore, a fluidly noncommunicating addressable ordered set of individual probes, corresponding to those on a genome-derived single exon microarray, is provided, with each probe in sufficient quantity to permit amplification, such as by PCR. As earlier mentioned, the ORF-specific 5' primers used for genomic amplification can have a first common sequence added thereto, and the ORF-specific 3' primers used for genomic amplification can have a second, different, common sequence added thereto, thus permitting, in this preferred embodiment, the use of a single set of 5' and 3' primers to amplify any one of the probes from the amplifiable ordered set.

Each discrete amplifiable probe can also be packaged with amplification primers, solutes, buffers, etc., and can be provided in dry (e.g., lyophilized) form or wet, in the latter case typically with addition of agents that retard evaporation.

In another aspect of the present invention, a genome-derived single-exon microarray is packaged together with such an ordered set of amplifiable probes corresponding to the probes, or one or more subsets of probes, thereon. In alternative embodiments, the ordered set of amplifiable probes is packaged separately from the genome-derived single exon microarray.

In some embodiments, the microarray and/or ordered probe set are further packaged with recordable media that provide probe identification and addressing information, and that can additionally contain annotation information, such as gene expression data. Such recordable media can be packaged with the microarray, with the ordered probe set, or with both.

If the microarray is constructed on a substrate that incorporates recordable media, such as is described in

international patent application no. WO 98/12559, then separate packaging of the genome-derived single exon microarray and the bioinformatic information is not required.

- 5           The amount of amplifiable probe material should be sufficient to permit at least one amplification sufficient for subsequent hybridization assay.

          Although the use of high density genome-derived microarrays on solid planar substrates is presently a  
10 preferred approach for the physical confirmation and characterization of the expression of sequences predicted to encode protein, other types of microarrays (as herein defined) can also be used.

- Furthermore, as earlier mentioned, experimental  
15 verification of the function predicted from genomic sequence in process 200 can be bioinformatic, rather than, or additional to, physical verification.

          For example, where the function desired to be identified is protein coding, the predicted ORFs can be  
20 compared bioinformatically to sequences known or suspected of being expressed.

- Thus, the sequences output from process 300 (or process 200), can be used to query expression databases, such as EST databases, SNP ("single nucleotide  
25 polymorphism") databases, known cDNA and mRNA sequences, SAGE ("serial analysis of gene expression") databases, and more generalized sequence databases that allow query for expressed sequences. Such query can be done by any sequence query algorithm, such as BLAST ("basic local  
30 alignment search tool"). The results of such query - including information on identical sequences and information on nonidentical sequences that have diffuse or focal regions of sequence homology to the query sequence - can then be passed directly to process 500, or used to  
35 inform analyses subsequently undertaken in process 200,

process 300, or process 400.

Experimental data, whether obtained by physical or bioinformatic assay in process 400, is passed to process 500 where it is usefully related to the sequence data itself, a process colloquially termed "annotation". Such annotation can be done using any technique that usefully relates the functional information to the sequence, as, for example, by incorporating the functional data into the record itself, by linking records in a hierarchical or relational database, by linking to external databases, or by a combination thereof. Such database techniques are well within the skill in the art.

The annotated sequence data can be stored locally, uploaded to genomic sequence database 100, and/or displayed 800.

The methods and apparatus of the present invention rapidly produce functional information from genomic sequence. Coupled with the escalating pace at which sequence now accumulates, the rapid pace of sequence annotation produces a need for methods of displaying the information in meaningful ways.

FIG. 3 shows visual display 80 presenting a single genomic sequence annotated according to the present invention. Because of its nominal resemblance to artistic works of Piet Mondrian, visual display 80 is alternatively described herein as a "Mondrian".

Each of the visual elements of display 80 is aligned with respect to the genomic sequence being annotated (hereinafter, the "annotated sequence"). Given the number of nucleotides typically represented in an annotated sequence, representation of individual nucleotides would rarely be readable in hard copy output of display 80. Typically, therefore, the annotated sequence is schematized as rectangle 89, extending from the left border of display 80 to its right border. By convention

herein, the left border of rectangle 89 represents the first nucleotide of the sequence and the right border of rectangle 89 represents the last nucleotide of the sequence.

5           As further discussed below, however, the Mondrian visual display of annotated sequence can serve as a convenient graphical user interface for computerized representation, analysis, and query of information stored electronically. For such use, the individual nucleotides  
10 can conveniently be linked to the X axis coordinate of rectangle 89. This permits the annotated sequence at any point within rectangle 89 readily to be viewed, either automatically – for example, by time-delayed appearance of a small overlaid window upon movement of a cursor or other  
15 pointer over rectangle 89 – or through user intervention, as by clicking a mouse or other pointing device at a point in rectangle 89.

Visual display 80 is generated after user specification of the genomic sequence to be displayed.  
20 Such specification can consist of or include an accession number for a single clone (e.g., a single BAC accessioned into GenBank), wherein the starting and stopping nucleotides are thus absolutely identified, or alternatively can consist of or include an anchor or  
25 fulcrum point about which a chosen range of sequence is anchored, thus providing relative endpoints for the sequence to be displayed. For example, the user can anchor such a range about a given chromosomal map location, gene name, or even a sequence returned by query for similarity  
30 or identity to an input query sequence. When visual display 80 is used as a graphical user interface to computerized data, additional control over the first and last displayed nucleotide will typically be dynamically selectable, as by use of standard zooming and/or selection  
35 tools.

Field 81 of visual display 80 is used to present the output from process 200, that is, to present the bioinformatic prediction of those sequences having the desired function within the genomic sequence. Functional sequences are typically indicated by at least one rectangle 83 (83a, 83b, 83c), the left and right borders of which respectively indicate, by their X-axis coordinates, the starting and ending nucleotides of the region predicted to have function.

Where a single bioinformatic method or approach identifies a plurality of regions having the desired function, a plurality of rectangles 83 is disposed horizontally in field 81. Where multiple methods and/or approaches are used to identify function, each such method and/or approach can be represented by its own series of horizontally disposed rectangles 83, each such horizontally disposed series of rectangles offset vertically from those representing the results of the other methods and approaches.

Thus, rectangles 83a in FIG. 3 represent the functional predictions of a first method of a first approach for predicting function, rectangles 83b represent the functional predictions of a second method and/or second approach for predicting that function, and rectangles 83c represent the predictions of a third method and/or approach.

Where the function desired to be identified is protein coding, field 81 is used to present the bioinformatic prediction of sequences encoding protein. For example, rectangles 83a can represent the results from GRAIL or GRAIL II, rectangles 83b can represent the results from GENEFINDER, and rectangles 83c can represent the results from DICTION.

Optionally, and preferably, rectangles 83 collectively representing predictions of a single method



and/or approach are identically colored and/or textured, and are distinguishable from the color and/or texture used for a different method and/or approach.

Alternatively, or in addition, the color, hue, density, or texture of rectangles 83 can be used further to report a measure of the bioinformatic reliability of the prediction. For example, many gene prediction programs will report a measure of the reliability of prediction. Thus, increasing degrees of such reliability can be indicated, e.g., by increasing density of shading. Where display 80 is used as a graphical user interface, such measures of reliability, and indeed all other results output by the program, can additionally or alternatively be made accessible through linkage from individual rectangles 83, as by time-delayed window ("tool tip" window), or by pointer (e.g., mouse)-activated link.

As earlier described, increased predictive reliability can be achieved by requiring consensus among methods and/or approaches to determining function. Thus, field 81 can include a horizontal series of rectangles 83 that indicate one or more degrees of consensus in predictions of function.

Although FIG. 3 shows three series of horizontally disposed rectangles in field 81, display 80 can include as few as one such series of rectangles and as many as can discriminably be displayed, depending upon the number of methods and/or approaches used to predict a given function.

Furthermore, field 81 can be used to show predictions of a plurality of different functions. However, the increased visual complexity occasioned by such display makes more useful the ability of the user to select a single function for display. When display 80 is used as a graphical user interface for computer query and analysis, such function can usefully be indicated and user-

selectable, as by a series of graphical buttons or tabs (not shown in FIG. 3).

Rectangle 89 is shown in FIG. 3 as including interposed rectangle 84. Rectangle 84 represents the  
5 portion of annotated sequence for which predicted functional information has been assayed physically, with the starting and ending nucleotides of the assayed material indicated by the X axis coordinates of the left and right borders of rectangle 84. Rectangle 85, with optional  
10 inclusive circles 86 (86a, 86b, and 86c) displays the results of such physical assay.

Although a single rectangle 84 is shown in FIG. 3, physical assay is not limited to just one region of annotated genomic sequence. It is expected that an  
15 increasing percentage of regions predicted to have function by process 200 will be assayed physically, and that display 80 will accordingly, for any given genomic sequence, have an increasing number of rectangles 84 and 85, representing an increased density of sequence annotation.

20 Where the function desired to be identified is protein coding, rectangle 84 identifies the sequence of the probe used to measure expression. In embodiments of the present invention where expression is measured using genome-derived single exon microarrays, rectangle 84  
25 identifies the sequence included within the probe immobilized on the support surface of the microarray. As noted *supra*, such probe will often include a small amount of additional, synthetic, material incorporated during amplification and designed to permit reamplification of the  
30 probe, which sequence is typically not shown in display 80.

Rectangle 87 is used to present the results of bioinformatic assay of the genomic sequence. For example, where the function desired to be identified is protein coding, process 400 can include bioinformatic query of  
35 expression databases with the sequences predicted in

process 200 to encode exons. And as earlier discussed, because bioinformatic assay presents fewer constraints than does physical assay, often the entire output of process 200 can be used for such assay, without further subsetting thereof by process 300. Therefore, rectangle 87 typically need not have separate indicators therein of regions submitted for bioinformatic assay; that is, rectangle 87 typically need not have regions therein analogous to rectangles 84 within rectangle 89.

Rectangle 87 as shown in FIG. 3 includes smaller rectangles 880 and 88. Rectangles 880 indicate regions that returned a positive result in the bioinformatic assay, with rectangles 88 representing regions that did not return such positive results. Where the function desired to be predicted and displayed is protein coding, rectangles 880 indicate regions of the predicted exons that identify sequence with significant similarity in expression databases, such as EST, SNP, SAGE databases, with rectangles 88 indicating genes novel over those identified in existing expression data bases.

Rectangles 880 can further indicate, through color, shading, texture, or the like, additional information obtained from bioinformatic assay.

For example, where the function assayed and displayed is protein coding, the degree of shading of rectangles 880 can be used to represent the degree of sequence similarity found upon query of expression databases. The number of levels of discrimination can be as few as two (identity, and similarity, where similarity has a user-selectable lower threshold). Alternatively, as many different levels of discrimination can be indicated as can visually be discriminated.

Where display 80 is used as a graphical user interface, rectangles 880 can additionally provide links directly to the sequences identified by the query of

expression databases, and/or statistical summaries thereof. As with each of the precedingly-discussed uses of display 80 as a graphical user interface, it should be understood that the information accessed via display 80 need not be  
5 resident on the computer presenting such display, which often will be serving as a client, with the linked information resident on one or more remotely located servers.

Rectangle 85 displays the results of physical  
10 assay of the sequence delimited by its left and right borders.

Rectangle 85 can consist of a single rectangle, thus indicating a single assay, or alternatively, and increasingly typically, will consist of a series of  
15 rectangles (85a, 85b, 85c) indicating separate physical assays of the same sequence.

Where the function assayed is gene expression, and where gene expression is assayed as herein described using simultaneous two-color fluorescent detection of  
20 hybridization to genome-derived single exon microarrays, individual rectangles 85 can be colored to indicate the degree of expression relative to control. Conveniently, shades of green can be used to depict expression in the sample over control values, and shades of red used to  
25 depict expression less than control, corresponding to the spectra of the Cy3 and Cy5 dyes conventionally used for respective labeling thereof. Additional functional information can be provided in the form of circles 86 (86a, 86b, 86c), where the diameter of the circle can be used to  
30 indicate expression intensity. As discussed *infra*, such relative expression (expression ratios) and absolute expression (signal intensity) can be expressed using normalized values.

Where display 80 is used as a graphical user  
35 interface, rectangle 85 can be used as a link to further

information about the assay. For example, where the assay is one for gene expression, each rectangle 85 can be used to link to information about the source of the hybridized mRNA, the identity of the control, raw or processed data from the microarray scan, or the like.

FIG. 4 is rendition of display 80 representing gene prediction and gene expression for a hypothetical BAC, showing conventions used in the Examples presented *infra*. BAC sequence ("Chip seq.") 89 is presented, with the physically assayed region thereof (corresponding to rectangle 84 in FIG. 3) shown in white. Algorithmic gene predictions are shown in field 81, with predictions by GRAIL shown, predictions by GENEFINDER, and predictions by DICTION shown. Within rectangle 87, regions of sequence that, when used to query expression databases, return identical or similar sequences ("EST hit") are shown as white rectangles (corresponding to rectangles 880 in FIG. 3), gray indicates low homology, and black indicates unknowns (where black and gray would correspond to rectangles 88 in FIG. 3).

Although FIGS. 3 and 4 show a single stretch of sequence, uninterrupted from left to right, longer sequences are usefully represented by vertical stacking of such individual Mondrians, as shown in FIGS. 9 and 10.

#### Single Exon Probes Useful For Measuring Gene Expression

The methods and apparatus of the present invention rapidly produce functional information from genomic sequence. Where the function to be identified is protein coding, the methods and apparatus of the present invention rapidly identify and confirm the expression of portions of genomic sequence that function to encode protein. As a direct result, the methods and apparatus of the present invention rapidly yield large numbers of

single-exon nucleic acid probes, the majority from previously unknown genes, each of which is useful for measuring and/or surveying expression of a specific gene in one or more tissues or cell types.

5           It is, therefore, another aspect of the present invention to provide genome-derived single exon nucleic acid probes useful for gene expression analysis, and particularly for gene expression analysis by microarray.

          Using the methods and genome-derived single-exon  
10 microarrays of the present invention, we have for example readily identified a large number of unique ORFs from human genomic sequence. Using single exon probes that encompass these ORFs, we have demonstrated, through microarray hybridization analysis, the expression of these ORFs in  
15 HeLa cells.

          As would immediately be appreciated by one of skill in the art, each single exon probe having demonstrable expression in HeLa cells is currently available for use in measuring the level of its ORF's  
20 expression in HeLa cells.

          Expression in HeLa cells provides a first level screen for demonstrating the expression of exons predicted from genomic sequence.

          HeLa cells are derived from human cervical cells.  
25 Accordingly, it would be appreciated by one of skill in the art that each single exon probe having demonstrable expression in HeLa cells is available for measuring the level of its ORF expression in other human cervical epithelial cells thus making such detection of expression  
30 useful in grading and/or staging of diseases of cervix, notably cervical carcinoma.

          The utility is specific to the probe; at sufficiently high hybridization stringency, which stringencies are well known in the art — see Ausubel et al.  
35 and Maniatis et al. — each probe reports the level of

expression of message specifically containing that ORF.

It should be appreciated, however, that the probes of the present invention, for which expression in the HeLa cells has been demonstrated are useful for both  
5 measurement in the HeLa cells or other human cervical epithelial cells and for survey of expression in other tissues.

Significant among such advantages is the presence of probes for novel genes.

10 As mentioned above and further detailed in Examples 1 and 2, the methods described enable ORFs which are not present in existing expression databases to be identified. And the fewer the number of tissues in which the ORF can be shown to be expressed, the more likely the  
15 ORF will prove to be part of a novel gene: as further discussed in Example 2, ORFs whose expression was measurable in only a single of the tested tissues were represented in existing expression databases at a rate of only 11%, whereas 36% of ORFs whose expression was  
20 measurable in 9 tissues were present in existing expression databases, and fully 45% of those ORFs expressed in all ten tested tissues were present in existing expressed sequence databases.

Either as tools for measuring gene expression or  
25 tools for surveying gene expression, the genome-derived single exon probes of the present invention have significant advantages over the cDNA or EST-based probes that are currently available for achieving these utilities.

The genome-derived single exon probes of the  
30 present invention are useful in constructing genome-derived single exon microarrays; the genome-derived single exon microarrays, in turn, are useful devices for measuring and for surveying gene expression in the human.

Gene expression analysis using microarrays -  
35 conventionally using microarrays having probes derived from

expressed message - is well-established as useful in the biological research arts (see Lockhart et al. *Nature* 405, 827-836).

Microarrays have been used to determine gene  
5 expression profiles in cells in response to drug treatment  
(see, for example, Kaminski et al., "Global Analysis of  
Gene Expression in Pulmonary Fibrosis Reveals Distinct  
Programs Regulating Lung Inflammation and Fibrosis," *Proc.  
Natl. Acad. Sci. USA* 97(4):1778-83 (2000); Bartosiewicz et  
10 al., "Development of a Toxicological Gene Array and  
Quantitative Assessment of This Technology," *Arch. Biochem.  
Biophys.* 376(1):66-73 (2000)), viral infection (see for  
example, Geiss et al., "Large-scale Monitoring of Host Cell  
Gene Expression During HIV-1 Infection Using cDNA  
15 Microarrays," *Virology* 266(1):8-16 (2000)) and during cell  
processes such as differentiation, senescence and apoptosis  
(see, for example, Shelton et al., "Microarray Analysis of  
Replicative Senescence," *Curr. Biol.* 9(17):939-45 (1999);  
Voehringer et al., "Gene Microarray Identification of Redox  
20 and Mitochondrial Elements That Control Resistance or  
Sensitivity to Apoptosis," *Proc. Natl. Acad. Sci. USA*  
97(6):2680-5 (2000)).

Microarrays have also been used to determine  
abnormal gene expression in diseased tissues (see, for  
25 example, Alon et al., "Broad Patterns of Gene Expression  
Revealed by Clustering Analysis of Tumor and Normal Colon  
Tissues Probed by Oligonucleotide Arrays," *Proc. Natl.  
Acad. Sci. USA* 96(12):6745-50 (1999); Perou et al.,  
"Distinctive Gene Expression Patterns in Human Mammary  
30 Epithelial Cells and Breast Cancers," *Proc. Natl. Acad. Sci.  
USA* 96(16):9212-7 (1999); Wang et al., "Identification of  
Genes Differentially Over-expressed in Lung Squamous Cell  
Carcinoma Using Combination of cDNA Subtraction and  
Microarray Analysis," *Oncogene* 19(12):1519-28 (2000);  
35 Whitney et al., "Analysis of Gene Expression in Multiple



Sclerosis Lesions Using cDNA Microarrays," *Ann. Neurol.* 46(3):425-8 (1999)), in drug discovery screens (see, for example, Scherf et al., "A Gene Expression Database for the Molecular Pharmacology of Cancer," *Nat. Genet.* 24(3):236-44 (2000)) and in diagnosis to determine appropriate treatment strategies (see, for example, Sgroi et al., "In vivo Gene Expression Profile Analysis of Human Breast Cancer Progression," *Cancer Res.* 59(22):5656-61 (1999)).

In microarray-based gene expression screens of pharmacological drug candidates upon cells, each probe provides specific useful data. In particular, it should be appreciated that even those probes that show no change in expression are as informative as those that do change, serving, in essence, as negative controls.

For example, where gene expression analysis is used to assess toxicity of chemical agents on cells, the failure of the agent to change a gene's expression level is evidence that the drug likely does not affect the pathway of which the gene's expressed protein is a part. Analogously, where gene expression analysis is used to assess side effects of pharmacological agents - whether in lead compound discovery or in subsequent screening of lead compound derivatives - the inability of the agent to alter a gene's expression level is evidence that the drug does not affect the pathway of which the gene's expressed protein is a part.

WO 99/58720 provides methods for quantifying the relatedness of a first and second gene expression profile and for ordering the relatedness of a plurality of gene expression profiles. The methods so described permit useful information to be extracted from a greater percentage of the individual gene expression measurements from a microarray than methods previously used in the art.

Other uses of microarrays are described in Gerhold et al., *Trends Biochem. Sci.* 24(5):168-173 (1999)

and Zweiger, *Trends Biotechnol.* 17(11):429-436 (1999);  
Schena et al.

The invention particularly provides genome-  
derived single-exon probes known to be expressed in HeLa  
5 cells.

The individual single exon probes can be provided  
in the form of substantially isolated and purified nucleic  
acid, typically, but not necessarily, in a quantity  
sufficient to perform a hybridization reaction.

10 Such nucleic acid can be in any form directly  
hybridizable to the message that contains the probe's ORF,  
such as double stranded DNA, single-stranded DNA  
complementary to the message, single-stranded RNA  
complementary to the message, or chimeric DNA/RNA molecules  
15 so hybridizable. The nucleic acid can alternatively or  
additionally include either nonnative nucleotides,  
alternative internucleotide linkages, or both, so long as  
complementary binding can be obtained. For example, probes  
can include phosphorothioates, methylphosphonates,  
20 morpholino analogs, and peptide nucleic acids (PNA), as are  
described, for example, in U.S. Patent Nos. 5,142,047;  
5,235,033; 5,166,315; 5,217,866; 5,184,444; 5,861,250.

Usefully, however, such probes are provided in a  
form and quantity suitable for amplification, where the  
25 amplified product is thereafter to be used in the  
hybridization reactions that probe gene expression.  
Typically, such probes are provided in a form and quantity  
suitable for amplification by PCR or by other well known  
amplification technique. One such technique additional to  
30 PCR is rolling circle amplification, as is described, *inter  
alia*, in U.S. Patent Nos. 5,854,033 and 5,714,320 and  
international patent publications WO 97/19193 and  
WO 00/15779. As is well understood, where the probes are  
to be provided in a form suitable for amplification, the  
35 range of nucleic acid analogues and/or internucleotide

linkages will be constrained by the requirements and nature of the amplification enzyme.

Where the probe is to be provided in form suitable for amplification, the quantity need not be  
5 sufficient for direct hybridization for gene expression analysis, and need be sufficient only to function as an amplification template, typically at least about 1, 10 or 100 pg or more.

Each discrete amplifiable probe can also be  
10 packaged with amplification primers, either in a single composition that comprises probe template and primers, or in a kit that comprises such primers separately packaged therefrom. As earlier mentioned, the ORF-specific 5' primers used for genomic amplification can have a first  
15 common sequence added thereto, and the ORF-specific 3' primers used for genomic amplification can have a second, different, common sequence added thereto, thus permitting, in this embodiment, the use of a single set of 5' and 3' primers to amplify any one of the probes. The probe  
20 composition and/or kit can also include buffers, enzyme, etc., required to effect amplification.

As mentioned earlier, when intended for use on a genome-derived single exon microarray of the present invention, the genome-derived single exon probes of the  
25 present invention will typically average at least about 100, 200, 300, 400 or 500 bp in length, including (and typically, but not necessarily centered about) the ORF. Furthermore, when intended for use on a genome-derived single exon microarray of the present invention, the  
30 genome-derived single exon probes of the present invention will typically not contain a detectable label.

When intended for use in solution phase hybridization, however – that is, for use in a hybridization reaction in which the probe is not first  
35 bound to a support substrate (although the target may

indeed be so bound) – length constraints that are imposed in microarray-based hybridization approaches will be relaxed, and such probes will typically be labeled.

In such case, the only functional constraint that dictates the minimum size of such probe is that each such probe must be capable of specifically identifying in a hybridization reaction the exon from which it is drawn. In theory, a probe of as little as 17 nucleotides is capable of uniquely identifying its cognate sequence in the human genome. For hybridization to expressed message – a subset of target sequence that is much reduced in complexity as compared to genomic sequence – even fewer nucleotides are required for specificity.

Therefore, the probes of the present invention can include as few as 20, 25 or 50 bp or ORF, or more. In particular embodiments, the ORF sequences are given in SEQ ID NOS. 9,291 - 18,392, respectively, for probe SEQ ID NOS. 1 - 9,290. The minimum amount of ORF required to be included in the probe of the present invention in order to provide specific signal in either solution phase or microarray-based hybridizations can readily be determined for each of ORF SEQ ID NOS. 9,291 - 18,392 individually by routine experimentation using standard high stringency conditions.

Such high stringency conditions are described, *inter alia*, in Ausubel et al. and Maniatis et al. For microarray-based hybridization, standard high stringency conditions can usefully be 50% formamide, 5X SSC, 0.2 µg/µl poly(dA), 0.2 µg/µl human c<sub>0</sub>t1 DNA, and 0.5 % SDS, in a humid oven at 42°C overnight, followed by successive washes of the microarray in 1X SSC, 0.2% SDS at 55°C for 5 minutes, and then 0.1X SSC, 0.2% SDS, at 55°C for 20 minutes. For solution phase hybridization, standard high stringency conditions can usefully be aqueous hybridization at 65°C in 6X SSC. Lower stringency conditions, suitable

for cross-hybridization to mRNA encoding structurally- and functionally-related proteins, can usefully be the same as the high stringency conditions but with reduction in temperature for hybridization and washing to room  
5 temperature (approximately 25°C).

When intended for use in solution phase hybridization, the maximum size of the single exon probes of the present invention is dictated by the proximity of other expressed exons in genomic DNA: although each single  
10 exon probe can include intergenic and/or intronic material contiguous to the ORF in the human genome, each probe of the present invention will include portions of only one expressed exon.

Thus, each single exon probe will include no more  
15 than about 25 kb of contiguous genomic sequence, more typically no more than about 20 kb of contiguous genomic sequence, more usually no more than about 15 kb, even more usually no more than about 10 kb. Usually, probes that are maximally about 5 kb will be used, more typically no more  
20 than about 3 kb.

It will be appreciated that the Sequence Listing appended hereto presents, by convention, only that strand of the probe and ORF sequence that can be directly translated reading from 5' to 3' end. As would be well  
25 understood by one of skill in the art, single stranded probes must be complementary in sequence to the ORF as present in an mRNA; it is well within the skill in the art to determine such complementary sequence. It will further be understood that double stranded probes can be used in  
30 both solution-phase hybridization and microarray-based hybridization if suitably denatured.

Thus, it is an aspect of the present invention to provide single-stranded nucleic acid probes that have sequence complementary to those described herein above and  
35 below, and double-stranded probes one strand of which has

sequence complementary to the probes described herein.

The probes can, but need not, contain intergenic and/or intronic material that flanks the ORF, on one or both sides, in the same linear relationship to the ORF that  
5 the intergenic and/or intronic material bears to the ORF in genomic DNA. The probes do not, however, contain nucleic acid derived from more than one expressed ORF.

And when intended for use in solution hybridization, the probes of the present invention can  
10 usefully have detectable labels. Nucleic acid labels are well known in the art, and include, *inter alia*, radioactive labels, such as  $^3\text{H}$ ,  $^{32}\text{P}$ ,  $^{33}\text{P}$ ,  $^{35}\text{S}$ ,  $^{125}\text{I}$ ,  $^{131}\text{I}$ ; fluorescent labels, such as Cy3, Cy5, Cy5.5, Cy7, SYBR<sup>®</sup>

Green and other labels described in Haugland,  
15 *Handbook of Fluorescent Probes and Research Chemicals*, 7th ed., Molecular Probes Inc., Eugene, OR (2000), or fluorescence resonance energy transfer tandem conjugates thereof; labels suitable for chemiluminescent and/or enhanced chemiluminescent detection; labels suitable for  
20 ESR and NMR detection; and labels that include one member of a specific binding pair, such as biotin, digoxigenin, or the like.

The probes, either in quantity sufficient for hybridization or sufficient for amplification, can be  
25 provided in individual vials or containers.

Alternatively, such probes can usefully be packaged as a plurality of such individual genome-derived single exon probes.

When provided as a collection of plural  
30 individual probes, the probes are typically made available in amplifiable form in a spatially-addressable ordered set, typically one per well of a microtiter dish. Although a 96 well microtiter plate can be used, greater efficiency is obtained using higher density arrays.

35 If, as earlier mentioned, the ORF-specific

5' primers used for genomic amplification had a first common sequence added thereto, and the ORF-specific 3' primers used for genomic amplification had a second, different, common sequence added thereto, a single set of 5' and 3' primers can be used to amplify all of the probes from the amplifiable ordered set.

Such collections of genome-derived single exon probes can usefully include a plurality of probes chosen for the common attribute of expression in the human HeLa cells.

In such defined subsets, typically at least 50, 60, 75, 80, 85, 90 or 95% or more of the probes will be chosen by their expression in the defined tissue or cell type.

The single exon probes of the present invention, as well as fragments of the single exon probes comprising selectively hybridizable portions of the probe ORF, can be used to obtain the full length cDNA that includes the ORF by (i) screening of cDNA libraries; (ii) rapid amplification of cDNA ends ("RACE"); or (iii) other conventional means, as are described, *inter alia*, in Ausubel et al. and Maniatis et al.

It is another aspect of the present invention to provide genome-derived single exon nucleic acid microarrays useful for gene expression analysis, where the term "microarray" has the meaning given in the definitional section of this description, *supra*.

The invention particularly provides genome-derived single-exon nucleic acid microarrays comprising a plurality of probes known to be expressed in human HeLa cells. In preferred embodiments, the present invention provides human genome-derived single exon microarrays comprising a plurality of probes drawn from the group consisting of SEQ ID NOS.: 1 - 9,290.

When used for gene expression analysis, the

genome-derived single exon microarrays provide greater physical informational density than do the genome-derived single exon microarrays that have lower percentages of probes known to be expressed commonly in the tested tissue.

5 At a fixed probe density, for example, a given microarray surface area of the defined subset genome-derived single exon microarray can yield a greater number of expression measurements. Alternatively, at a given probe density, the same number of expression measurements can be obtained from

10 a smaller substrate surface area. Alternatively, at a fixed probe density and fixed surface area, probes can be provided redundantly, providing greater reliability in signal measurement for any given probe. Furthermore, with a higher percentage of probes known to be expressed in the

15 assayed tissue, the dynamic range of the detection means can be adjusted to reveal finer levels discrimination among the levels of expression.

Although particularly described with respect to their utility as probes of gene expression, particularly as

20 probes to be included on a genome-derived single exon microarray, each of the nucleic acids having SEQ ID NOS.: 1 - 9,290 contains an open-reading frame, set forth respectively in SEQ ID NOS.: 9,291 - 18,392, that encodes a protein domain. Thus, each of SEQ ID NOS. 1 - 9,290 can be

25 used, or that portion thereof in SEQ ID NOS. 9,291 - 18,392 used, to express a protein domain by standard *in vitro* recombinant techniques. See Ausubel et al. and Maniatis et al.

Additionally, kits are available commercially

30 that readily permit such nucleic acids to be expressed as protein in bacterial cells, insect cells, or mammalian cells, as desired (e.g., HAT<sup>™</sup> Protein Expression & Purification System, ClonTech Laboratories, Palo Alto, CA; Adeno-X<sup>™</sup> Expression System, ClonTech Laboratories, Palo

35 Alto, CA; Protein Fusion & Purification (pMAL<sup>™</sup>) System, New



England Biolabs, Beverly, MA)

Furthermore, shorter peptides can be chemically synthesized using commercial peptide synthesizing equipment and well known techniques. Procedures are described, *inter alia*, in Chan et al. (eds.), Fmoc Solid Phase Peptide Synthesis: A Practical Approach (Practical Approach Series, (Paper)), Oxford Univ. Press (March 2000) (ISBN: 0199637245); Jones, Amino Acid and Peptide Synthesis (Oxford Chemistry Primers, No 7) , Oxford Univ. Press (August 1992) (ISBN: 0198556683); and Bodanszky, Principles of Peptide Synthesis (Springer Laboratory), Springer Verlag (December 1993) (ISBN: 0387564314).

It is, therefore, another aspect of the invention to provide peptides comprising an amino acid sequence translated from SEQ ID NOS.: 9,291 - 18,392. Such amino acid sequences are set out in SEQ ID NOS: 18,393 - 26,941. Any such recombinantly-expressed or synthesized peptide of at least 8, and preferably at least about 15, amino acids, can be conjugated to a carrier protein and used to generate antibody that recognizes the peptide. Thus, it is a further aspect of the invention to provide peptides that have at least 8, preferably at least 15, consecutive amino acids.

The following examples are offered by way of illustration and not by way of limitation.

#### EXAMPLE 1

Preparation of Single Exon Microarrays from ORFs Predicted in Human Genomic Sequence

#### Bioinformatics Results

All human BAC sequences in fewer than 10 pieces that had been accessioned in a five month period immediately preceding this study were downloaded from

GenBank. This corresponds to ~2200 clones, totaling ~350 MB of sequence, or approximately 10% of the human genome.

After masking repetitive elements using the program CROSS\_MATCH, the sequence was analyzed for open  
5 reading frames using three separate gene finding programs. The three programs predict genes using independent algorithmic methods developed on independent training sets: GRAIL uses a neural network, GENEFINDER uses a hidden Markoff model, and DICTION, a program proprietary to  
10 Genetics Institute, operates according to a different heuristic. The results of all three programs were used to create a prediction matrix across the segment of genomic DNA.

The three gene finding programs yielded a range  
15 of results. GRAIL identified the greatest percentage of genomic sequence as putative coding region, 2% of the data analyzed. GENEFINDER was second, calling 1%, and DICTION yielded the least putative coding region, with 0.8% of genomic sequence called as coding region.

20 The consensus data were as follows. GRAIL and GENEFINDER agreed on 0.7% of genomic sequence, GRAIL and DICTION agreed on 0.5% of genomic sequence, and the three programs together agreed on 0.25% of the data analyzed. That is, 0.25% of the genomic sequence was identified by  
25 all three of the programs as containing putative coding region.

ORFs predicted by any two of the three programs ("consensus ORFs") were assorted into "gene bins" using two criteria: (1) any 7 consecutive exons within a 25 kb window  
30 were placed together in a bin as likely contributing to a single gene, and (2) all ORFs within a 25 kb window were placed together in a bin as likely contributing to a single gene if fewer than 7 exons were found within the 25 kb window.

35

PCR

The largest ORF from each gene bin that did not span repetitive sequence was then chosen for amplification, as were all consensus ORFs longer than 500 bp. This method  
5 approximated one exon per gene; however, a number of genes were found to be represented by multiple elements.

Previously, we had determined that DNA fragments fewer than 250 bp in length do not bind well to the amino-modified glass surface of the slides used as support  
10 substrate for construction of microarrays; therefore, amplicons were designed in the present experiments to approximate 500 bp in length.

Accordingly, after selecting the largest ORF per gene bin, a 500 bp fragment of sequence centered on the ORF  
15 was passed to the primer picking software, PRIMER3 (available online for use at <http://www-genome.wi.mit.edu/cgi-bin/primer/> ). A first additional sequence was commonly added to each ORF-unique 5' primer, and a second, different, additional sequence was  
20 commonly added to each ORF-unique 3' primer, to permit subsequent reamplification of the amplicon using a single set of "universal" 5' and 3' primers, thus immortalizing the amplicon. The addition of universal priming sequences also facilitates sequence verification, and can be used to  
25 add a cloning site should some ORFs be found to warrant further study.

The ORFs were then PCR amplified from genomic DNA, verified on agarose gels, and sequenced using the universal primers to validate the identity of the amplicon  
30 to be spotted in the microarray.

Primers were supplied by Operon Technologies (Alameda, CA). PCR amplification was performed by standard techniques using human genomic DNA (Clontech, Palo Alto, CA) as template. Each PCR product was verified by SYBR®  
35 green (Molecular Probes, Inc., Eugene, OR) staining of

agarose gels, with subsequent imaging by Fluorimager (Molecular Dynamics, Inc., Sunnyvale, CA). PCR amplification was classified as successful if a single band appeared.

5           The success rate for amplifying ORFs of interest directly from genomic DNA using PCR was approximately 75%. FIG. 5 graphs the distribution of predicted ORF (exon) length and distribution of amplified PCR products, with ORF length shown in red and PCR product length shown in blue  
10 (which may appear black in the figure). Although the range of ORF sizes is readily seen to extend to beyond 900 bp, the mean predicted exon size was only 229 bp, with a median size of 150 bp (n=9498). With an average amplicon size of 475  $\pm$  25 bp, approximately 50% of the average PCR  
15 amplification product contained predicted coding region, with the remaining 50% of the amplicon containing either intron, intergenic sequence, or both.

          Using a strategy predicated on amplifying about 500 bp, it was found that long exons had a higher PCR  
20 failure rate. To address this, the bioinformatics process was adjusted to amplify 1000, 1500 or 2000 bp fragments from exons larger than 500 bp. This improved the rate of successful amplification of exons exceeding 500 bp, constituting about 9.2% of the exons predicted by the gene  
25 finding algorithms.

          Approximately 75% of the probes disposed on the array (90% of those that successfully PCR amplified) were sequence-verified by sequencing in both the forward and reverse direction using MegaBACE sequencer (Molecular  
30 Dynamics, Inc., Sunnyvale, CA), universal primers, and standard protocols.

          Some genomic clones (BACs) yielded very poor PCR and sequencing results. The reasons for this are unclear, but may be related to the quality of early draft sequence  
35 or the inclusion of vector and host contamination in some

submitted sequence data.

Although the intronic and intergenic material flanking coding regions could theoretically interfere with hybridization during microarray experiments, subsequent  
5 empirical results demonstrated that differential expression ratios were not significantly affected by the presence of noncoding sequence. The variation in exon size was similarly found not to affect differential expression ratios significantly; however, variation in exon size was  
10 observed to affect the absolute signal intensity (data not shown).

The 350 MB of genomic DNA was, by the above-described process, reduced to 9750 discrete probes, which were spotted in duplicate onto glass slides using  
15 commercially available instrumentation (MicroArray GenII Spotter and/or MicroArray GenIII Spotter, Molecular Dynamics, Inc., Sunnyvale, CA). Each slide additionally included either 16 or 32 *E. coli* genes, the average hybridization signal of which was used as a measure of  
20 background biological noise.

Each of the probe sequences was BLASTed against the human EST data set, the NR data set, and SwissProt GenBank (May 7, 1999 release 2.0.9).

One third of the probe sequences (as amplified)  
25 produced an exact match (BLAST Expect ("E") values less than  $1 \text{ e}^{-100}$ ) to either an EST (20% of sequences) or a known mRNA (13% of sequences). A further 22% of the probe sequences showed some homology to a known EST or mRNA (BLAST E values from  $1 \text{ e}^{-5}$  to  $1 \text{ e}^{-99}$ ). The remaining 45% of  
30 the probe sequences showed no significant sequence homology to any expressed, or potentially expressed, sequences present in public databases.

All of the probe sequences (as amplified) were then analyzed for protein similarities with the SwissProt  
35 database using BLASTX, Gish et al., *Nature Genet.* 3:266

(1993). The predicted functional breakdowns of the 2/3 of probes identical or homologous to known sequences are presented in Table 1.

5                      Table 1

Function of Predicted ORFs As Deduced From Comparative Sequence Analysis			
Total	V6 chip	V7 chip	Function Predicted from Comparative Sequence Analysis
211	96	115	Receptor
120	43	77	Zinc Finger
30	11	19	Homeobox
25	9	16	Transcription Factor
17	11	7	Transcription
118	57	61	Structural
95	39	56	Kinase
36	18	18	Phosphatase
83	31	52	Ribosomal
45	19	26	Transport
21	17	14	Growth Factor
17	12	5	Cytochrome
50	33	17	Channel

As can be seen, the two most common types of genes were transcription factors and receptors, making up 2.2% and 1.8% of the arrayed elements, respectively.

10

#### EXAMPLE 2

Gene Expression Measurements From Genome-Derived Single Exon Microarrays

15

The two genome-derived single exon microarrays prepared according to Example 1 were hybridized in a series of simultaneous two-color fluorescence experiments to (1) 5 Cy3-labeled cDNA synthesized from message drawn individually from each of brain, heart, liver, fetal liver, placenta, lung, bone marrow, HeLa, BT 474, or HBL 100 cells, and (2) Cy5-labeled cDNA prepared from message pooled from all ten tissues and cell types, as a control in 10 each of the measurements. Hybridization and scanning were carried out using standard protocols and Molecular Dynamics equipment.

Briefly, mRNA samples were bought from commercial sources (Clontech, Palo Alto, CA and Amersham Pharmacia 15 Biotech (APB)). Cy3-dCTP and Cy5-dCTP (both from APB) were incorporated during separate reverse transcriptions of 1 µg of polyA<sup>+</sup> mRNA performed using 1 µg oligo(dT)12-18 primer and 2 µg random 9mer primers as follows. After heating to 70°C, the RNA:primer mixture was snap cooled on ice. After 20 snap cooling on ice, added to the RNA to the stated final concentration was: 1X Superscript II buffer, 0.01 M DTT, 100µM dATP, 100 µM dGTP, 100 µM dTTP, 50 µM dCTP, 50 µM Cy3-dCTP or Cy5-dCTP 50 µM, and 200 U Superscript II enzyme. The reaction was incubated for 2 hours at 42°C. 25 After 2 hours, the first strand cDNA was isolated by adding 1 U Ribonuclease H, and incubating for 30 minutes at 37°C. The reaction was then purified using a Qiagen PCR cleanup column, increasing the number of ethanol washes to 5. Probe was eluted using 10 mM Tris pH 8.5.

30 Using a spectrophotometer, probes were measured for dye incorporation. Volumes of both Cy3 and Cy5 cDNA corresponding to 50 pmoles of each dye were then dried in a Speedvac, resuspended in 30 µl hybridization solution containing 50% formamide, 5X SSC, 0.2 µg/µl poly(dA), 0.2 35 µg/µl human c<sub>ot</sub>1 DNA, and 0.5 % SDS.

Hybridizations were carried out under a coverslip, with the array placed in a humid oven at 42°C overnight. Before scanning, slides were washed in 1X SSC, 0.2% SDS at 55°C for 5 minutes, followed by 0.1X SSC, 0.2% SDS, at 55°C for 20 minutes. Slides were briefly dipped in water and dried thoroughly under a gentle stream of nitrogen.

Slides were scanned using a Molecular Dynamics Gen3 scanner, as described. Schena (ed.), Microarray Biochip: Tools and Technology, Eaton Publishing Company/BioTechniques Books Division (2000) (ISBN: 1881299376).

Although the use of pooled cDNA as a reference permitted the survey of a large number of tissues, it attenuates the measurement of relative gene expression, since every highly expressed gene in the tissue/cell type-specific fluorescence channel will be present to a level of at least 10% in the control channel. Because of this fact, both signal and expression ratios (the latter hereinafter, "expression" or "relative expression") for each probe were normalized using the average ratio or average signal, respectively, as measured across the whole slide.

Data were accepted for further analysis only when signal was at least three times greater than biological noise, the latter defined by the average signal produced by the *E. coli* control genes.

The relative expression signal for these probes was then plotted as function of tissue or cell type, and is presented in FIG. 6.

FIG. 6 shows the distribution of expression across a panel of ten tissues. The graph shows the number of sequence-verified products that were either not expressed ("0"), expressed in one or more but not all tested tissues ("1" - "9"), and expressed in all tissues tested ("10").



Of 9999 arrayed elements on the two microarrays (including positive and negative controls and "failed" products), 2353 (51%) were expressed in at least one tissue or cell type. Of the gene elements showing significant  
5 signal - where expression was scored as "significant" if the normalized Cy3 signal was greater than 1, representing signal 5-fold over biological noise (0.2) - 39% (991) were expressed in all 10 tissues. The next most common class (15%) consisted of gene elements expressed in only a single  
10 tissue.

The genes expressed in a single tissue were further analyzed, and the results of the analyses are compiled in FIG. 7.

FIG. 7A is a matrix presenting the expression of  
15 all verified sequences that showed expression greater than 3 in at least one tissue. Each clone is represented by a column in the matrix. Each of the 10 tissues assayed is represented by a separate row in the matrix, and relative expression of a clone in that tissue is indicated at the  
20 respective node by intensity of green shading, with the intensity legend shown in panel B. The top row of the matrix ("EST Hit") contains "bioinformatic" rather than "physical" expression data - that is, presents the results returned by query of EST, NR and SwissProt databases using  
25 the probe sequence. The legend for "bioinformatic expression" (i.e., degree of homology returned) is presented in panel C. Briefly, white is known, black is novel, with gray depicting nonidentical with significant homology (white: E values < 1e-100; gray: E values from 1e-  
30 05 to 1e-99; black: E values > 1e-05).

As FIG. 7 readily shows, heart and brain were demonstrated to have the greatest numbers of genes that were shown to be uniquely expressed in the respective tissue. In brain, 200 uniquely expressed genes were  
35 identified; in heart, 150. The remaining tissues gave the

following figures for uniquely expressed genes: liver, 100; lung, 70; fetal liver, 150; bone marrow, 75; placenta, 100; HeLa, 50; HBL, 100; and BT474, 50.

It was further observed that there were many more  
5 "novel" genes among those that were up-regulated in only one tissue, as compared with those that were down-regulated in only one tissue. In fact, it was found that ORFs whose expression was measurable in only a single of the tested tissues were represented in sequencing databases at a rate  
10 of only 11%, whereas 36% of the ORFs whose expression was measurable in 9 of the tissues were present in public databases. As for those ORFs expressed in all ten tissues, fully 45% were present in existing expressed sequence databases. These results are not unexpected, since genes  
15 expressed in a greater number of tissues have a higher likelihood of being, and thus of having been, discovered by EST approaches.

#### Comparison of Signal from Known and Unknown Genes

20 The normalized signal of the genes found to have high homology to genes present in the GenBank human EST database were compared to the normalized signal of those genes not found in the GenBank human EST database. The data are shown in FIG. 8.

25 FIG. 8 shows the normalized Cy3 signal intensity for all sequence-verified products with a BLAST Expect ("E") value of greater than  $1e-30$  (designated "unknown") upon query of existing EST, NR and SwissProt databases, and shows in blue the normalized Cy3 signal intensity for all  
30 sequence-verified products with a BLAST Expect value of less than  $1e-30$  ("known"). Note that biological background noise has an averaged normalized Cy3 signal intensity of 0.2.

As expected, the most highly expressed of the  
35 ORFs were "known" genes. This is not surprising, since

very high signal intensity correlates with very commonly-expressed genes, which have a higher likelihood of being found by EST sequence.

However, a significant point is that a large  
5 number of even the high expressers were "unknown". Since the genomic approach used to identify genes and to confirm their expression does not bias exons toward either the 3' or 5' end of a gene, many of these high expression genes will not have been detected in an end-sequenced cDNA  
10 library.

The significant point is that presence of the gene in an EST database is not a prerequisite for incorporation into a genome-derived microarray, and further, that arraying such "unknown" exons can help to  
15 assign function to as-yet undiscovered genes.

#### Verification of Gene Expression

To ascertain the validity of the approach described above to identify genes from raw genomic  
20 sequence, expression of two of the probes was assayed using reverse transcriptase polymerase chain reaction (RT PCR) and northern blot analysis.

Two microarray probes were selected on the basis of exon size, prior sequencing success, and tissue-specific  
25 gene expression patterns as measured by the microarray experiments. The primers originally used to amplify the two respective ORFs from genomic DNA were used in RT PCR against a panel of tissue-specific cDNAs (Rapid-Scan gene expression panel 24 human cDNAs) (OriGene Technologies,  
30 Inc., Rockville, MD).

Sequence AL079300\_1 was shown by microarray hybridization to be present in cardiac tissue, and sequence AL031734\_1 was shown by microarray experiment to be present in placental tissue (data not shown). RT-PCR on these two  
35 sequences confirmed the tissue-specific gene expression as

measured by microarrays, as ascertained by the presence of a correctly sized PCR product from the respective tissue type cDNAs.

Clearly, all microarray results cannot, and indeed should not, be confirmed by independent assay methods, or the high throughput, highly parallel advantages of microarray hybridization assays will be lost. However, in addition to the two RT-PCR results presented above, the observation that 1/3 of the arrayed genes exist in expression databases provides powerful confirmation of the power of our methodology – which combines bioinformatic prediction with expression confirmation using genome-derived single exon microarrays – to identify novel genes from raw genomic data.

To verify that the approach further provides correct characterization of the expression patterns of the identified genes, a detailed analysis was performed of the microarrayed sequences that showed high signal in brain.

For this latter analysis, sequences that showed high (normalized) signal in brain, but which showed very low (normalized) signal (less than 0.5, determined to be biological noise) in all other tissues, were further studied. There were 82 sequences that fit these criteria, approximately 2% of the arrayed elements. The 10 sequences showing the highest signal in brain in microarray hybridizations are detailed in Table 2, along with assigned function, if known or reasonably predicted.

Table 2

Function of the Most Highly Expressed Genes Expressed Only in Brain

Microarray Sequence Name	Normal ized Signal	Expressi on Ratio	Homology to EST present in GenBank	Gene Function as described by GenBank
AP000217-1	5.2	+7.7	High	S-100 protein, b-chain, Ca <sup>2+</sup> binding protein expressed in central nervous system
AP000047-1	2.3		High	Unknown Function
AC006548-9	1.7		High	Similar to mouse membrane glyco-protein M6, expressed in central nervous system
AC007245-5	1.5		High	Similar to amphiphysin, a synaptic vesicle- associated protein. Ref 21
L44140-4	1.2	+2.0	High	Endothelial actin-binding protein found in nonmuscle filamin

AC004689-9	1.2	+3.5	High	Protein Phosphatase PP2A, neuronal/ downregulates activated protein kinases
AL031657-1	1.2	+3.0	High	Unknown function/ Contains the anhyrin motif, a common protein sequence motif
AC009266-2	1.1	+3.7	Low	Low homology to the Synaptotagmin I protein in rat/present at low levels throughout rat brain
AP000086-1	1.0	+2.7	Low	Unknown, very poor homology to collagen
AC004689-3	1.0		High	Protein Phosphatase PP2A, neuronal/ downregulates activated protein kinases

Of the ten sequences studied by these latter confirmatory approaches, eight were previously known. Of these eight, six had previously been reported to be  
5 important in the central nervous system or brain. The exon

giving the highest signal (AP00217-1) was found to be the gene encoding an S100B  $\text{Ca}^{2+}$  binding protein, reported in the literature to be highly and uniquely expressed in the central nervous system. Heizmann, *Neurochem. Res.* 9:1097  
5 (1997).

A number of the brain-specific probe sequences (including AC006548-9, AC009266-2) did not have homology to any known human cDNAs in GenBank but did show homology to rat and mouse cDNAs. Sequences AC004689-9 and AC004689-3  
10 were both found to be phosphatases present in neurons (Millward et al., *Trends Biochem. Sci.* 24(5):186-191 (1999)). Two microarray sequences, AP000047-1 and AP000086-1 have unknown function, with AP000086-1 being absent from GenBank. Functionality can now be narrowed  
15 down to a role in the central nervous system for both of these genes, showing the power of designing microarrays in this fashion.

Next, the function of the chip sequences with the highest (normalized) signal intensity in brain, regardless  
20 of expression in other tissues, was assessed. In this latter analysis, we found expression of many more common genes, since the sequences were not limited to those expressed only in brain. For example, looking at the 20 highest signal intensity spots in brain, 4 were similar to  
25 tubulin (AC00807905; AF146191-2; AC007664-4; AF14191-2), 2 were similar to actin (AL035701-2; AL034402-1), and 6 were found to be homologous to glyceraldehyde-3-phosphate dehydrogenase (GAPDH) (AL035604-1; Z86090-1; AC006064-L, AC006064-K; AC035604-3; AC006064-L). These genes are often  
30 used as controls or housekeeping genes in microarray experiments of all types.

Other interesting genes highly expressed in brain were a ferritin heavy chain protein, which is reported in the literature to be found in brain and liver (Joshi et  
35 al., *J. Neurol. Sci.* 134(Suppl):52-56 (1995)), a result

duplicated with the array. Other highly expressed chip  
 sequences included a translation elongation factor 1 $\alpha$   
 (AC007564-4), a DEAD-box homolog (AL023804-4), and a Y-  
 chromosome RNA-binding motif (Chai et al., *Genomics*  
 5 49(2):283-89 (1998)) (AC007320-3). A low homology analog  
 (AP00123-1/2) to a gene, DSCR1, thought to be involved in  
 trisomy 21 (Down's syndrome), showed high expression in  
 both brain and heart, in agreement with the literature  
 (Fuentes et al., *Mol. Genet.* 4(10):1935-44 (1995)).

10 As a further validation of the approach, we  
 selected the BAC AC006064 to be included on the array.  
 This BAC was known to contain the GAPDH gene, and thus  
 could be used as a control for the ORF selection process.  
 The gene finding and exon selection algorithms resulted in  
 15 choosing 25 exons from BAC AC006064 for spotting onto the  
 array, of which four were drawn from the GAPDH gene. Table  
 3 shows the comparison of the average expression ratio for  
 the 4 exons from BAC006064 compared with the average  
 expression ratio for 5 different dilutions of a  
 20 commercially available GAPDH cDNA (Clontech).

Table 3

Comparison of Expression Ratio, for each tissue, of GAPDH		
	AC006064 (n = 4)	Control ( n = 5)
Bone Marrow	-1.81 $\pm$ 0.11	-1.85 $\pm$ 0.08
Brain	-1.41 $\pm$ 0.11	-1.17 $\pm$ 0.05
BT474	1.85 $\pm$ 0.09	1.66 $\pm$ 0.12
Fetal Liver	-1.62 $\pm$ 0.07	-1.41 $\pm$ 0.05
HBL100	1.32 $\pm$ 0.05	2.64 $\pm$ 0.12
Heart	1.16 $\pm$ 0.09	1.56 $\pm$ 0.10
HeLa	1.11 $\pm$ 0.06	1.30 $\pm$ 0.15
Liver	-1.62 $\pm$ 0.22	-2.07 $\pm$



Lung	-4.95 ± 0.93	-3.75 ± 0.21
Placenta	-3.56 ± 0.25	-3.52 ± 0.43

Each tissue shows excellent agreement between the experimentally chosen exons and the control, again  
5 demonstrating the validity of the present exon mining approach. In addition, the data also show the variability of expression of GAPDH within tissues, calling into question its classification as a housekeeping gene and utility as a housekeeping control in microarray  
10 experiments.

### EXAMPLE 3

Representation of Sequence and Expression Data as a "Mondrian"

15

For each genomic clone processed for microarray as above-described, a plethora of information was accumulated, including full clone sequence, probe sequence within the clone, results of each of the three gene finding  
20 programs, EST information associated with the probe sequences, and microarray signal and expression for multiple tissues, challenging our ability to display the information.

Accordingly, we devised a new tool for visual  
25 display of the sequence with its attendant annotation which, in deference to its visual similarity to the paintings of Piet Mondrian, is hereinafter termed a "Mondrian". FIGS. 3 and 4 present the key to the information presented on a Mondrian.

30 FIG. 9 presents a Mondrian of BAC AC008172 (bases 25,000 to 130,000 shown), containing the carbamyl phosphate synthetase gene (AF154830.1). Purple background within the region shown as field 81 in FIG. 3 indicates all 37 known

exons for this gene.

As can be seen, GRAIL II successfully identified 27 of the known exons (73%), GENEFINDER successfully identified 37 of the known exons (100%), while DICTION 5 identified 7 of the known exons (19%).

Seven of the predicted exons were selected for physical assay, of which 5 successfully amplified by PCR and were sequenced. These five exons were all found to be from the same gene, the carbamyl phosphate synthetase gene 10 (AF154830.1).

The five exons were arrayed, and gene expression measured across 10 tissues. As is readily seen in the Mondrian, the five chip sequences on the array show identical expression patterns, elegantly demonstrating the 15 reproducibility of the system.

FIG. 10 is a Mondrian of BAC AL049839. We selected 12 exons from this BAC, of which 10 successfully sequenced, which were found to form between 5 and 6 genes. Interestingly, 4 of the genes on this BAC are protease 20 inhibitors. Again, these data elegantly show that exons selected from the same gene show the same expression patterns, depicted below the red line. From this figure, it is clear that our ability to find known genes is very good. A novel gene is also found from 86.6 kb to 88.6 kb, 25 upon which all the exon finding programs agree. We are confident we have two exons from a single gene since they show the same expression patterns and the exons are proximal to each other. Backgrounds in the following colors indicate a known gene (top to bottom):

30 red = kallistatin protease inhibitor (P29622);  
purple = plasma serine protease inhibitor (P05154);  
turquoise =  $\alpha$ 1 anti-chymotrypsin (P01011); mauve = 40S ribosomal protein (P08865). Note that chip sequence 8 and 12 did not sequence verify.

35

EXAMPLE 4Genome-Derived Single Exon Probes Useful For Measuring  
Human Gene Expression

5

The protocols set forth in Examples 1 and 2, *supra*, were applied to additional human genomic sequence as it became newly available in GenBank to identify unique exons in the human genome that could be shown to be  
10 expressed at significant levels in HeLa cell line.

These unique exons are within longer probe sequences. Each probe was completely sequenced on both strands prior to its use on a genome-derived single exon microarray; sequencing confirms the exact chemical  
15 structure of each probe. An added benefit of sequencing is that it placed us in possession of a set of single base-incremented fragments of the sequenced nucleic acid, starting from the sequencing primer 3' OH. (Since the single exon probes were first obtained by PCR amplification  
20 from genomic DNA, we were of course additionally in possession of an even larger set of single base incremented fragments of each of the 9,290 single exon probes, each fragment corresponding to an extension product from one of the two amplification primers.)

25 The structures of the 9,290 unique single exon probes are clearly presented in the Sequence Listing as SEQ ID Nos.: 1 - 9,290. The 16 nt 5' primer sequence and 16 nt 3' primer sequence present on the amplicon are not included in the sequence listing. The sequences of the exons  
30 present within each of these probes is presented in the Sequence Listing as SEQ ID Nos.: 9,291 - 18,392, respectively. It will be noted that some amplicons have more than one exon, some exons are contained in more than one amplicon.

35 As detailed in Example 2, expression was

demonstrated by disposing the amplicons as single exon probes on nucleic acid microarrays and then performing two-color fluorescent hybridization analysis; significant expression is based on a statistical confidence that the  
5 signal is significantly greater than negative biological control spots. The negative biological control is formed from spotted DNA sequences from a different species. Here, 32 sequences from E.Coli were spotted in duplicate to give a total of 64 spots.

10 For each hybridisation (each slide, each colour) the median value of the signal from all of the spots is determined. The normalised signal value is the arithmetic mean of the signal from duplicate spots divided by the population median.

15 Control spots are eliminated if there is more than a five-fold difference between each one of the duplicate spots raw signals.

The median of the signal from the remaining control spots is calculated and all subsequent calculations  
20 are done with normalised signals.

Control spots having a signal of greater than median + 2.4 (the value 2.4 is roughly 12 times the observed standard deviation of control spot populations) are eliminated. Spots with such high signals are considered  
25 to be "outliers".

The mean and standard deviation of the modified control spot populations are calculated.

The mean + 3x the standard deviation (mean + (3\*SD)) is used as the signal threshold qualifier for that  
30 particular hybridisation. Thus, individual thresholds are determined for each channel and each hybridisation.

This means that, assuming that the data is distributed normally, there is a 99% confidence that any signal exceeding the threshold is significant.

35 The probes and their expression data are

presented in Table 4, set forth respectively in Example 5. Example 5 presents the subset of probes that is significantly expressed in the human HeLa cells and thus presents the subset of probes that was recognized to be  
5 useful for measuring expression of their cognate genes in human HeLa cells.

The sequence of each of the exon probes identified by SEQ ID NOS.: 9,291 - 18,392 was individually used as a BLAST (or, for SWISSPROT, BLASTX) query to  
10 identify the most similar sequence in each of dbEST, SwissProt (BLASTX), and NR divisions of GenBank. Because the query sequences are themselves derived from genomic sequence in GenBank, only nongenic hits from NR were scored.

15 The smallest in value of the BLAST (or BLASTX) expect ("E") scores for each query sequence across the three database divisions was used as a measure of the "expression novelty" of the probe's ORF. Table 4 is sorted in descending order based on this measure, reported as  
20 "Most Similar (top) Hit BLAST E Value". Those sequences for which no "Hit E Value" is listed are those exons which were found to have no similar sequences.

As sorted, Table 4 thus lists its respective probes (by "AMPLICON SEQ ID NO.:" and additionally by the  
25 SEQ ID NO.: of the exon contained within the probe:"EXON SEQ ID NO.:" from least similar to sequences known to be expressed (i.e., highest BLAST E value), at the beginning of the table, to most similar to sequences known to be expressed (i.e., lowest BLAST E value), at the bottom of  
30 the table.

Table 4 further provides, for each listed probe, the accession number of the database sequence that yielded the "Most Similar (top) Hit BLAST E Value", along with the name of the database in which the database sequence is  
35 found ("Top Hit Database Source").

Table 4 further provides SEQ ID NOS.

corresponding to the predicted amino acid sequences where they have been determined for the probe and exon nucleotide sequences. These are set out as PEPTIDE SEQ ID NOS.:. The  
5 peptide sequences for a given exon are predicted as follows: Since each chip exon is a consensus sequence drawn from predictions from various exon finding programs (i.e. Grail, GeneFinder and GenScan), the multiple initial ORFs are first determined in a uniform way according to each  
10 prediction. In particular, the reading frame for predicting the first amino acid in the peptide sequence always starts with the first base of any codon and ends with the last base of non-termination codon. Next, for each strand of the exon, initial ORFs are merged into one or more final ORFs  
15 in an exhaustive process based on the following criteria: 1) the merging ORFs must be overlapping, and 2) the merging ORFs must be in the same frame.

The Sequence Listing, which is a superset of all of the data presented in Table 4, further includes, for  
20 each probe, the most similar hit, with accession number and BLAST E value, from the each of the three queried databases.

Table 4 further lists, for each probe, a portion of the descriptor for the top hit ("Top Hit Descriptor") as  
25 provided in the sequence database. For those ORFs that are similar in sequence, but nonidentical to known sequences (e.g., those with BLAST E values between about  $1e-05$  and  $1e-100$ ), the descriptor reveals the likely function of the protein encoded by the probe's ORF.

30 Using BLAST E value cutoffs of  $1e-05$  (i.e.,  $1 \times 10^{-5}$ ) and  $1e-100$  (i.e.,  $1 \times 10^{-100}$ ) as evidence of similarity to sequences known to be expressed is of course arbitrary: in Example 2, *supra*, a BLAST E value of  $1e-30$  was used as the boundary when only two classes were to be defined for  
35 analysis (unknown,  $>1e-30$ ; known  $<1e-30$ ) (see also FIG. 8).

Furthermore, even when the "Most Similar (Top) Hit BLAST E Value" is low, e.g., less than about  $1e-100$  - which is probative evidence that the query sequence has previously been shown to be expressed - the top hit is highly unlikely  
5 exactly to match the probe sequence.

First, such expression entries typically will not have the intronic and/or intergenic sequence present within the single exon probes listed in the Table. Second, even the ORF itself is unlikely in such cases to be present  
10 identically in the databases, since most of the EST and mRNA clones in existing databases include multiple exons, without any indication of the location of exon boundaries.

As noted, the data presented in Table 4 represent a proper subset of the data present within the attached  
15 sequence listing. For each amplicon probe (SEQ ID NOs.: 1 - 9,290) and probe exon (SEQ ID NOs.: 9,291 - 18,392, respectively), the sequence listing further provides, through iterated annotation fields <220> and <223>:

(a) the accession number of the BAC from which  
20 the sequence was derived ("MAP TO"), thus providing a link to the chromosomal map location and other information about the genomic milieu of the probe sequence;

(b) the most similar sequence provided by BLAST query of the EST database, with accession number and BLAST  
25 E value for the "hit";

(c) the most similar sequence provided by BLAST query of the GenBank NR database, with accession number and BLAST E value for the "hit"; and

(d) the most similar sequence provided by BLASTX  
30 query of the SWISSPROT database, with accession number and BLAST E value for the "hit".

#### EXAMPLE 5

35 Genome-Derived Single Exon Probes Useful For Measuring

Expression of Genes in Human HeLa cells

Table 4 (382 pages) presents expression, homology, and functional information for the genome-derived single exon probes that are expressed significantly in human HeLa cell line.



## CLAIMS

1. A spatially-addressable set of single exon nucleic acid probes for measuring gene expression in a sample derived  
5 from human HeLa cells or other human cervical epithelial cells comprising a plurality single exon nucleic probes, said probes comprising any one of the nucleotide sequences set out in SEQ ID NOS: 1 - 9,290 or a complementary sequence, or a portion of such a sequence.
- 10 2. A spatially-addressable set of single exon nucleic acid probes as claimed in claim 1 wherein each of said plurality of probes is separately and addressably amplifiable.
- 15 3. A spatially-addressable set of single exon nucleic acid probes as claimed in claim 1 wherein each of said plurality of probes is separately and addressably isolatable from said plurality.
- 20 4. A spatially-addressable set of single exon nucleic acid probes as claimed in any of claims 1 to 3 wherein said probes comprise any one of the nucleotide sequences set out in SEQ ID NOS.: 9,291 - 18,392.
- 25 5. A spatially-addressable set of single exon nucleic acid probes as claimed in any of claims 1 to 4, wherein each of said plurality of probes is amplifiable using at least one common primer.
- 30 6. A spatially-addressable set of single exon nucleic acid probes as claimed in any of claims 1 to 5 wherein the set comprises between 50 - 20,000 single exon nucleic acid probes.
- 35 7. A spatially-addressable set of single exon nucleic acid

probes as claimed in any of claims 1 to 6, wherein the average length of the single exon nucleic acid probes is between 200 and 500 bp.

- 5 8. A spatially-addressable set of single exon nucleic acid probes as claimed in any of claims 1 to 7, wherein at least 50% of said single exon nucleic acid probes lack prokaryotic and bacteriophage vector sequence.
- 10 9. A spatially-addressable set of single exon nucleic acid probes as claimed in any of claims 1 to 8, wherein at least 50% of said single exon nucleic acid probes lack homopolymeric stretches of A or T.
- 15 10. A spatially-addressable set of single exon nucleic acid probes as claimed in any of claims 1 - 9 characterised in that said set of probes is addressably disposed upon a substrate.
- 20 11. A spatially-addressable set of single exon nucleic acid probes as claimed in claim 10 wherein said substrate is selected from glass, amorphous silicon, crystalline silicon and plastic.
- 25 12. A microarray comprising a spatially addressable set of single exon nucleic acid probes as claimed in any of claims 1 - 11.
- 30 13. A single exon nucleic acid probe for measuring human gene expression in a sample derived from human HeLa cells or other human cervical epithelial cells comprising a nucleotide sequence as set out in any of SEQ ID NOs.: 1 - 9,290 or a complementary sequence or a fragment thereof wherein said probe hybridizes at high stringency to a
- 35 nucleic acid molecule expressed in the human HeLa cells or

other human cervical epithelial cells.

14. A single exon nucleic acid probe as claimed in claim 13 comprising a nucleotide sequence as set out in any of SEQ ID NOs.: 9,291 - 18,392 or a complementary sequence or a fragment thereof.

15. A single exon nucleic acid probe for measuring human gene expression in a sample derived from human HeLa cells or other human cervical epithelial cells which is a nucleic acid molecule having a sequence encoding a peptide comprising a peptide sequence as set out in any of SEQ ID NOs.: 18,393 - 26,941, or a complementary sequence or a fragment thereof wherein said probe hybridizes at high stringency to a nucleic acid expressed in the human HeLa cells or other human cervical epithelial cells.

16. A single exon nucleic acid probe as claimed in any one of claims 13 to 15 wherein said single exon nucleic acid probe comprises between 15 and 25 contiguous nucleotides of said SEQ ID NO.

17. A single exon nucleic acid probe as claimed in any one of claims 13 to 15, wherein said probe is between 3 - 25 kb in length.

18. A single exon nucleic acid probe as claimed in any one of claims 13 - 17, wherein said probe is DNA, RNA or PNA.

19. A single exon nucleic acid probe as claimed in any one of claims 13 - 18, wherein said probe is detectably labeled.

20. A single exon nucleic acid probe as claimed in any one of claims 13 - 19, wherein said probe lacks prokaryotic and

bacteriophage vector sequence.

21. A single exon nucleic acid probe as claimed in any one of claims 13 - 20, wherein said probe lacks homopolymeric  
5 stretches of A or T.

22. A method of measuring gene expression in a sample derived from human HeLa cells or other human cervical epithelial cells, comprising:

10       contacting the microarray of claim 12, with a first collection of detectably labeled nucleic acids, said first collection of nucleic acids derived from mRNA of human HeLa cells or other human cervical epithelial cells; and then  
15       measuring the label detectably bound to each probe of said microarray.

23. A method of identifying exons in a eukaryotic genome, comprising:

20       algorithmically predicting at least one exon from genomic sequence of said eukaryote; and then detecting specific hybridization of detectably labeled nucleic acids to a single exon probe,  
wherein said detectably labeled nucleic acids are derived  
25       from mRNA from the HeLa cells or other human cervical epithelial cells of said eukaryote, said probe is a single exon probe having a fragment identical in sequence to, or complementary in sequence to, said predicted exon, said probe is included within a microarray according to claim  
30       12, and said fragment is selectively hybridizable at high stringency.

24. A method of assigning exons to a single gene, comprising:

35       identifying a plurality of exons from genomic

sequence according to the method of claim 23; and  
then

measuring the expression of each of said exons in a  
plurality of tissues and/or cell types using  
5 hybridization to single exon microarrays having a  
probe with said exon,

wherein a common pattern of expression of said exons in  
said plurality of tissues and/or cell types indicates that  
the exons should be assigned to a single gene.

10

25. A nucleic acid sequence as set out in any of SEQ ID  
Nos: 1 - 18,392 which encodes a peptide.

26. A peptide encoded by a sequence as set out in any of  
15 SEQ ID Nos: 1 - 18,392.

27. A peptide comprising a sequence as set out in any of  
SEQ ID Nos: 18,393 - 26,941.

20

Page 1 of 382  
Table 4  
Single Exon Probes Expressed in HELA Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
450	9709	18849	5.87				
899	10134	19296	11.93				
1052	10278		2.08				
1309	10525	19685	19.17				
1593	10806	19982	2.78				
1613	10826	20001	12.21				
1700	10912	20098	1.72				
1721	10933	20116	1.1				
1727	10939	20122	9.25				
1856	11063	20254	1.76				
1947	11151	20353	2.13				
2131	11330	20549	1.94				
2244	11439	20663	2.03				
3149	12384	21517	3.28				
3426	12651	21781	1				
3489	12713	21849	8.63				
3535	12758		0.67				
3637	12858	21977	0.97				
3923	13139		1.02				
4179	13383	22484	1.57				
4248	13451	22542	7.61				
4266	13469	22561	0.64				
4266	13469	22562	0.64				
4330	13531		1.28				
4386	13587	22689	0.79				
4854	14043	23137	1.05				
4899	14087		0.89				
5070	14250	23333	5.18				
5404	14632		5.28				
5488	14714		6.43				
5525	14632		4.42				
5546	14770	24137	3.03				
5669	18082	24282	1.69				
5688	14908	24301	1.91				

Page 2 of 382  
Table 4  
Single Exon Probes Expressed in HELA Cells

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6484	15681	25150	2.19				
6830	16123	25580	5.79				
7275	16494		2.73				
7422	16078	26126	1.85				
7598	16798		3.09				
7899	17115	26647	2.51				
7987	16432	25919	2.03				
7997	16432	25920	2.03				
8034	17170		2.59				
8748	17691		1.72				
9085	17892	23899	1.79				
9279	18041		1.22				
5639	14909	24302	15.7	9.9E+00	AJ239028.1	NT	Homo sapiens LSS gene, partial, exons 15, 16, 17 and 18
6458	15683	25134	2.2	9.8E+00	U32716.1	NT	Haemophilus influenzae Rd section 31 of 163 of the complete genome
2874	12112	21240	3.14	9.4E+00	AB043785.1	NT	Mus musculus AT3 gene for antithrombin, complete cds
6766	15981	25417	3.22	9.3E+00	P11210	SWISSPROT	IMMEDIATE-EARLY PROTEIN 1 (IE1) (IMMEDIATE-EARLY PHOSPHOPROTEIN PP89)
5326	14558	23629	2.48	9.1E+00	AF085609.1	NT	Leuciscus cephalus orientalis cytochrome b (cyt b) gene, partial cds; mitochondrial gene for mitochondrial product
5326	14558	23630	2.48	9.1E+00	AF085609.1	NT	Leuciscus cephalus orientalis cytochrome b (cyt b) gene, partial cds; mitochondrial gene for mitochondrial product
5676	14896	24288	5.52	8.9E+00	BE971806.1	EST_HUMAN	601851038R1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:3934592 3'
5824	15041	24444	2.15	8.7E+00	AB019788.1	NT	Cynops pyrrhogaster CpTbx3 premature mRNA, partial cds
5824	15041	24445	2.15	8.7E+00	AB019788.1	NT	Cynops pyrrhogaster CpTbx3 premature mRNA, partial cds
448	9700	18836	1.88	8.4E+00	5031804	NT	Homo sapiens insulin receptor substrate 1 (IRS1) mRNA
6896	15602	25068	2.76	8.1E+00	AJ131719.1	NT	Zea mays mRNA for legumain-like protease (see2a)
7728	16926		2.49	8.0E+00	P41820	SWISSPROT	BREFELDIN A RESISTANCE PROTEIN
6229	15410		1.77	7.5E+00	AL445065.1	NT	Thermoplasma acidophilum complete genome, segment 3/5
5572	14796	24170	4.33	7.4E+00	BF700517.1	EST_HUMAN	802128878F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:4285506 5'
6703	15898	25359	2.97	7.4E+00	P04929	SWISSPROT	HISTIDINE-RICH GLYCOPROTEIN PRECURSOR
6703	15898	25360	2.97	7.4E+00	P04929	SWISSPROT	HISTIDINE-RICH GLYCOPROTEIN PRECURSOR
2834	12172	21305	3.8	7.2E+00	L12051.1	NT	Lycopodium esculentum Mill. GTPase (SAR2) mRNA, complete cds
2834	12172	21306	3.8	7.2E+00	L12051.1	NT	Lycopodium esculentum Mill. GTPase (SAR2) mRNA, complete cds
6960	16138		11.08	7.1E+00	AL161596.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 91
7824	17137	26688	4.08	7.1E+00	P05850	SWISSPROT	HYPOTHETICAL 17.3 KDA PROTEIN IN MRDA-PHPB INTERGENIC REGION

Page 3 of 382  
Table 4  
Single Exon Probes Expressed in HELA Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7068	16245	25720	3.26	7.0E+00	P46810	SWISSPROT	ARGININE KINASE (AK)
7802	16995	26509	1.94	7.0E+00	Q22469	SWISSPROT	WD-40 REPEAT PROTEIN MS13
6553	15749	25210	5.33	6.9E+00	P35679	SWISSPROT	60S RIBOSOMAL PROTEIN L4 (L2)
7137	16314	25795	4.45	6.8E+00	Q03570	SWISSPROT	HYPOTHETICAL 157.0 KDA PROTEIN C38C10.5 IN CHROMOSOME III
7097	16274	25752	2.93	6.6E+00	Q9ZE07	SWISSPROT	URIDYLATE KINASE (UK) (URIDINE MONOPHOSPHATE KINASE) (UMP KINASE)
7097	16274	25763	2.93	6.6E+00	Q9ZE07	SWISSPROT	URIDYLATE KINASE (UK) (URIDINE MONOPHOSPHATE KINASE) (UMP KINASE)
7888	16887		2.54	6.6E+00	Q10309	SWISSPROT	PROBABLE CATION-TRANSPORTING ATPASE C8C3.05C
6824	16018	25483	6.58	6.5E+00	P03374	SWISSPROT	ENV POLYPROTEIN [CONTAINS: COAT PROTEIN GP52; COAT PROTEIN GP36]
5885	15102	24513	6.98	5.9E+00	AF155142.1	NT	Mus musculus mixed lineage kinase 3 (Mlck3) and two pore domain K <sup>+</sup> channel subunit (Kcnk6) genes, complete cds
3497	12721		0.84	5.8E+00	7681557	NT	Homo sapiens DESCI protein (DESC1), mRNA
8011	16446	25936	2.42	5.6E+00	Q55278	SWISSPROT	LYCOPENE BETA CYCLASE
7360	16576		1.76	5.5E+00	AF175425.1	NT	Mus musculus DNA methyltransferase (Dnmt1) gene, exons 30, 31, and 32
8010	16445	25935	3.03	5.5E+00	P11990	SWISSPROT	PNEUMOLYSIN (THIOL-ACTIVATED CYTOLYSIN)
8222	17352		1.85	5.5E+00	AL161571.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 67
4795	13984	23089	1.28	5.3E+00	L43126.1	NT	Bovine immunodeficiency-like virus surface envelope gene, 5' end of cds
6492	15689		3.71	5.3E+00	P54098	SWISSPROT	DNA POLYMERASE GAMMA (MITOCHONDRIAL DNA POLYMERASE CATALYTIC SUBUNIT)
8147	17278	26824	1.66	5.3E+00	Q27905	SWISSPROT	PROBABLE ANTIBACTERIAL PEPTIDE POLYPROTEIN PRECURSOR
7749	16945		2.12	5.2E+00	Q10138	SWISSPROT	HYPOTHETICAL 61.1 KD PROTEIN C23E2.03C IN CHROMOSOME I
7189	16366	25846	4.81	5.0E+00	AF162445.2	NT	Canis familiaris skeletal muscle chloride channel ClC-1 (CLCN1) mRNA, complete cds
7838	17030	26546	12.07	5.0E+00	Z83960.1	NT	Mycobacterium tuberculosis H37Rv complete genome; segment 103/162
4038	13248		12.96	4.8E+00	AF165255.1	NT	Eunice australis histone H3 (H3) gene, partial cds
6636	15831		4.93	4.8E+00	AW750067.1	EST_HUMAN	PMO-BT0547-310100-002-b04 BT0547 Homo sapiens cDNA
284	9568	18700	2.43	4.7E+00	BF240552.1	EST_HUMAN	601875654F1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:4099716 5'
295	9568	18700	2	4.7E+00	BF240552.1	EST_HUMAN	601875654F1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:4099716 5'
3241	12475	21606	1.02	4.7E+00	AL163280.2	NT	Homo sapiens chromosome 21 segment HS21C080
8131	17265	26809	1.9	4.5E+00	AE001044.1	NT	Archaeoglobus fulgidus section 63 of 172 of the complete genome
8235	17364	26802	1.67	4.5E+00	BF668841.1	EST_HUMAN	602123238F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4280216 5'
3005	12241	21371	0.96	4.4E+00	BF530893.1	EST_HUMAN	602072585F1 NCI_CGAP_Bm87 Homo sapiens cDNA clone IMAGE:4215284 5'
3005	12241	21372	0.96	4.4E+00	BF530893.1	EST_HUMAN	602072585F1 NCI_CGAP_Bm87 Homo sapiens cDNA clone IMAGE:4215284 5'
6268	15448	24887	2.48	4.3E+00	Y13402.1	NT	Plasmodium falciparum R26R+var1 gene, exon 1
7438	16847	26140	8.75	4.3E+00	AF240788.1	NT	Homo sapiens glutathione S-transferase theta 2 (GSTT2) and glutathione S-transferase theta 1 (GSTT1) genes, complete cds



Page 4 of 382  
Table 4  
Single Exon Probes Expressed in HELA Cells

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5448	14874		3.45	4.2E+00	P16444	SWISSPROT	MICROSOMAL DIPEPTIDASE PRECURSOR (MDP) (DEHYDROPEPTIDASE-1) (RENAL DIPEPTIDASE) (RDP)
5988	15270	24697	1.82	4.2E+00	P13983	SWISSPROT	EXTENSIN PRECURSOR (CELL WALL HYDROXYPROLINE-RICH GLYCOPROTEIN)
5988	15270	24698	1.82	4.2E+00	P13983	SWISSPROT	EXTENSIN PRECURSOR (CELL WALL HYDROXYPROLINE-RICH GLYCOPROTEIN)
6757	15952	25410	8.13	4.2E+00	AI060013.1	EST_HUMAN	wf67g03.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2360692 3'
6363	15543	24998	7.72	4.1E+00	O23810	SWISSPROT	YY1 PROTEIN PRECURSOR
6409	15590	25050	3.79	4.1E+00	P28964	SWISSPROT	GENE 68 PROTEIN
6409	15590	25051	3.79	4.1E+00	P28964	SWISSPROT	GENE 68 PROTEIN
6430	15627	25092	4.55	4.1E+00	U57503.1	NT	Pan troglodytes novel repetitive solo LTR element in the RNU2 locus
7482	16670		2.88	4.1E+00	P08716	SWISSPROT	HYPOTHETICAL PROTEIN HVLFI
7543	16748		15.02	4.1E+00	BE885880.1	EST_HUMAN	601507510F1 NIH_MGC_71.Homo sapiens cDNA clone IMAGE:3908051 5'
3520	12744		0.69	4.0E+00	P38229	SWISSPROT	GLC7-INTERACTING PROTEIN 1
8009	16444	25934	1.69	4.0E+00	P14546	SWISSPROT	CYTOCHROME C OXIDASE POLYPEPTIDE III
8082	17217	26751	4.02	4.0E+00	P07564	SWISSPROT	GENOME POLYPROTEIN [CONTAINS: CAPSID PROTEIN C (CORE PROTEIN); MATRIX PROTEIN (ENVELOPE GLYCOPROTEIN M); MAJOR ENVELOPE PROTEIN E; NONSTRUCTURAL PROTEINS NS1, NS2A, NS2B, NS4A AND NS4B; HELICASE (NS3); RNA-DIRECTED RNA POLYMERASE (NS5)]
8082	17217	26752	4.02	4.0E+00	P07564	SWISSPROT	GENOME POLYPROTEIN [CONTAINS: CAPSID PROTEIN C (CORE PROTEIN); MATRIX PROTEIN (ENVELOPE GLYCOPROTEIN M); MAJOR ENVELOPE PROTEIN E; NONSTRUCTURAL PROTEINS NS1, NS2A, NS2B, NS4A AND NS4B; HELICASE (NS3); RNA-DIRECTED RNA POLYMERASE (NS5)]
3477	12701	21837	4.32	3.9E+00	X64518.1	NT	N. labeurum chitinase gene 50 for class I chitinase C
4312	13513		0.93	3.9E+00	AF055466.1	NT	Mus musculus seminal vesicle secretory protein 99 (MSVSP99) gene, promoter region
5515	14740	24105	2.78	3.9E+00	BE814357.1	EST_HUMAN	MRO-BN0070-300500-02B-105 BN0070 Homo sapiens cDNA
5515	14740	24106	2.78	3.9E+00	BE814357.1	EST_HUMAN	MRO-BN0070-300500-02B-105 BN0070 Homo sapiens cDNA
6029	15237	24660	4.25	3.9E+00	P39298	SWISSPROT	HYPOTHETICAL TRANSCRIPTIONAL REGULATOR IN AIDS-RPSF INTERGENIC REGION
6238	15419	24859	3.77	3.9E+00	M23907.1	NT	Human MHC class II lymphocyte antigen (DPw4-beta-1) gene, exon 2
6566	15762	25225	2.27	3.8E+00	X65865.1	NT	X.laavis mRNA for M4 muscarinic receptor
7929	16405	25689	3.21	3.9E+00	Y18000.1	NT	Homo sapiens NF2 gene
2593	11779		1.77	3.8E+00	AE001562.1	NT	Helicobacter pylori, strain J99 section 123 of 132 of the complete genome
3996	13209	22314	12.62	3.7E+00	AL161539.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 39
7969	17148	26683	2.5	3.7E+00	BF669279.1	EST_HUMAN	602120551F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:4277748 5'
7969	17148	26684	2.5	3.7E+00	BF669279.1	EST_HUMAN	602120551F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:4277748 5'
8390	17471		1.73	3.7E+00	AB013746.3	NT	Gallus gallus mRNA for hypoxia-inducible factor-1 alpha, complete cds

Page 5 of 382  
Table 4  
Single Exon Probes Expressed in HELA Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
600	9847	18865	3.46	3.6E+00	AV761055.1	EST_HUMAN	AV761055 MDS Homo sapiens cDNA clone MDSBUE10 5'
4812	14001		0.96	3.6E+00	AL161472.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 2
6667	15862	25321	4.86	3.6E+00	AE004447.1	NT	Pseudomonas aeruginosa PA01, section 8 of 529 of the complete genome
6667	15862	25322	4.86	3.6E+00	AE004447.1	NT	Pseudomonas aeruginosa PA01, section 8 of 529 of the complete genome
							Escherichia coli glycerophosphate dehydrogenase (glpD) gene, partial cds; and the translation start site has been verified (glpE), the translation start site has been verified (glpG), and repressor protein (glpR) genes, complete cds
7430	16640		4.12	3.6E+00	M96795.1	NT	Cryptosporidium felis heat shock protein 70 (HSP70) gene, partial cds
3214	12448	21580	1.13	3.5E+00	AF221538.1	NT	Brassica napus RPBSd mRNA, complete cds
1501	10714	19886	2.55	3.4E+00	AF254577.1	NT	DNA-DIRECTED RNA POLYMERASE II LARGEST SUBUNIT
6237	15418	24858	2.38	3.4E+00	P04052	SWISSPROT	Saccharomyces cerevisiae MSS1 gene, complete cds
7155	16332	25815	3.86	3.4E+00	AF013167.1	NT	Homo sapiens DiGeorge syndrome critical region, centromeric end
8063	17198	26736	2.13	3.4E+00	L77570.1	NT	D. rerio zp-50 POU gene
507	9759	18868	1.73	3.2E+00	X88422.1	NT	D. rerio zp-50 POU gene
4004	9759	18868	0.95	3.2E+00	X88422.1	NT	Homo sapiens carcinoembryonic antigen-related cell adhesion molecule 1 (biliary glycoprotein) (CEACAM1), mRNA
4739	13930	23034	1.09	3.2E+00	4502404	NT	PHOSPHOGLYCERATE KINASE, CYTOSOLIC
5491	14717	24074	2.88	3.2E+00	P12783	SWISSPROT	PHOSPHOGLYCERATE KINASE, CYTOSOLIC
5491	14717	24075	2.88	3.2E+00	P12783	SWISSPROT	PHOSPHOGLYCERATE KINASE, CYTOSOLIC
5780	15007	24410	1.78	3.2E+00	P18931	SWISSPROT	NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 4
5780	15007	24411	1.78	3.2E+00	P18931	SWISSPROT	NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 4
6405	15586	25044	2.53	3.2E+00	Y13655.1	NT	Chlamydomonas reinhardtii chloroplast DNA for rps9, ycf4, ycf3, rps18 genes
6405	15586	25045	2.53	3.2E+00	Y13655.1	NT	Chlamydomonas reinhardtii chloroplast DNA for rps9, ycf4, ycf3, rps18 genes
6773	15968		9.1	3.2E+00	P13061	SWISSPROT	PERIPLASMIC [NIFE] HYDROGENASE SMALL SUBUNIT (NIFE HYDROGENLYASE SMALL CHAIN)
7122	16299	26781	3.21	3.2E+00	AB018081.2	NT	Onyias latipes OIG08 gene for guanylyl cyclase C, complete cds
7650	16850	26348	1.75	3.2E+00	AJ235270.1	NT	Rickettsia prowazekii strain Macrid E, complete genome, segment 1/4
8350	17444		1.93	3.2E+00	L33836.1	NT	Sus scrofa choline acetyltransferase gene, promoter region
5602	14826	24202	2.1	3.1E+00	Q10135	SWISSPROT	HYPOPHOSPHATE 142.5 KD PROTEIN C23E2.02 IN CHROMOSOME 1
6656	15651	25309	4.85	3.1E+00	P49894	SWISSPROT	TYPE I IODOETHYRONE DEIODINASE (TYPE-I DEIODINASE) (DIOI) (TYPE 1 DI) (SDI)
6656	15651	25310	4.85	3.1E+00	P49894	SWISSPROT	TYPE I IODOETHYRONE DEIODINASE (TYPE-I DEIODINASE) (DIOI) (TYPE 1 DI) (SDI)
							GLUTAMATE [NMDA] RECEPTOR SUBUNIT EPSILON 3 PRECURSOR (N-METHYL D-ASPARTATE RECEPTOR SUBTYPE 2C) (NR2C) (NMDAR2C)
6842	16047		3.67	3.1E+00	Q14957	SWISSPROT	DEOXYHYPUISINE SYNTHASE (DHS)
7178	16355	25833	7.65	3.1E+00	P49365	SWISSPROT	DEOXYHYPUISINE SYNTHASE (DHS)

Page 6 of 382  
Table 4  
Single Exon Probes Expressed in HELA Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7999	16434		2.92	3.1E+00	P33515	SWISSPROT	GENOME POLYPROTEIN [CONTAINS: CAPSID PROTEIN C (CORE PROTEIN); MATRIX PROTEIN (ENVELOPE PROTEIN M); MAJOR ENVELOPE PROTEIN E; NONSTRUCTURAL PROTEINS NS1, NS2A, NS2B, NS4A AND NS4B; HELICASE (NS3); RNA-DIRECTED RNA POLYMERASE (NS5)]
8016	17155		3.7	3.1E+00	S56660.1	NT	retinoid acid nuclear receptor isoform beta 2 [mice, embryonal carcinoma cell line, PCC7-MZ1, mRNA, 2671 nt]
6144	15328		12.2	3.0E+00	P18406	SWISSPROT	CYR61 PROTEIN PRECURSOR (3CH61)
7241	16461	25950	1.7	3.0E+00	Q16181	SWISSPROT	CDC10 PROTEIN HOMOLOG
7579	16784	26277	6.87	3.0E+00	P51842	SWISSPROT	RETINAL GUANYLYL CYCLASE 2 PRECURSOR (GUANYLYL CYCLASE 2F, RETINAL) (RETGC-2) (ROD OUTER SEGMENT MEMBRANE GUANYLYL CYCLASE 2) (ROS-GC2) (GUANYLYL CYCLASE F) (GC-F)
7579	16784	26278	6.87	3.0E+00	P51842	SWISSPROT	RETINAL GUANYLYL CYCLASE 2 PRECURSOR (GUANYLYL CYCLASE 2F, RETINAL) (RETGC-2) (ROD OUTER SEGMENT MEMBRANE GUANYLYL CYCLASE 2) (ROS-GC2) (GUANYLYL CYCLASE F) (GC-F)
1979	11183	20391	2.21	2.9E+00	AE002225.2	NT	Chlamydia pneumoniae AR39, section 53 of 94 of the complete genome
6046	15214	24634	1.71	2.9E+00	Z38879.1	NT	F. pringlei gdsA gene for P-protein of the glycine cleavage system
6170	15352	24789	4.54	2.9E+00	O14514	SWISSPROT	BRAIN-SPECIFIC ANGIOGENESIS INHIBITOR 1 PRECURSOR
6170	15352	24790	4.54	2.9E+00	O14514	SWISSPROT	BRAIN-SPECIFIC ANGIOGENESIS INHIBITOR 1 PRECURSOR
6279	15459	24900	5.32	2.9E+00	P46589	SWISSPROT	ADHERENCE FACTOR (ADHESION AND AGGREGATION MEDIATING SURFACE ANTIGEN)
1456	10669	18842	4.19	2.8E+00	AF186398.1	NT	Buxus harlandii malate K (malK) gene, partial cds; chloroplast gene for chloroplast product
1610	10823		2.03	2.8E+00	AL161552.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 52
6210	15391	24835	4.9	2.8E+00	8393724	NT	Mus musculus endomucin (LOC53423), mRNA
236	9515	18643	13.15	2.7E+00	8679306	NT	Mus musculus per-hexamer repeat gene 3 (Pbx3), mRNA
238	9515	18644	13.15	2.7E+00	8679306	NT	Mus musculus per-hexamer repeat gene 3 (Pbx3), mRNA
5487	14693	24046	1.64	2.7E+00	L14005.1	NT	Homo sapiens apoa polymorphism Kringle IV gene, exons 1 and 2
4677	13871	22670	5.06	2.6E+00	AF068749.1	NT	Mus musculus sphingosine kinase (SPHK1b) mRNA, complete cds
5465	14691	24043	2.01	2.6E+00	8755601	NT	Mus musculus SRY-box containing gene 13 (Sox13), mRNA
5465	14691	24044	2.01	2.6E+00	8755601	NT	Mus musculus SRY-box containing gene 13 (Sox13), mRNA
5582	14806		2.36	2.6E+00	Y17062.1	NT	Mycobacterium fortuitum furA II gene
6376	15556		5.52	2.6E+00	AF235502.1	NT	Mus musculus SH2-containing inositol 5-phosphatase (Ship) gene, exons 18 through 27, and complete cds
6980	16158	25630	2.9	2.6E+00	AL161540.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 40
7597	16800	26292	1.74	2.6E+00	AF143675.1	NT	Hantavirus Z10 segment M G1/G2 glycoprotein (Z10) gene, complete cds
9012	18264		2.67	2.6E+00	11419220	NT	Homo sapiens ATP-binding cassette, sub-family B (MDR/TP), member 4 (ABCB4), mRNA
1460	10873	19845	2.95	2.5E+00	AJ271844.1	NT	Aspergillus nidulans recQ gene for DNA helicase, exons 1-4

Page 7 of 382  
Table 4  
Single Exon Probes Expressed in HELA Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1460	10673	19848	2.95	2.5E+00	AJ271844.1	NT	Aspergillus nidulans recQ gene for DNA helicase, exons 1-4
5578	14802	24174	2.14	2.5E+00	P13485	SWISSPROT	TEICHOIC ACID BIOSYNTHESIS PROTEIN F
5578	14802	24175	2.14	2.5E+00	P13485	SWISSPROT	TEICHOIC ACID BIOSYNTHESIS PROTEIN F
8347	17442		2.33	2.5E+00	AF280685.1	NT	Mus musculus EIF4H gene, partial cds; LIMK1 gene, complete cds; and ELN gene, partial cds
2875	12212	21350	1.58	2.4E+00	M24282.1	NT	Chicken alpha-3 collagen type VI mRNA, 3' and
4928	14116	23212	7.8	2.4E+00	4503352	NT	Homo sapiens double C2-like domains, alpha (DOC2A) mRNA
5660	14883	24271	4.18	2.4E+00	P02843	SWISSPROT	VITELLOGENIN I PRECURSOR (YOLK PROTEIN 1)
8632	16728		2.7	2.4E+00	AE001486.1	NT	Helicobacter pylori, strain J99 section 47 of 132 of the complete genome
8728	15923	25382	12.95	2.4E+00	P24091	SWISSPROT	ENDOCHITINASE B PRECURSOR (CHN-B)
7149	16326		6.73	2.4E+00	P09099	SWISSPROT	XYLOLOSE KINASE (XYLOKINASE)
7175	16352	25829	2.32	2.4E+00	BE328702.1	EST_HUMAN	h63706.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:3133187 3'
7175	16352	25830	2.32	2.4E+00	BE328702.1	EST_HUMAN	h63706.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:3133187 3'
7645	16845	26343	1.91	2.4E+00	Y14079.1	NT	Bacillus subtilis chromosomal DNA, region 75 degrees: glpFKD operon and downstream
7898	17114	26646	2.65	2.4E+00	AF158652.2	NT	Frederia x ananassa cytosolic ascorbate peroxidase (ApxSC) gene, ApxSC-c allele, complete cds
1280	10475	19837	10.92	2.3E+00	Z48724.1	NT	G. domesticus artificial single chain antibody gene (L3)
4101	13308		1.51	2.3E+00	AJ401081.1	NT	Bos taurus partial cytb gene for cytochrome b
5284	14437	23511	2.28	2.3E+00	U12024.1	NT	Asylanex mexicanus green opsin gene (g101) gene, complete cds
8277	15457	24898	2.33	2.3E+00	6878554	NT	Rattus norvegicus ATPase, Ca++ transporting, ubiquitous (Atp2a3), mRNA
6330	18388		3.14	2.3E+00	P07189	SWISSPROT	MAJOR CENTROMERE AUTOANTIGEN B (CENTROMERE PROTEIN B) (CENP-B)
7380	16598	26083	1.72	2.3E+00	Q07076	SWISSPROT	ANNEXIN VII (SYNEXIN)
8247	17376	26910	2.87	2.3E+00	BF541987.1	EST_HUMAN	602069121F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:4068173 5'
8247	17376	26911	2.87	2.3E+00	BF541987.1	EST_HUMAN	602069121F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:4068173 5'
8578	17594	24002	4.79	2.3E+00	BE885237.1	EST_HUMAN	601433673F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3918643 5'
3993	13207	22313	0.95	2.2E+00	AF020528.1	NT	Magnaporthe grisea Class IV chitin synthase (chs4) gene, complete cds
4302	13503	22599	3.87	2.2E+00	D87071.1	NT	Rat gene for regucalcin, exon1 (non-coding exon)
4302	13503	22600	3.87	2.2E+00	D87071.1	NT	Rat gene for regucalcin, exon1 (non-coding exon)
							SORTILIN-RELATED RECEPTOR PRECURSOR (SORTING PROTEIN-RELATED RECEPTOR CONTAINING LDLR CLASS A REPEATS) (SORLA-1) (LOW-DENSITY LIPOPROTEIN RECEPTOR RELATIVE WITH 11 LIGAND-BINDING REPEATS) (LDLR RELATIVE WITH 11 LIGAND-BINDING REPEATS) (LR11) (>
5380	14590	23667	10.24	2.2E+00	O88307	SWISSPROT	

Page 8 of 382  
Table 4  
Single Exon Probes Expressed in HELA Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5360	14590	23668	10.24	2.2E+00	Q88307	SWISSPROT	SORTILIN-RELATED RECEPTOR PRECURSOR (SORTING PROTEIN-RELATED RECEPTOR CONTAINING LDLR CLASS A REPEATS) (MSORLA-1) (LOW-DENSITY LIPOPROTEIN RECEPTOR RELATIVE WITH 11 LIGAND-BINDING REPEATS) (LDLR RELATIVE WITH 11 LIGAND-BINDING REPEATS) (LR11) (>)
5695	14915	24309	9.16	2.2E+00	BE250383.1	EST_HUMAN	600943401T1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:2959777 3'
5815	15032	24433	4.17	2.2E+00	Q00335	SWISSPROT	MINOR VIRION STRUCTURAL PROTEIN MU-2
5932	15148	24558	2.98	2.2E+00	P51459	SWISSPROT	INSULIN-LIKE GROWTH FACTOR II PRECURSOR (IGF-II) (SOMATOMEDIN A)
6087	14514		3.74	2.2E+00	AA594574.1	EST_HUMAN	n195b02.s1 NCI_CGAP_Cot10 Homo sapiens cDNA clone IMAGE:1058379 3'
6338	15518	24966	18.81	2.2E+00	AA449012.1	EST_HUMAN	z05g10.f1 Soares_t0101.f09 Homo sapiens cDNA clone IMAGE:785634 5'
6864	16054		19.58	2.2E+00	BE741678.1	EST_HUMAN	601594733F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3948581 5'
6946	18075		2.79	2.2E+00	Q04706	SWISSPROT	TRANSPONSON TY1 PROTEIN A
7090	16267	25743	2.51	2.2E+00	AI290373.1	EST_HUMAN	q165b03.x1 Soares_placenta_816c9weeks_2N8HP81c9W Homo sapiens cDNA clone IMAGE:1893965 3' similar to gb:Y00433 GLUTATHIONE PEROXIDASE (HUMAN);
7090	16267	25744	2.51	2.2E+00	AI290373.1	EST_HUMAN	q165b03.x1 Soares_placenta_816c9weeks_2N8HP81c9W Homo sapiens cDNA clone IMAGE:1893965 3' similar to gb:Y00433 GLUTATHIONE PEROXIDASE (HUMAN);
7109	16286	25767	2.44	2.2E+00	BF246782.1	EST_HUMAN	601855591F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4075391 5'
7200	16377	25858	3.22	2.2E+00	AF183416.1	NT	Homo sapiens ovarian granulosa cell 13.0 kDa protein HGR74 homolog mRNA, complete cds
7977	16412	25898	4.63	2.2E+00	P07911	SWISSPROT	UROMODULIN PRECURSOR (TAMM-HORSFALL URINARY GLYCOPROTEIN) (THP)
8138	17271	26816	4.81	2.2E+00	P10407	SWISSPROT	EARLY E1A 28 KD PROTEIN
876	11971	18945	8.07	2.1E+00	AF132812.2	NT	Mus musculus pre-T cell receptor alpha gene, enhancer region and upstream region
2978	12215	21351	1.86	2.1E+00	AF208532.1	NT	Homo sapiens fatty acid omega-hydroxylase CYP4A11 (CYP4A11) gene, complete cds
3565	12788		1.24	2.1E+00	AW449368.1	EST_HUMAN	UHH-B13-ekt-s-08-0-JJ.s1 NCI_CGAP_Sub5 Homo sapiens cDNA clone IMAGE:2734550 3'
6000	15282	24715	3.28	2.1E+00	O70159	SWISSPROT	ALPHA-2HS-GLYCOPROTEIN PRECURSOR (FETUIN-A)
6103	15197	24615	5.28	2.1E+00	N28575.1	EST_HUMAN	y08a10.s1 Soares_melanocyte_2N8HM Homo sapiens cDNA clone IMAGE:270818 3' similar to gb:M55654
1204	10423	19578	1.81	2.0E+00	AF180527.1	NT	TRANSCRIPTION INITIATION FACTOR TFIIID (HUMAN);
1204	10423	19579	1.81	2.0E+00	AF180527.1	NT	Homo sapiens p22Dokdel (DOKDEL) mRNA, complete cds
1343	10557	19723	0.84	2.0E+00	AF204927.1	NT	Homo sapiens p22Dokdel (DOKDEL) mRNA, complete cds
1554	10768		2.32	2.0E+00	P25582	SWISSPROT	PUTATIVE RNA METHYLTRANSFERASE SPB1
2117	11316	20533	6.95	2.0E+00	Z78279.1	NT	R.novgicus mRNA for collagen alpha1 type I
2117	11316	20534	6.95	2.0E+00	Z78279.1	NT	R.novgicus mRNA for collagen alpha1 type I
4078	13288	22386	1.88	2.0E+00	AW664496.1	EST_HUMAN	h13c05.x1 NCI_CGAP_GL1 Homo sapiens cDNA clone IMAGE:2972168 3' similar to gb:X01677 GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE, LIVER (HUMAN);

Page 9 of 382  
Table 4  
Single Exon Probes Expressed in HELA Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4078	13288	22387	1.88	2.0E+00	AW684496.1	EST_HUMAN	h13cd5.x1 NCI_CGAP_GU1 Homo sapiens cDNA clone IMAGE:2972168 3' similar to gb:X01677
8472	15689	25138	6.44	2.0E+00	AB008676.1	NT	GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE, LIVER (HUMAN);
8472	15669	25139	6.44	2.0E+00	AB008676.1	NT	Escherichia coli 0157 DNA, map position at 46 min., complete cds
8472	15669	25140	6.44	2.0E+00	AB008676.1	NT	Escherichia coli 0157 DNA, map position at 46 min., complete cds
8752	15947	25405	5.02	2.0E+00	F31500.1	EST_HUMAN	HSPD22703 HM3 Homo sapiens cDNA clone s4000117B08
8824	18222	23694	6.38	2.0E+00	5834843	NT	Gallus gallus mitochondrion, complete genome
5489	14716	24071	4.76	1.9E+00	8754389	NT	Mus musculus inositol 1,4,5-trisphosphate receptor 1 (ltp1), mRNA
5489	14715	24072	4.76	1.9E+00	8754389	NT	Mus musculus inositol 1,4,5-trisphosphate receptor 1 (ltp1), mRNA
5979	15193		2.35	1.9E+00	Q63627	SWISSPROT	CTD-BINDING SR-LIKE PROTEIN RA4
8617	15813	25271	2.81	1.9E+00	P02467	SWISSPROT	COLLAGEN ALPHA 2(I) CHAIN PRECURSOR
8617	15813	25272	2.81	1.9E+00	P02467	SWISSPROT	COLLAGEN ALPHA 2(I) CHAIN PRECURSOR
8672	15867		2.61	1.9E+00	BF360206.1	EST_HUMAN	CM3-MT0114-010900-323-h12 MT0114 Homo sapiens cDNA
3058	12294	21419	2.04	1.8E+00	P21004	SWISSPROT	PROTEIN B8 PRECURSOR
3084	12320	21441	2.25	1.8E+00	U04356.1	NT	Synechococcus sp. PCC7942 copper transporting P-ATPase (ctaA) and ATP synthase epsilon subunit (atpE) genes, complete cds
3084	12320	21442	2.25	1.8E+00	U04356.1	NT	Synechococcus sp. PCC7942 copper transporting P-ATPase (ctaA) and ATP synthase epsilon subunit (atpE) genes, complete cds
5599	14823		1.79	1.8E+00	P18502	SWISSPROT	HEDGEHOG RECEPTOR (PATCHED PROTEIN)
5709	14828	24323	1.93	1.8E+00	BF311999.1	EST_HUMAN	601897854F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4127364 5'
6733	15928	25387	3.27	1.8E+00	O43281	SWISSPROT	EMBRYONAL FYN-ASSOCIATED SUBSTRATE (HEFS)
7163	16340		2.67	1.8E+00	AF111849.1	NT	Homo sapiens PRO0530 mRNA, complete cds
8709	18195		5.06	1.8E+00	AF314254.1	NT	Chlamydomonas reinhardtii alternative oxidase 1 (AOX1) gene, nuclear gene encoding mitochondrial protein
8792	17719		3.48	1.8E+00	9506404	NT	Rattus norvegicus Actin-related protein complex 1b (Arpct1b), mRNA
9100	18095	23803	1.32	1.8E+00	BF212412.1	EST_HUMAN	601813714F1 NIH_MGC_54 Homo sapiens cDNA clone IMAGE:4048251 5'
9285	18043		1.45	1.8E+00	BF316805.1	EST_HUMAN	601903309F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4135586 5'
1116	10340	19480	2.08	1.7E+00	Q60114	SWISSPROT	LEVANSUCRASE (BETA-D-FRUCTOFURANOSYL TRANSFERASE)(SUCROSE 6-FRUCTOSYL TRANSFERASE)
2238	11431	20658	2.49	1.7E+00	AL163280.2	NT	Homo sapiens chromosome 21 segment HS21C080
2340	11533	20756	2.43	1.7E+00	AI141067.1	EST_HUMAN	oz43h05.x1 Soares_NHMPu_S1 Homo sapiens cDNA clone IMAGE:1678137 3'
5665	14887	24277	3.48	1.7E+00	Q91TR8	SWISSPROT	COUP TRANSCRIPTION FACTOR 1 (COUP-TF1)(COUP-TF I)
8817	18074	25476	3.96	1.7E+00	O60479	SWISSPROT	HOMEBOX PROTEIN DLX-3
8817	18074	25477	3.96	1.7E+00	O60479	SWISSPROT	HOMEBOX PROTEIN DLX-3

Page 10 of 382  
Table 4  
Single Exon Probes Expressed in HELA Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8124	17258	26800	2.25	1.7E+00	W22424.1	EST_HUMAN	67B7 Human retina cDNA Tsp5091-cleaved sublibrary Homo sapiens cDNA not directional
8660	17637	23975	1.61	1.7E+00	AI678443.1	EST_HUMAN	tu82407.x1 NCL_CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2257549.3 similar to contains MSR1.H1
9178	17689	23857	2.33	1.7E+00	AI198573.1	EST_HUMAN	q550b01.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1753417.3 similar to contains L1.H1.L1
2002	11205	20418	14.44	1.6E+00	AF198339.1	NT	Homo sapiens lens epithelium-derived growth factor gene, alternatively spliced, complete cds
2010	11213	20422	3.58	1.6E+00	AF077374.1	NT	Homo sapiens small proline-rich protein (SPRR3) gene, exons 1, 2, and 3 and complete cds
2016	11218	20427	1.35	1.6E+00	Y11344.1	NT	Mus musculus ST6GalNAcII gene, exon 2
2248	11443		1.07	1.6E+00	X88373.1	NT	B.napus gene encoding endo-polygalacturonase
2915	12153	21288	1.34	1.6E+00	W58428.1	EST_HUMAN	zd25f01.r1 Soares_fetal_heart_NH-H19W Homo sapiens cDNA clone IMAGE:341689.5 similar to
4009	13221		6.38	1.6E+00	BF570077.1	EST_HUMAN	gb: D29805 N-ACETYLACTOSAMINE SYNTHASE (HUMAN);
4345	13547	22638	1.97	1.6E+00	AF155827.1	NT	60218605T1 NIH_MGC_45 Homo sapiens cDNA clone IMAGE:4310591.3
4345	13547	22639	1.87	1.6E+00	AF155827.1	NT	Homo sapiens proliferation-associated SNF2-like protein (SMARCA6) mRNA, complete cds
5027	14212	23285	0.63	1.6E+00	AF075394.1	NT	Homo sapiens cytochrome c oxidase subunit I (COI) gene, mitochondrial gene encoding mitochondrial protein, partial cds
5027	14212	23298	0.63	1.6E+00	AF075394.1	NT	Urotauthis chinensis cytochrome c oxidase subunit I (COI) gene, mitochondrial gene encoding mitochondrial protein, partial cds
5113	14293	23380	1.96	1.6E+00	Y11344.1	NT	Mus musculus ST6GalNAcII gene, exon 2
5113	14293	23381	1.96	1.6E+00	Y11344.1	NT	Mus musculus ST6GalNAcII gene, exon 2
5583	14807	24180	2.43	1.6E+00	L04808.1	NT	Brachydanio rerio MHC class II DA-beta-2701 gene, 3' end
6182	15364	24804	2.64	1.6E+00	BE697287.1	EST_HUMAN	RC0-CT0415-200700-032-c10 CT0415 Homo sapiens cDNA
6590	15788	25245	3.83	1.6E+00	AJ297131.1	NT	Mus musculus SIL, MAP_17, CYP_a, SCL & CYP_b genes
7420	14848	24227	6.93	1.6E+00	AF005631.1	NT	Homo sapiens transglutaminase type I (Tgase1) gene, promoter region
8197	17329	26871	3.2	1.6E+00	AF104313.1	NT	Homo sapiens unknown mRNA
9221	18000		1.43	1.6E+00	AV764043.1	EST_HUMAN	AV764043 MDS Homo sapiens cDNA clone MDSDAH08.5
34	9330	18435	5.46	1.5E+00	U53449.1	NT	Rattus norvegicus jun dimerization protein 2 (jdp-2) mRNA, complete cds
237	9516	18645	2.45	1.5E+00	AEO2201.2	NT	Chlamydomonas reinhardtii AR39, section 32 of 94 of the complete genome
627	9872		1.95	1.5E+00	6752861	NT	Mus musculus a disintegrin and metalloproteinase domain (ADAM) 15 (metagardim) (Adam15), mRNA
1882	11089	20280	3.71	1.5E+00	AF275265.1	NT	Mus musculus receptor protein tyrosine phosphatase-rho (Ptptr) gene, exons 10 and 11 and partial cds
2373	11566	20787	2.06	1.5E+00	AJ131402.1	NT	Polyoma virus A RNA complete genome, isolate U
2481	11871	20889	1.63	1.5E+00	6678350	NT	Mus musculus T-cell lymphoma invasion and metastasis 1 (Tiam1), mRNA

Page 11 of 382  
Table 4  
Single Exon Probes Expressed in HELA Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3103	11568	20787	1.67	1.5E+00	AJ131402.1	NT	Potato virus A RNA complete genome, isolate U
3353	12581	21721	0.82	1.5E+00	AE001946.1	NT	Delinococcus reidiolurans R1 section 82 of 229 of the complete chromosome 1
5029	15048	24450	2.76	1.5E+00	R17879.1	EST_HUMAN	yg10602.r1 Soares infant brain 1N1B Homo sapiens cDNA clone IMAGE:31693 5'
6148	15332	24768	18.56	1.5E+00	P47179	SWISSPROT	HYPOTHETICAL 118.4 KD PROTEIN IN BAT2-DAL5 INTERGENIC REGION PRECURSOR
8148	15332	24769	18.56	1.5E+00	P47179	SWISSPROT	HYPOTHETICAL 118.4 KD PROTEIN IN BAT2-DAL5 INTERGENIC REGION PRECURSOR
7026	16203	25680	11.13	1.5E+00	BF378754.1	EST_HUMAN	RCO-TN0078-150900-034-g05 TN0078 Homo sapiens cDNA
7132	16309	25780	3.83	1.5E+00	AA017989.1	EST_HUMAN	ze388g08.r1 Soares retina N2b4HR Homo sapiens cDNA clone IMAGE:361306 5'
7132	16309	25791	3.83	1.5E+00	AA017989.1	EST_HUMAN	ze388g08.r1 Soares retina N2b4HR Homo sapiens cDNA clone IMAGE:361308 5'
7937	17077	26605	4.16	1.5E+00	AL134187.1	EST_HUMAN	DKFZp547P243_s1 547 (synonym: hibr1) Homo sapiens cDNA clone DKFZp547P243 3'
8074	17209		8.7	1.5E+00	X07380.1	NT	Malze mitochondrial tRNA-Ser gene and tRNA-Pha pseudogene
8494	17537		1.33	1.5E+00	6753287	NT	Mus musculus caspase 8 associated protein 2 (Casp8ap2), mRNA
8653	18290	23687	1.24	1.5E+00	D63480.1	NT	Human mRNA for KIAA0146 gene, partial cds
8885	17780		3.71	1.5E+00	AL445065.1	NT	Thermoplasma acidophilum complete genome; segment 3/5
8988	17852		1.25	1.5E+00	6878492	NT	Rattus norvegicus 5-Lipoxygenase (Alox5), mRNA
31	9327	18431	1.22	1.4E+00	7661685	NT	Homo sapiens DKFZP586M0122 protein (DKFZP586M0122), mRNA
31	9327	18432	1.22	1.4E+00	7661685	NT	Homo sapiens DKFZP586M0122 protein (DKFZP586M0122), mRNA
1711	10923	20108	1.26	1.4E+00	H19859.1	EST_HUMAN	yn57e03.r1 Soares adult brain N2b5HB55Y Homo sapiens cDNA clone IMAGE:172540 5'
2242	11437		1.38	1.4E+00	AF053357.1	NT	Helicobacter pylori glutamine synthetase (glnA) gene, complete cds
2302	11496		9.69	1.4E+00	U67922.1	NT	Ovis aries p10n protein gene, complete cds
2629	11812	21030	1.38	1.4E+00	X74463.1	NT	Human papillomavirus type 7 genomic DNA
2729	11808	21122	2.38	1.4E+00	AF064564.2	NT	Fugu rubripes neurofibromatosis type 1 (NF1), A-kinase anchor protein (AKAP84), BAW protein (BAW), and WSB1 protein (WSB1) genes, complete cds
2729	11808	21123	2.38	1.4E+00	AF064564.2	NT	Fugu rubripes neurofibromatosis type 1 (NF1), A-kinase anchor protein (AKAP84), BAW protein (BAW), and WSB1 protein (WSB1) genes, complete cds
4243	13446	22536	1.72	1.4E+00	AW900455.1	EST_HUMAN	WSB1 protein (WSB1) genes, complete cds
4243	13446	22837	1.72	1.4E+00	AW900455.1	EST_HUMAN	GMO-NN1005-140300-288-108 NN1005 Homo sapiens cDNA
4557	12273	21401	1.2	1.4E+00	AE002324.2	NT	CMLydia muridarum, section 55 of 85 of the complete genome
4557	12273	21402	1.2	1.4E+00	AE002324.2	NT	CMLydia muridarum, section 55 of 85 of the complete genome
4584	13778		1.41	1.4E+00	BF681547.1	EST_HUMAN	602156887F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4297566 5'
5455	14681		5.66	1.4E+00	AB032983.1	NT	Homo sapiens mRNA for KIAA1157 protein, partial cds
5780	14998	24400	2.74	1.4E+00	Q13472	SWISSPROT	DNA TOPOISOMERASE III ALPHA
5784	18387		4.59	1.4E+00	AB020712.1	NT	Homo sapiens mRNA for KIAA0905 protein, complete cds
5832	15049	24454	2.62	1.4E+00	Q82777	SWISSPROT	SYNAPSIN II
5832	15049	24455	2.62	1.4E+00	Q82777	SWISSPROT	SYNAPSIN II



Page 12 of 382  
Table 4  
Single Exon Probes Expressed in HELA Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6203	15384	24826	2.21	1.4E+00	AJ133269.1	NT	Homo sapiens carvedin-1/2 locus, Contig1, D7S522, genes CAV2 (exons 1, 2a, and 2b), CAV1 (exons 1 and 2)
6715	15910		8.09	1.4E+00	AJ271735.1	NT	Homo sapiens Xq pseudautosomal region, segment 1/2
6827	16021	25487	5.92	1.4E+00	BE094867.1	EST_HUMAN	RC1-BT0313-301298-012-035 BT0313 Homo sapiens cDNA
7637	18837	26333	2.22	1.4E+00	AA195528.1	EST_HUMAN	z36609.r1 Soares NHMPu_S1 Homo sapiens cDNA clone IMAGE:865512 5' similar to contains element MER22 repetitive element;
7778	19973	28488	6.19	1.4E+00	AB006682.1	NT	Homo sapiens APECED mRNA for AIRE-1, complete cds
7843	17083	26611	3.76	1.4E+00	BE962107.2	EST_HUMAN	601655184R1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3845805 3'
7843	17083	26612	3.76	1.4E+00	BE962107.2	EST_HUMAN	601655184R1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3845805 3'
7885	17144	26677	2.89	1.4E+00	U30780.1	NT	Pneumocystis carinii f. sp. ratti guanine nucleotide binding protein alpha subunit (pcg1) gene, complete cds
7885	17144	26678	2.89	1.4E+00	U30780.1	NT	Pneumocystis carinii f. sp. ratti guanine nucleotide binding protein alpha subunit (pcg1) gene, complete cds
8491	18214		1.8	1.4E+00	AL161500.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 12
8899	18382		1.27	1.4E+00	11545836	NT	Homo sapiens cutaneous T-cell lymphoma tumor antigen se70-2 (SE70-2), mRNA
9287	18033		1.22	1.4E+00	AF224669.1	NT	Homo sapiens mannosidase, beta A, lysosomal (MANBA) gene, and ubiquitin-conjugating enzyme E2D 3 (UBE2D3) genes, complete cds
577	9826		1.79	1.3E+00	Z73840.1	NT	M.mucedo gene encoding 4-Dihydropyrimidin-thiopyran dehydrogenase
912	10147	19308	2.87	1.3E+00	AJ271192.1	NT	Cantharellus sp. partial 25S rRNA gene, isolate Tibet
1137	10360		17.3	1.3E+00	Y19213.1	NT	Homo sapiens putative psih-IbA pseudogene for hair keratin, exons 2 to 7
1304	10520	19679	11.83	1.3E+00	4507998	NT	Homo sapiens zinc finger protein 157 (ZNF157) mRNA
1304	10520	19680	11.83	1.3E+00	4507998	NT	Homo sapiens zinc finger protein 157 (ZNF157) mRNA
1364	10579		0.94	1.3E+00	U61730.2	NT	Cox lacryme-jobi dihydrodipicolinate synthase (dapA) gene, complete cds
1589	10802		1.91	1.3E+00	AE002338.2	NT	Chlamydia muridarum, section 66 of 85 of the complete genome
2515	11704		1.75	1.3E+00	BE968735.2	EST_HUMAN	601681233R1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3915945 3'
2890	12127	21260	0.62	1.3E+00	6755621	NT	Mus musculus alpha-spectrin 1, erythroid (Spn1), mRNA
3575	12798	21924					Fugu rubripes gamma-aminobutyric acid receptor beta subunit gene, partial cds; 55kd erythrocyte membrane protein (P55), synaptic vesicle-associated integral membrane protein (VAMP-1), procollagen C-proteinase enhancer protein (PCOLCE) genes, complete c>
5668	14888	24278	9.72	1.3E+00	AW362834.1	EST_HUMAN	PM0-CT0288-291199-004-108 CT0289 Homo sapiens cDNA
5668	14888	24278	9.72	1.3E+00	AW362834.1	EST_HUMAN	PM0-CT0288-291199-004-108 CT0289 Homo sapiens cDNA
6559	15765	25218	2.2	1.3E+00	AJ009812.1	NT	Sus scrofa plp gene
6919	16112		3.28	1.3E+00	AF042084.1	NT	Homo sapiens heparan glucosaminyl N-deacetylase/N-sulfotransferase-2 gene, complete cds
6924	16117	25582	2.21	1.3E+00	X72019.1	NT	S.alba phr-1 mRNA for photolyase

Page 13 of 382  
Table 4  
Single Exon Probes Expressed in HELA Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6924	16117	25583	2.21	1.3E+00	X72019.1	NT	S. alba pht-1 mRNA for photolysis
6982	16180	25631	2.37	1.3E+00	O00754	SWISSPROT	LYSOSOMAL ALPHA-MANNOSIDASE PRECURSOR (MANNOSIDASE, ALPHA B) (LYSOSOMAL ACID ALPHA-MANNOSIDASE) (LAMAN)
7026	16205	25682	5.79	1.3E+00	BE963379.2	EST_HUMAN	601657145R1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3866195 3'
7284	16503		4.82	1.3E+00	Q14117	SWISSPROT	DIHYDROPYRIMIDINASE (DHPASE) (HYDANTOINASE) (DHP)
7480	16688	26170	2.44	1.3E+00	P25289	SWISSPROT	MRNA 3'-END PROCESSING PROTEIN RNA15
7501	16708	26195	2.26	1.3E+00	Z18892.2	NT	Mus musculus desmin gene
8072	17207	26740	3.07	1.3E+00	D42042.1	NT	Human mRNA for KIAA0085 gene, partial cds
8144	17276	26820	2.63	1.3E+00	Z88682.1	NT	Bacillus subtilis genomic DNA 23.9KB fragment
8639	17627		2.58	1.3E+00	AF187873.1	NT	Cavia porcellus inwardly-rectifying potassium channel Kir2.2 (KCNJ12) gene, complete cds
8821	17738	23930	4.23	1.3E+00	BF348043.1	EST_HUMAN	602023185F1 NCI_CGAP_Bn67 Homo sapiens cDNA clone IMAGE:4158452 5'
8833	18106		2.07	1.3E+00	P33464	SWISSPROT	E1 GLYCOPROTEIN PRECURSOR (MATRIX GLYCOPROTEIN) (MEMBRANE GLYCOPROTEIN)
8832	17814		1.4	1.3E+00	AF187035.1	NT	Stimulin liliun cytochrome b gene, complete cds; mitochondrial gene for mitochondrial product
656	9902	19028	8.36	1.2E+00	AA676246.1	EST_HUMAN	z122d08.s1 Soares fetal liver spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:431535 3'
833	10071	19226	1.12	1.2E+00	P05228	SWISSPROT	HISTIDINE-RICH PROTEIN PRECURSOR (CLONE PFHRP-III)
833	10071	19227	1.12	1.2E+00	P05228	SWISSPROT	HISTIDINE-RICH PROTEIN PRECURSOR (CLONE PFHRP-III)
833	10071	19228	1.12	1.2E+00	P05228	SWISSPROT	HISTIDINE-RICH PROTEIN PRECURSOR (CLONE PFHRP-III)
888	10123		1.52	1.2E+00	8924234	NT	Homo sapiens hypothetical protein PRO3077 (PRO3077), mRNA
1169	10390	19542	3.71	1.2E+00	AF080245.2	NT	Elaeis delfera sesquiterpene synthase mRNA, complete cds
1213	10431	19587	1.74	1.2E+00	AJ252242.1	NT	pea seed-borne mosaic virus complete genome
1213	10431	19588	1.74	1.2E+00	AJ252242.1	NT	pea seed-borne mosaic virus complete genome
1978	11182	20390	1	1.2E+00	AF140631.1	NT	Homo sapiens G-protein coupled receptor 14 (GPR14) gene, complete cds
3074	12310	21431	1.07	1.2E+00	AB020681.1	NT	Homo sapiens mRNA for KIAA0874 protein, partial cds
3129	12364	21404	6.74	1.2E+00	AL161563.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 63
3129	12364	21495	6.74	1.2E+00	AL161563.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 63
3254	12487		2.72	1.2E+00	P54910	SWISSPROT	CONJUGAL TRANSFER PROTEIN TRBE PRECURSOR
3331	12590	21698	0.66	1.2E+00	AF188740.1	NT	Homo sapiens LHX3 gene, intron 2
3693	12813	22031	7.58	1.2E+00	U75902.1	NT	Mus musculus subtilisin-like serine protease LPC (PC7) gene, exons 1 to 9, partial cds
3964	13178	22282	2.14	1.2E+00	BF373570.1	EST_HUMAN	MR0-F10175-050900-203-g06.1 F10175 Homo sapiens cDNA
4286	12560	21698	1.04	1.2E+00	AF188740.1	NT	Homo sapiens LHX3 gene, intron 2
4487	13695		2.05	1.2E+00	M87060.1	NT	Rattus rattus cardiac AE3 gene, exons 1-23
4559	13753	22851	1.8	1.2E+00	AF156495.1	NT	Homo sapiens post-synaptic density 95 (DLG4) gene, complete cds
4587	13781		6.87	1.2E+00	Y09200.1	NT	T. pinnaum chloroplast rbcL gene, partial
5489	14695	24048	2.08	1.2E+00	AW813278.1	EST_HUMAN	MR3-ST0191-140200-013-c05 ST0191 Homo sapiens cDNA

Page 14 of 382  
Table 4  
Single Exon Probes Expressed in HELA Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5734	14953	24351	2.5	1.2E+00	X74885.1	NT	D. hydei ey1 repeat cluster DNA, fragment D
5758	14977	24376	4.03	1.2E+00	BE003113.1	EST_HUMAN	QV4-BN090-270400-190-q03 BN090 Homo sapiens cDNA
5804	15021	24422	37.27	1.2E+00	AA759254.1	EST_HUMAN	ah84g12.s1 Soares_testis_NHT Homo sapiens cDNA clone 1322374 3'
5877	15094	24508	2.08	1.2E+00	AW813276.1	EST_HUMAN	MR3-ST0191-140200-013-c05 ST0191 Homo sapiens cDNA
6055	15223	24842	2.84	1.2E+00	AJ002141.1	NT	Mus musculus DSPP gene
6356	15536	24860	2.81	1.2E+00	X74207.1	NT	L. lactis pyrD and pyrF genes
6644	15839	25299	5.07	1.2E+00	AB033030.1	NT	Homo sapiens mRNA for KIAA1204 protein, partial cds
6772	15967	25425	2.48	1.2E+00	AW377210.1	EST_HUMAN	MR2-CT0222-201099-001-q07 CT0222 Homo sapiens cDNA
6876	16067	25538	2.56	1.2E+00	Z32850.1	NT	R. communis gene for pyrophosphate-dependent phosphofructokinase beta subunit
6965	16143	25612	2.48	1.2E+00	D11745.1	EST_HUMAN	HUMHM01A01 Liver HepG2 cell line. Homo sapiens cDNA clone hmo1a01
7048	16225	25700	4.49	1.2E+00	X56832.1	NT	H. sapiens ENO3 gene for muscle specific enolase
7886	17102	26633	2.36	1.2E+00	AW817817.1	EST_HUMAN	PM0-ST0264-161198-001-q01 ST0264 Homo sapiens cDNA
7923	17136		5.4	1.2E+00	BE160761.1	EST_HUMAN	PM1-HT0422-160200-007-g10 HT0422 Homo sapiens cDNA
7982	18427	25914	3.52	1.2E+00	U50147.1	NT	Rattus norvegicus synapse-associated protein 102 mRNA, complete cds
8005	18185	23757	20.83	1.2E+00	AL163203.2	NT	Homo sapiens chromosome 21 segment HS21C003
8025	17618		2.04	1.2E+00	AP001515.1	NT	Bacillus halodurans genomic DNA, section 9/14
470	9723	18854	1.47	1.1E+00	D86980.1	NT	Human mRNA for KIAA0227 gene, partial cds
1733	10945	20128	2.18	1.1E+00	AW995393.1	EST_HUMAN	QV0-BN0042-170300-163-g12 BN0042 Homo sapiens cDNA
3303	12534	21668	8.21	1.1E+00	AL163213.2	NT	Homo sapiens chromosome 21 segment HS21C013
3303	12534	21667	8.21	1.1E+00	AL163213.2	NT	Homo sapiens chromosome 21 segment HS21C013
3461	12686	21822	0.85	1.1E+00	8922841	NT	Homo sapiens hypothetical protein FLJ10749 (FLJ10749), mRNA
3555	12778	21907	1.18	1.1E+00	AI808360.1	EST_HUMAN	wf54h11.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2359461 3' similar to SW:P531_HUMAN Q12888 P53-BINDING PROTEIN 53BP1 ;
3699	12919	22036	1.52	1.1E+00	AE003886.1	NT	Xyella fastidiosa, section 32 of 229 of the complete genome
3699	12919	22037	1.52	1.1E+00	AE003886.1	NT	Xyella fastidiosa, section 32 of 229 of the complete genome
3807	13025		0.75	1.1E+00	X85374.1	NT	H. parahaeemolyticus hphIM(A), hphIM(C), hphIR and menB genes
3919	13135	22252	1.03	1.1E+00	8922841	NT	Homo sapiens hypothetical protein FLJ10749 (FLJ10749), mRNA
3997	13210	22315	0.89	1.1E+00	8755205	NT	Mus musculus proteasome (prosome, macropain) subunit, beta type 7 (Psmb7), mRNA
4188	13402		7.87	1.1E+00	5835331	NT	R. uniconis complete mitochondrial genome
4888	13880		1.06	1.1E+00	U34992.1	NT	Carcharias plumbeus Ig lambda light chain gene, complete cds
5016	14203	23260	3.61	1.1E+00	U18466.1	NT	African swine fever virus, complete genome
5102	14282	23367	1.13	1.1E+00	X78425.1	NT	E. faecalis pbp5 gene
5251	14424	23501	0.82	1.1E+00	P25396	SWISSPROT	TELLURITE RESISTANCE PROTEIN TEHA
5335	14566	23640	1.89	1.1E+00	6978530	NT	Rattus norvegicus Aquaporin 4 (Aqp4), mRNA

Page 15 of 382  
Table 4  
Single Exon Probes Expressed in HELA Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5497	14723	24081	22.14	1.1E+00	BE060184.1	EST_HUMAN	601652776R1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:3825835 3'
6286	15467	24908	2.16	1.1E+00	Z72338.1	NT	Herpes simplex virus type 1 (strain KOS) UL41 gene
6286	15467	24909	2.16	1.1E+00	Z72338.1	NT	Herpes simplex virus type 1 (strain KOS) UL41 gene
6294	15475	24917	7.18	1.1E+00	AL161588.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 84
6503	15700	25166	4.96	1.1E+00	BF93996.1	EST_HUMAN	602082582F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4246628 5'
7052	16229	25705	7.08	1.1E+00	AL161515.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 27
7073	16250	25723	22.71	1.1E+00	6754021	NT	Mus musculus guanine nucleotide binding protein (G protein), gamma 3 subunit (Gng3), mRNA
7244	16464	25954	2.93	1.1E+00	11067364	NT	Homo sapiens KIAA0626 gene product (KIAA0626), mRNA
7296	16515		4.08	1.1E+00	AF068942.1	NT	Klebsoridium fluitans cytochrome c oxidase subunit 2 (cox2) gene, mitochondrial gene encoding mitochondrial protein, partial cds
7684	14493		5.98	1.1E+00	8922673	NT	Homo sapiens hypothetical protein FLJ11280 (FLJ11280), mRNA
7689	16868	26370	3.89	1.1E+00	AF012862.1	NT	Petrosselinum crispum cytosolic glucose-6-phosphate dehydrogenase 1 (cG6PDH1) mRNA, complete cds
7689	16868	26371	3.89	1.1E+00	AF012862.1	NT	Petrosselinum crispum cytosolic glucose-6-phosphate dehydrogenase 1 (cG6PDH1) mRNA, complete cds
7895	17111	26642	5.2	1.1E+00	AI808699.1	EST_HUMAN	wf76e11.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2361548 3'
8103	17237	26774	1.83	1.1E+00	D89501.1	NT	Human PBI gene, complete cds
8103	17237	26776	1.83	1.1E+00	D89501.1	NT	Human PBI gene, complete cds
8575	17591		2.98	1.1E+00	P07866	SWISSPROT	LOW TEMPERATURE ESSENTIAL PROTEIN
8682	17652	23979	2.49	1.1E+00	AF216696.1	NT	Taenia solium immunogenic protein Ts76 mRNA, partial cds
8811	18182		1.81	1.1E+00	AF234169.1	NT	Dicystotellium discoideum isopentenyl pyrophosphate isomerase (Dip) mRNA, complete cds
99	9392		2.09	1.0E+00	U23808.1	NT	Xenopus laevis rhodopsin gene, complete cds
113	9401	18530	1.22	1.0E+00	D88425.1	NT	Cavia cobaya mRNA for serine/threonine kinase, complete cds
424	9677		2.34	1.0E+00	AB021684.1	NT	Marchantia polymorpha genes for 26S rRNA, 5S rRNA, 18S rRNA, 5.8S rRNA and 26S rRNA
583	9832	18950	1.38	1.0E+00	AJ251660.1	NT	Giardia tigrina mRNA for homeodomain transcription factor (so gene)
683	9926	19057	6.39	1.0E+00	AL163218.2	NT	Homo sapiens chromosome 21 segment HS21C018
685	9928		0.94	1.0E+00	AF125984.1	NT	Aedes aegypti mucin-like protein MUC1 mRNA, complete cds
1392	11993		1.65	1.0E+00	X80416.1	NT	V. canteri Algal-CAM mRNA
1728	10940	20123	1.15	1.0E+00	AB006531.1	NT	Plautia stali intestine virus RNA for nonstructural polyprotein, capsid protein precursor, complete cds
2643	11826	21041	0.95	1.0E+00	AF131205.1	NT	Mus musculus Serf1 protein (Serf1), survival of motor neuron protein (Snm), neuronal apoptosis inhibitory protein-rs6 (Naip-rs6), and neuronal apoptosis inhibitory protein-rs3 (Naip-rs3) genes, complete cds

Page 16 of 382  
Table 4  
Single Exon Probes Expressed in HELA Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2829	12068	21189	4.6	1.0E+00	P24008	SWISSPROT	3-OXO-5-ALPHA-STEROID 4-DEHYDROGENASE 1 (STEROID 5-ALPHA-REDUCTASE 1)(SR TYPE 1)
2829	12068	21190	4.6	1.0E+00	P24008	SWISSPROT	3-OXO-5-ALPHA-STEROID 4-DEHYDROGENASE 1 (STEROID 5-ALPHA-REDUCTASE 1)(SR TYPE 1)
2922	12160		1.25	1.0E+00	O14226	SWISSPROT	HYPOTHETICAL 67.9 KD PROTEIN C6F12.08C IN CHROMOSOME 1
3163	12398	21533	1.17	1.0E+00	AA628453.1	EST_HUMAN	at2g008.s1 Soares_tetis_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:1032830 3' similar to
3577	9392		1.17	1.0E+00	U23808.1	NT	WP:C4208.3 CE04204; contains element MER22 MER22 repetitive element;
3661	12882	22003	1.81	1.0E+00	AJ223816.1	NT	Xenopus laevis rhodopsin gene, complete cds
4046	13256	22357	0.84	1.0E+00	AF223381.1	NT	Agaricus bisporus mRNA for tyrosinase
5165	14361		0.87	1.0E+00	AF200817.1	NT	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced
5279	14450		0.6	1.0E+00	AL163216.2	NT	Pilot whale morbillivirus phosphoprotein (P) gene, partial cds
5315	14547	23618	2.5	1.0E+00	Z97022.1	NT	Homo sapiens chromosome 21 segment HS21C018
5592	14816	24190	4.53	1.0E+00	AF248054.1	NT	Hordeum vulgare gene encoding cysteine proteinase
5592	14816	24191	4.53	1.0E+00	AF248054.1	NT	Bos taurus micromolar calcium activated neutral protease 1 (CAPN1) gene, exons 11-20, and partial cds
5715	14933	24329	4.68	1.0E+00	P04501	SWISSPROT	Bos taurus micromolar calcium activated neutral protease 1 (CAPN1) gene, exons 11-20, and partial cds
5716	14934	24330	1.62	1.0E+00	AW452782.1	EST_HUMAN	FIBER PROTEIN
5870	15088	24501	1.87	1.0E+00	U75802.1	NT	U1-H-B13-ab-d-09-Q-U1.s1 NCI_CGAP_Sub5 Homo sapiens cDNA clone IMAGE:3068969 3'
6284	15465		8.44	1.0E+00	P20273	SWISSPROT	Mus musculus subtilisin-like serine protease LPC (PC7) gene, exons 1 to 9, partial cds
6387	15567	25024	8.14	1.0E+00	AA775191.1	EST_HUMAN	B-CELL RECEPTOR CD22 PRECURSOR (LEU-14)(B-LYMPHOCYTE CELL ADHESION MOLECULE) (BL-CAM)
6505	14499		2.37	1.0E+00	D10852.1	NT	ac79b08.s1 Stralagene lung (#837210) Homo sapiens cDNA clone IMAGE:888791 3'
6580	15776	25235	3.41	1.0E+00	Q02207	SWISSPROT	Rattus norvegicus mRNA for N-acetylglucosaminyltransferase III, complete cds
6580	15776	25238	3.41	1.0E+00	Q02207	SWISSPROT	PEROXISOMAL HYDRATASE-DEHYDROGENASE-EPIMERASE (HDE) (MULTIFUNCTIONAL BETA-OXIDATION PROTEIN) (MFP) [INCLUDES: 2-ENOYL-COA HYDRATASE ; D-3-HYDROXYACYL COA DEHYDROGENASE]
6634	18073		2.74	1.0E+00	BE147331.1	EST_HUMAN	PEROXISOMAL HYDRATASE-DEHYDROGENASE-EPIMERASE (HDE) (MULTIFUNCTIONAL BETA-OXIDATION PROTEIN) (MFP) [INCLUDES: 2-ENOYL-COA HYDRATASE ; D-3-HYDROXYACYL COA DEHYDROGENASE]
6969	16147	25618	2.2	1.0E+00	AV689554.1	EST_HUMAN	RC1-H107229-181009-011-008 HT07228 Homo sapiens cDNA
7209	16386	25667	32.49	1.0E+00	AA004982.1	EST_HUMAN	AV689554 GKG Homo sapiens cDNA clone GKCCYA11 5'
							z194a02.r1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:428906 5'

Page 17 of 382  
Table 4  
Single Exon Probes Expressed in HELA Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7209	16388	25868	32.49	1.0E+00	AA004982.1	EST_HUMAN	219402.r1 Soares_fetal_liver spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:428906 5'
7545	16750	26244	1.94	1.0E+00	S80825.1	NT	PBR1=proline-rich protein (intron 3) [human, Genomic, 898 nt]
8066	17201		1.96	1.0E+00	L47613.1	NT	Picea glauca EMB13 mRNA
8457	17514		3.4	1.0E+00	P15306	SWISSPROT	THROMBOMODULIN PRECURSOR (FETOMODULIN) (TM)
8801	17726		2.13	1.0E+00	AW976184.1	EST_HUMAN	EST388293 MAGE sequences, MAGN Homo sapiens cDNA
2601	11785	21005	1	9.9E-01	AL163302.2	NT	Homo sapiens chromosome 21 segment HS21C102
3583	12805		1.14	9.9E-01	AF174585.1	NT	Apple mosaic virus RNA 2 putative polymerase gene, complete cds
5505	14730	24092	8.2	9.9E-01	P49657	SWISSPROT	SERINE/THREONINE PROTEIN KINASE MINIBRAIN
6938	16082		3.4	9.9E-01	Q28842	SWISSPROT	B2 BRADYKININ RECEPTOR (BK-2 RECEPTOR)
529	9780	18903	2.91	9.8E-01	P22567	SWISSPROT	AMINO-ACID ACETYLTRANSFERASE (N-ACETYLGLUTAMATE SYNTHASE) (AGS) (NAGS)
2259	11454		1.63	9.8E-01	AJ003108.1	NT	Callithrix jacchus UBE1 gene derived retroposon on the Y chromosome
3767	13005	22120	0.63	9.8E-01	BE957439.2	EST_HUMAN	601653583R2 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:3838461 3'
3787	13005	22121	0.63	9.8E-01	BE957439.2	EST_HUMAN	601653583R2 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:3838461 3'
6164	15347	24784	4.67	9.8E-01	AJ302158.1	NT	Enterobacteriaceae sp. JM983 partial groES gene for GroES-like protein and partial groEL gene for GroEL-like protein, isolate JM983
6164	15347	24785	4.67	9.8E-01	AJ302158.1	NT	Enterobacteriaceae sp. JM983 partial groES gene for GroES-like protein and partial groEL gene for GroEL-like protein, isolate JM983
7566	16771	26262	4.32	9.8E-01	BE258705.1	EST_HUMAN	601110258F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3350750 5'
7566	16771	26263	4.32	9.8E-01	BE258705.1	EST_HUMAN	601110258F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3350750 5'
							Homo sapiens X28 region near ALD locus containing dual specificity phosphatase 9 (DUSP9), ribosomal protein L18a (RPL18a), Ca2+/Calmodulin-dependent protein kinase 1 (CAMK1), creatine transporter (CRTR), CDM protein (CDM), adrenoleukodystrophy protein >
8688	17657		1.26	9.8E-01	U52111.2	NT	Drosophila melanogaster sodium channel protein (para) gene, exons 9,10,11,12 and optional segments b, c, d and e, partial cds
6147	15331	24767	3.07	9.7E-01	U26716.1	NT	UHH-B14-act-e-07-Q-UJ.s1 NCJ_CGAP_Sub8 Homo sapiens cDNA clone IMAGE:3085140 3'
7729	16927		4.82	9.7E-01	BF511209.1	EST_HUMAN	Botrytis cinerea strain T4 cDNA library under conditions of nitrogen deprivation
9272	18035		1.38	9.7E-01	AL114281.1	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 49
9289	18047	23827	5.82	9.7E-01	AL161649.2	NT	Bromus inermis putative cytosolic phosphoglucomutase (pgm1) mRNA, complete cds
4430	13630	22724	1	9.6E-01	AF187925.1	NT	Bromus inermis putative cytosolic phosphoglucomutase (pgm1) mRNA, complete cds
4430	13630	22725	1	9.6E-01	AF187925.1	NT	Bromus inermis putative cytosolic phosphoglucomutase (pgm1) mRNA, complete cds
4452	13651	22746	1.53	9.6E-01	AW768674.1	EST_HUMAN	PM2-JM0053-240300-005-f12 UM0053 Homo sapiens cDNA
5552	14776	24143	3.47	9.6E-01	Z70556.1	NT	Parvovirus B19 DNA, patient C, genome position 2448-2894
5552	14776	24144	3.47	9.6E-01	Z70556.1	NT	Parvovirus B19 DNA, patient C, genome position 2448-2894
6596	15792		2.23	9.6E-01	X95275.1	NT	P. falciparum complete genome map of plasid-like DNA (IR-A)
7654	16854	26353	1.69	9.6E-01	AF041427.1	NT	Homo sapiens ribosomal protein s4 Y isoform gene, complete cds

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Single Exon Probes Expressed in HELA Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8051	17187	28726	4.97	9.6E-01	AV752605.1	EST_HUMAN	AV752605 NP0 Homo sapiens cDNA clone NPDBAG06 5'
8051	17187	28727	4.97	9.6E-01	AV752605.1	EST_HUMAN	AV752605 NP0 Homo sapiens cDNA clone NPDBAG06 5'
8356	17449		1.59	9.6E-01	11421722	NT	Homo sapiens centrosomal protein 2 (CEP2), mRNA
9010	18260	23680	2.28	9.6E-01	U91423.1	NT	Sphyrna tiburo NADH dehydrogenase subunit 2 (NADH2) gene, mitochondrial gene encoding mitochondrial protein, partial cds
2438	11629	20850	1.21	9.5E-01	7705591	NT	Homo sapiens CGI-125 protein (LOC51003), mRNA
3765	12983	22097	2.06	9.5E-01	BE902340.1	EST_HUMAN	601675639F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3958473 5'
3765	12983	22098	2.06	9.5E-01	BE902340.1	EST_HUMAN	601675639F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3958473 5'
7798	16989	28504	1.76	9.5E-01	BF218771.1	EST_HUMAN	601885163F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4103630 5'
7987	16422	25909	1.85	9.5E-01	AW263789.1	EST_HUMAN	U1-H-812-shp-1-03-Q-U1.s1 NCI_CGAP_Sub4 Homo sapiens cDNA clone IMAGE:2727677 3'
3165	12400		3.84	9.4E-01	AF165980.1	NT	Bartonella clarridgeiae RNA polymerase beta subunit (rpoB) gene, partial cds
3184	12419		2.15	9.4E-01	AF080595.1	NT	Pimpinella brachycarpa zinc finger protein (ZFP1) mRNA, complete cds
8630	17622		1.65	9.4E-01	BE781251.1	EST_HUMAN	601466703F1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3689929 5'
9009	18176		1.61	9.4E-01	11419857	NT	Homo sapiens epidermal growth factor receptor (avian erythroblastic leukemia viral (v-erb-b) oncogene homolog) (EGFR), mRNA
1705	10917		1.15	9.3E-01	AF242382.1	NT	Homo sapiens phytyl-CoA hydroxylase (PHYH) gene, exon 5
2598	11783	21003	1.61	9.3E-01	BE071172.1	EST_HUMAN	RC5-BT0503-271199-011-B01 BT0503 Homo sapiens cDNA
4013	13225	22325	0.76	9.3E-01	M20219.1	NT	Bovine papillomavirus type 2, complete genome
4013	13225	22328	0.76	9.3E-01	M20219.1	NT	Bovine papillomavirus type 2, complete genome
5524	14749	24116	4.02	9.3E-01	L36189.1	NT	Spodoptera frugiperda methylenetetrahydrofolate dehydrogenase mRNA, complete cds
9128	17939	23879	1.56	9.3E-01	11440288	NT	Homo sapiens inositol 1,4,5-trisphosphate receptor, type 2 (ITPR2), mRNA
9135	17944		2.19	9.3E-01	AF271207.1	NT	Aedes triseriatus putative large subunit ribosomal protein rPL34, mRNA, complete cds
3205	12439	21574	3.6	9.2E-01	BE622702.1	EST_HUMAN	601441338T1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3918184 3'
4894	14082		0.79	9.2E-01	BF129973.1	EST_HUMAN	601817814F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:4041363 5'
5649	14872	24259	4.49	9.2E-01	BF037586.1	EST_HUMAN	601461153F1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3864861 5'
7156	16333	25816	5.03	9.2E-01	11430963	NT	Homo sapiens lysosomal aspartase-like protein 1 (LALP1), mRNA
7240	16460	25949	1.69	9.2E-01	BE563811.1	EST_HUMAN	601334943F1 NIH_MGC_39 Homo sapiens cDNA clone IMAGE:3688714 5'
8213	17344	26883	2.06	9.2E-01	BF132402.1	EST_HUMAN	601820312F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:4052018 5'
1602	10816	19992	1.14	9.1E-01	T66675.1	EST_HUMAN	ye5201.s1 Soares fetal liver spleen 1NLS Homo sapiens cDNA clone IMAGE:121369 3' similar to contains Alu repetitive element
2084	11284		1.18	9.1E-01	8923058	NT	Homo sapiens hypothetical protein FLJ20048 (FLJ20048), mRNA
3170	12405	21538	1.28	9.1E-01	T26418.1	EST_HUMAN	AB200G8R Infant brain, LLNL array of Dr. M. Soares 1NIB Homo sapiens cDNA clone LLAB200G8 5'

Page 19 of 382  
Table 4  
Single Exon Probes Expressed in HELA Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3170	12405	21539	1.28	9.1E-01	T26418.1	EST_HUMAN	AB20038R Infant brain, LLNL array of Dr. M. Soares 1N1B Homo sapiens cDNA clone LLAB20038 5'
5878	15095	24509	2.86	9.1E-01	Q61704	SWISSPROT	INTER-ALPHA-TRYPsin INHIBITOR HEAVY CHAIN H3 PRECURSOR (ITI HEAVY CHAIN H3)
6325	15508	24952	17.68	9.1E-01	AA806623.1	EST_HUMAN	cb71g08.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1336882 3'
6393	15573	25029	2.35	9.1E-01	U72895.1	NT	Rattus norvegicus Rab3 GDP/GTP exchange protein mRNA, complete cds
8726	18254		15.31	9.1E-01	AF050113.1	NT	Homo sapiens uncoupling protein-3 (UCP3) gene, complete cds
3172	12407	21542	0.6	9.0E-01	7681625	NT	Homo sapiens DKFZP584M2423 protein (DKFZP584M2423), mRNA
4373	13575	22671	2	9.0E-01	AF088810.1	NT	Homo sapiens neuradn III-alpha gene, partial cds
5268	14441	23514	0.61	9.0E-01	AI086302.1	EST_HUMAN	ox10b05.s1 Soares_fetal_liver_spleen_INFLS_S1 Homo sapiens cDNA clone IMAGE:1655889 3' similar to contains Alu repetitive element
5534	14758	24125	2.39	8.9E-01	AF028188.1	NT	Fugu rubripes neural cell adhesion molecule L1 homolog (L1-CAM) gene, complete cds; putative protein 1 (PUT1) gene, partial cds; mitosis-specific chromosome segregation protein SMC1 homolog (SMC1) gene, complete cds; and calcium channel alpha-1 subunit>
8251	17379	26913	2.66	8.9E-01	AE003944.1	NT	Xylella fastidiosa, section 90 of 229 of the complete genome
8557	17578		4.11	8.9E-01	AE002186.2	NT	Chlamydia pneumoniae AR39, section 21 of 94 of the complete genome
4539	13734	22832	1.91	8.8E-01	Q28350	SWISSPROT	PUTATIVE F420-DEPENDENT NADP REDUCTASE
5205	14380	23468	3.86	8.8E-01	AW856840.1	EST_HUMAN	RC2-CT0298-150200-015-001 CT0298 Homo sapiens cDNA
7647	18847	28345	3.06	8.8E-01	Z28337.1	NT	M.aeruginosa (HUB 5-2-4) DNA from plasmid PMA1
8372	18344		2.12	8.8E-01	D90911.1	NT	Synechocystis sp. PCC6803 complete genome, 13/27, 1576593-1719643
471	9724	18855	1.29	8.7E-01	AF106953.2	NT	Homo sapiens SOS1 (SOS1) gene, partial cds
2827	12068	21187	5.87	8.7E-01	AA595863.1	EST_HUMAN	nm051f1.s1 NCI_CGAP_P4.1 Homo sapiens cDNA clone IMAGE:1076877
5031	14218		2.76	8.7E-01	AF121970.1	NT	Pseudomonas aeruginosa topoisomerase (top), putative transcriptional regulatory protein OhbR (ohbR), ortho-halobenzoate 1,2-dioxygenase beta-ISP protein OhbA (ohbA), OhbC (ohbC), ortho-halobenzoate 1,2-dioxygenase alpha-ISP protein OhbB (ohbB), and put-
7408	19620	26112	6.23	8.7E-01	BF363970.1	EST_HUMAN	QV0-NN1021-100800-337-c03 NN1021 Homo sapiens cDNA
8226	17356	26894	3.87	8.7E-01	BF107894.1	EST_HUMAN	601823684R1 NIH_MGC_79 Homo sapiens cDNA clone IMAGE:4043584 3'
8226	17356	26895	3.87	8.7E-01	BF107894.1	EST_HUMAN	601823684R1 NIH_MGC_79 Homo sapiens cDNA clone IMAGE:4043564 3'
8775	18144		2.27	8.7E-01	AV661898.1	EST_HUMAN	AV661898 GLC Homo sapiens cDNA clone GLOCYG07 3'
481	9733		1.49	8.6E-01	X17012.1	NT	Rat IGF1 gene for insulin-like growth factor II
868	10104	19267	7.46	8.6E-01	W69089.1	EST_HUMAN	zd44e03.r1 Soares_fetal_heart_NbH19W Homo sapiens cDNA clone IMAGE:343516 5'
2235	11430	20855	0.95	8.6E-01	4503210	NT	Homo sapiens cytochrome P450, subfamily XXVIA (steroid 27-hydroxylase, cerebrotendinous xanthomatosis), polypeptide 1 (CYP27A1b) mRNA
3599	12820	21941	1.09	8.6E-01	AL161565.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 65
3784	13002	22117	1.49	8.6E-01	U49724.1	NT	Drosophila melanogaster maelin (Ornietin) mRNA, complete cds



Page 20 of 382  
Table 4  
Single Exon Probes Expressed in HELA Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5614	14837	24214	7.93	8.8E-01	X60547.1	NT	Chicken lipoprotein lipase gene
5614	14837	24215	7.93	8.8E-01	X60547.1	NT	Chicken lipoprotein lipase gene
5989	15184	24600	1.77	8.8E-01	AF143732.1	NT	Grus canadensis recombination activating protein 1 (RAG-1) gene, partial cds
5989	15184	24601	1.77	8.8E-01	AF143732.1	NT	Grus canadensis recombination activating protein 1 (RAG-1) gene, partial cds
8982	18092		1.56	8.8E-01	AL112162.1	NT	Batrytis cinerea strain T4 cDNA library under conditions of nitrogen deprivation
4491	13689	22781	0.85	8.5E-01	AF101029.1	EST_HUMAN	we09h02.x1 NCL_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:2340627 3'
6301	15482	24926	2.42	8.5E-01	BE542612.1	EST_HUMAN	601087107F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3453505 5'
7180	18357	25835	2.22	8.5E-01	AB008799.1	NT	Cyanidium caldarium gene for SigC, complete cds
7180	18357	25838	2.22	8.5E-01	AB008799.1	NT	Cyanidium caldarium gene for SigC, complete cds
8711	18256		2.74	8.5E-01	11418543	NT	Homo sapiens human immunodeficiency virus type 1 enhancer-binding protein 1 (HIVEP1), mRNA
8717	17672		4	8.5E-01	9507003	NT	Rattus norvegicus protein tyrosine phosphatase, non-receptor type 5 (Ptpn5), mRNA
5440	18055	23820	2.81	8.4E-01	L78726.1	NT	Human fibroblast growth factor receptor 3 (FGFR3) gene, intron 7
5440	18055	23821	2.81	8.4E-01	L78726.1	NT	Human fibroblast growth factor receptor 3 (FGFR3) gene, intron 7
7057	16234		4.37	8.4E-01	AJ248287.1	NT	Pyrococcus abyssi complete genome, segment 5/8
749	9990	18133	2.79	8.3E-01	M93437.1	NT	Thermus thermophilus cytochrome c-552 (cycA) and CycB (cycB) genes, complete cds
3060	12298	21420	3.24	8.3E-01	AL161506.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 18
3798	13016	22129	0.71	8.3E-01	AB010879.1	NT	Nicotiana tabacum mRNA for chloroplast ribosomal protein L10, complete cds
3988	13202	22310	3.75	8.3E-01	Y19177.1	NT	Streptomyces antibioticus polyketide biosynthetic gene cluster
5308	14540	23545	2.38	8.3E-01	AL161540.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 40
7140	16317	26769	4.76	8.3E-01	AF108133.1	NT	Mus musculus neuro-d4 gene, exons 3 through 12 and partial cds
7266	16485	25977	2.68	8.3E-01	AE000803.1	NT	Methanobacterium thermoautotrophicum from bases 1270510 to 1283409 (section 109 of 148) of the complete genome
7282	16501		2.2	8.3E-01	7212472	NT	Phytophthora infestans mitochondrion, complete genome
7851	17041	26558	2.88	8.3E-01	AF020503.1	NT	Homo sapiens FRA3B common fragile region, diadenosine triphosphate hydrolase (FHIT) gene, exon 5
2018	11220	20428	2.47	8.2E-01	AB000489.1	NT	Rattus norvegicus mRNA for RPHO-1, complete cds
2059	11260		1.69	8.2E-01	AF145889.1	NT	Mus musculus trophinin (Tm) gene, complete cds
2639	11822		1.02	8.2E-01	AW376990.1	EST_HUMAN	IL3-CT0219-161189-031-Q08 CT0219 Homo sapiens cDNA
3879	13095	22212	0.61	8.2E-01	AB014574.1	NT	Homo sapiens mRNA for KIAA0674 protein, partial cds
4111	13318	22417	0.99	8.2E-01	Z72584.1	NT	S. cerevisiae chromosome VII reading frame ORF YGL062w
4111	13318	22418	0.99	8.2E-01	Z72584.1	NT	S. cerevisiae chromosome VII reading frame ORF YGL062w
6040	15248	24670	3.49	8.2E-01	AW379433.1	EST_HUMAN	GM4-HT0243-081199-037-601 HT0243 Homo sapiens cDNA
6196	18072	24818	4.4	8.2E-01	Z12126.1	NT	S. cerevisiae MET, LEU4, and POL1 genes encoding MET4 protein, alpha-isopropylmalate (alpha-IPM) synthetase (partial), and DNA polymerase alpha (partial)

Page 21 of 382  
Table 4  
Single Exon Probes Expressed in HELA Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7094	18271	26748	2.43	8.2E-01	AF052859.1	NT	Homo sapiens thiodoxin-related protein mRNA, complete cds
7184	16361	25840	3.28	8.2E-01	Q8J70	SWISSPROT	MCKUSICK-KAUFMAN/BARDET-BIEDL SYNDROMES PUTATIVE CHAPERONIN
7184	16361	25841	3.28	8.2E-01	Q8J70	SWISSPROT	MCKUSICK-KAUFMAN/BARDET-BIEDL SYNDROMES PUTATIVE CHAPERONIN
8155	17287	26831	3.09	8.2E-01	L10127.1	NT	Molluscum contagiosum virus type 1 ORF1 and ORF2 DNA
8221	17351	26889	7.78	8.2E-01	P10383	SWISSPROT	OVARIAN TUMOR LOCUS PROTEIN
8227	17357	26896	6.68	8.2E-01	H87398.1	EST_HUMAN	yw14d02.r1 Soares_placenta_8td8weeks_2NHP80c9W Homo sapiens cDNA clone IMAGE:252195 5'
8734	17680	23952	1.91	8.2E-01	AJ001261.1	NT	similar to gb:M36072.60S RIBOSOMAL PROTEIN L7A (HUMAN);
2714	11893		1.1	8.1E-01	AF191839.1	NT	Mus musculus mRNA for NIPSNAP2 protein
3435	12660	21791	3.11	8.1E-01	AF055066.1	NT	Mus musculus TANK binding kinase TBK1 (Tbk1) mRNA, complete cds
3435	12660	21792	3.11	8.1E-01	AF055066.1	NT	Homo sapiens MHC class 1 region
4941	14126		0.62	8.1E-01	AF202634.1	NT	Homo sapiens MHC class 1 region
5943	15159	24571	2.59	8.1E-01	Q13491	SWISSPROT	Drosophila melanogaster Na/K-ATPase beta subunit isoform 4 (JYbeta2) mRNA, complete cds
5943	15159	24572	2.59	8.1E-01	Q13491	SWISSPROT	NEURONAL MEMBRANE GLYCOPROTEIN M6-B
8017	17156	26691	3.58	8.1E-01	BE938558.1	EST_HUMAN	RCO-TN0080-220800-025-d10 TN0080 Homo sapiens cDNA
8017	17156	26692	3.58	8.1E-01	BE938558.1	EST_HUMAN	RCO-TN0080-220800-025-d10 TN0080 Homo sapiens cDNA
8430	17498	24013	1.53	8.1E-01	AE001711.1	NT	Thermotoga maritima section 23 of 138 of the complete genome
180	9460		2.95	8.0E-01	AJ271510.1	NT	Staphylococcus aureus partial pla gene for phosphate acyltransferase allele 15
293	9567	18698	9.28	8.0E-01	AJ132772.1	NT	Bos taurus tub and rtf genes
2003	11206		1.53	8.0E-01	BF530962.1	EST_HUMAN	602072473F1 NCJ CGAP Bm67 Homo sapiens cDNA clone IMAGE:4215091 5'
3284	12515	21648	1.71	8.0E-01	AB006193.1	NT	Mus musculus gene for oviductal glycoprotein, complete cds
4530	13726	22623	5.64	8.0E-01	X83739.2	NT	G.gallus mRNA for nicotinic acetylcholine receptor (nAChR) beta 3 subunit
5001	14188	23278	1.29	8.0E-01		NT	Mus musculus myosin IXb (Myo9b), mRNA
6828	15825	25287	2.21	8.0E-01	Y11095.1	NT	Rice stripe virus RNA 3
480	9713	18948	1.61	7.9E-01	D11476.1	NT	Lymnaea disper nuclear polyhedrosis virus gene for DNA polymerase, complete cds
722	9984		1.09	7.9E-01	AE002130.1	NT	Ureaplasma urealyticum section 31 of 59 of the complete genome
1584	10797		25.24	7.9E-01	AB040885.1	NT	Homo sapiens mRNA for KIAA1452 protein, partial cds
1631	10845		1	7.9E-01	U32739.1	NT	Haemophilus influenzae Rd section 54 of 163 of the complete genome
2228	11424	20650	6.52	7.9E-01	AB004816.1	NT	Oryctolagus cuniculus mRNA for mitsugumin28, complete cds
2228	11425	20651	2.33	7.9E-01	AF130459.1	NT	Danio rerio Trp4-associated protein Tap1A (tap1A) mRNA, complete cds
3490	12714	21850	2.71	7.9E-01	AF228664.1	NT	Gallus gallus SOX8 transcription factor (SOX8) mRNA, complete cds
4287	13489		0.71	7.9E-01	BE263612.1	EST_HUMAN	601192033F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3535785 5'
4613	13807	22899	1.03	7.9E-01	6753745	NT	Mus musculus embigin (Emb), mRNA
4613	13807	22900	1.03	7.9E-01	6753745	NT	Mus musculus embigin (Emb), mRNA

Page 22 of 382  
Table 4  
Single Exon Probes Expressed in HELA Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6497	15694	25158	4.39	7.9E-01	X80986.1	NT	P. sativum GR gene
6834	16126	25594	4.56	7.9E-01	U01812.1	NT	Giardia lamblia variant-specific surface protein G3M-B (vspG3M-B) mRNA, partial cds
7089	16266	25742	2.99	7.9E-01	P19719	SWISSPROT	SMALL HYDROPHOBIC PROTEIN
7577	16782		2.29	7.9E-01	7662471	NT	Homo sapiens KIAA1072 protein (KIAA1072), mRNA
7784	16960	28470	3	7.9E-01	P19022	SWISSPROT	NEURAL-CADHERIN PRECURSOR (N-CADHERIN)
888	10121		2.22	7.8E-01	Z43785.1	EST_HUMAN	HSC1KH041 normalized infant brain cDNA Homo sapiens cDNA clone c-1kh04
2240	11435	20659	4.11	7.8E-01	AW959567.1	EST_HUMAN	EST1371637 MAGE resequences, MAGF Homo sapiens cDNA
4712	13903	23003	0.74	7.8E-01	U87305.1	NT	Rattus norvegicus transmembrane receptor Unc5H1 mRNA, complete cds
5082	14242		1.12	7.8E-01	AW753353.1	EST_HUMAN	RC3-CT0254-130100-023-c02 CT0254 Homo sapiens cDNA
5227	14401		1.33	7.8E-01	Z43785.1	EST_HUMAN	HSC1KH041 normalized infant brain cDNA Homo sapiens cDNA clone c-1kh04
5697	14917	24311	2.41	7.8E-01	AF115958.1	NT	Sphenodon punctatus alpha enolase mRNA, partial cds
8705	18234		1.54	7.8E-01	L29260.1	NT	Arabidopsis thaliana 1-amino-1-cyclopropanecarboxylate synthase (ACS5) gene, complete cds
141	9423	18556	5.87	7.7E-01	AF184345.1	NT	Lycopersicon hirsutum ADP-glucose pyrophosphorylase large subunit (AGP-L1) mRNA, complete cds
733	9974						Mus musculus major histocompatibility locus class II region: major histocompatibility protein class II alpha chain (Iaalpha) and major histocompatibility protein class II beta chain (Ib beta) genes, complete cds; butyrophilin-like (NGR), butyrophilin-like
2872	11854	21070	2.1	7.7E-01	AF050157.1	NT	CITRATE SYNTHASE
3576	12800	21928	4.2	7.7E-01	AF118085.1	NT	Homo sapiens PRO1975 mRNA, complete cds
4390	13591	22683	3.15	7.7E-01	AF199488.1	NT	Coturnix coturnix japonica sub-species japonica beta-actin mRNA, partial cds
4390	13591	22694	3.16	7.7E-01	AF199488.1	NT	Coturnix coturnix japonica sub-species japonica beta-actin mRNA, partial cds
5263	14436		1.46	7.7E-01	L78833.1	NT	Human BRCA1, Rho7 and vati genes, complete cds, and lp35 gene, partial cds
8479	9423	18556	1.35	7.7E-01	AF184345.1	NT	Lycopersicon hirsutum ADP-glucose pyrophosphorylase large subunit (AGP-L1) mRNA, complete cds
8586	17596		5.33	7.7E-01	11497621	NT	Archaeoglobus fulgidus, complete genome
5707	14926	24320	4.05	7.6E-01	AF059510.1	NT	Arabidopsis thaliana 3-methylcrotonyl-CoA carboxylase non-biotinylated subunit (MCCB) mRNA, complete cds
5707	14926	24321	4.05	7.6E-01	AF059510.1	NT	Arabidopsis thaliana 3-methylcrotonyl-CoA carboxylase non-biotinylated subunit (MCCB) mRNA, complete cds
6501	15698	25163	2.5	7.6E-01	6857752	NT	Mus musculus advinlin (Advin-pending), mRNA
6501	15698	25164	2.5	7.6E-01	6857752	NT	Mus musculus advinlin (Advin-pending), mRNA
6849	16038	25502	7.49	7.6E-01	P30372	SWISSPROT	MUSCARINIC ACETYLCHOLINE RECEPTOR M2
6849	16038	25503	7.49	7.6E-01	P30372	SWISSPROT	MUSCARINIC ACETYLCHOLINE RECEPTOR M2
7697	17113	26844	2.88	7.6E-01	X86347.1	NT	H. aspersa mRNA for neurofilament NF70

Page 23 of 382  
Table 4  
Single Exon Probes Expressed in HELA Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7897	17113	28845	2.88	7.6E-01	X86347.1	NT	H. aspersa mRNA for neurofilament NF70
8201	17333		6.71	7.6E-01	AL161592.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 88
8334	17432		3.62	7.6E-01	AB020702.1	NT	Homo sapiens mRNA for KIAA0895 protein, partial cds
519	9770		1.25	7.5E-01	AL163301.2	NT	Homo sapiens chromosome 21 segment HS21C101
591	9839	18958	1.51	7.5E-01	AF020503.1	NT	Homo sapiens FRA3B common fragile region, diadenosine triphosphate hydrolase (FHT) gene, exon 5
7768	16964	26477	1.71	7.5E-01	AB047819.1	NT	Homo sapiens GCMa/GCM1 gene for chorion-specific transcription factor GCMa, complete cds
8658	17635		4.34	7.5E-01	AF163151.2	NT	Homo sapiens dentin sialophosphoprotein precursor (DSPP) gene, complete cds
9204	17989	23863	1.8	7.5E-01	AE000823.1	NT	Methanobacterium thermoautotrophicum from bases 317350 to 328792 (section 29 of 148) of the complete genome
1138	10361	19510	1.26	7.4E-01	AI598146.1	EST_HUMAN	h14009.x1 NCI_CGAP_Bm25 Homo sapiens cDNA clone IMAGE:2167577 3' similar to contains Alu repetitive element; contains element MIR repetitive element ;
2311	11505	20726	0.93	7.4E-01	AB011108.1	NT	Homo sapiens mRNA for KIAA0534 protein, partial cds
3707	12627	22045	0.58	7.4E-01	AF112538.1	NT	Malva pusilla actin (Act1) mRNA, complete cds
4289	13500	22596	6.84	7.4E-01	AL163246.2	NT	Homo sapiens chromosome 21 segment HS21C046
6804	15888	25458	9.91	7.4E-01	BE747503.1	EST_HUMAN	601573026F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3834174 5'
8168	17300	26843	1.64	7.4E-01	AB021490.2	NT	Oryzias latipes gene for membrane guanylyl cyclase OIGC1, complete cds
8168	17300	26844	1.84	7.4E-01	AB021490.2	NT	Oryzias latipes gene for membrane guanylyl cyclase OIGC1, complete cds
8302	17410		2.98	7.4E-01		NT	Mus musculus complement component 1 inhibitor (C1inh), mRNA
8415	17488		1.42	7.4E-01	AI472641.1	EST_HUMAN	ta13h01.x1 NCI_CGAP_Lym5 Homo sapiens cDNA clone IMAGE:2043985 3'
3952	13167		0.66	7.3E-01	AP000062.1	NT	Aeropyrum pernix genomic DNA, section 57
4818	13612	22802	0.67	7.3E-01	AE001166.1	NT	Borrelia burgdorferi (section 52 of 70) of the complete genome
4711	13902	23002	5.85	7.3E-01	AF225421.1	NT	Homo sapiens HT017 mRNA, complete cds
5130	14308	23399	0.91	7.3E-01	O43103	SWISSPROT	FERRICHRONE SIDEROPHORE PEPTIDE SYNTHETASE
5936	15152	24562	6.03	7.3E-01	L35772.1	NT	Mus musculus antigen (OD72) gene
5936	15152	24563	6.03	7.3E-01	L35772.1	NT	Mus musculus antigen (OD72) gene
6310	15491	24935	8.23	7.3E-01	M26511.1	NT	V. alginolyticus sucrose (scrB) gene, complete cds
6310	15491	24936	8.23	7.3E-01	M26511.1	NT	V. alginolyticus sucrose (scrB) gene, complete cds
7968	17147	26881	3.69	7.3E-01	AA678019.1	EST_HUMAN	z25508.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:431799 3'
7968	17147	26882	3.69	7.3E-01	AA678019.1	EST_HUMAN	z25508.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:431799 3'
841	10078		2.68	7.2E-01	L29281.1	NT	Rattus norvegicus initiation factor-2 kinase (eIF-2a) mRNA, complete cds
1927	11131	20326	4.35	7.2E-01	X79140.1	NT	N. labacum Nelf-4A13 mRNA
2424	11615	20837	2.18	7.2E-01	AB000605.1	NT	Gallus gallus gene for melanocortin 2-receptor, complete cds
3031	12267	21394	1.35	7.2E-01	AF198100.1	NT	Fowlpox virus, complete genome

Page 24 of 382  
Table 4  
Single Exon Probes Expressed in HELA Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3430	12855	21785	3.04	7.2E-01	AF065608.1	NT	Giardia intestinalis variant-specific surface protein (vsp417-6) gene, vsp417-6(A-I) allele, complete cds
3582	12813	21834	1.13	7.2E-01	AB002307.1	NT	Human mRNA for KIA0309 gene, partial cds
4039	13249		0.81	7.2E-01	AF108093.1	NT	Homo sapiens IA-2 gene, intron 18
4780	13969	23071	3.66	7.2E-01	D90314.1	NT	L. mesenteroides gene for sucrose phosphorylase (EC 2.4.1.7)
6335	15515		6.78	7.2E-01	9625875	NT	Human herpesvirus 3, complete genome
7325	16541	26030	6.68	7.2E-01	U82623.1	NT	[Rattus norvegicus cytochrome mRNA, complete cds
7715	16914	26423	1.7	7.2E-01	S76838.1	NT	Dbs=Dbi guanine nucleotide exchange factor homolog [mice, 32D murine hemopoietic cell line, mRNA, 3923 nt]
8857	17760		4.26	7.2E-01	AP000063.1	NT	Aeropyrum pernix genomic DNA, section 8/7
899	9941	19075	12.1	7.1E-01	D21070.1	NT	Rana catesbeiana mRNA for bullfrog skeletal muscle calcium release channel (ryanodine receptor) alpha isoform(RyR1), complete cds
3027	12263	21391	15.67	7.1E-01	AJ270777.1	NT	Homo sapiens partial TCF-4 gene for T-cell transcription factor-4, exons 15-16
4190	13394	22493	3.47	7.1E-01	7305360	NT	Mus musculus otogelin (Otog), mRNA
4190	13394	22494	3.47	7.1E-01	7305360	NT	Mus musculus otogelin (Otog), mRNA
6063	15253	24677	7.74	7.1E-01	U36232.1	NT	Drosophila melanogaster 8-pyruvyltetrahydropterin synthase (pt) gene, complete cds
8840	18160		1.97	7.1E-01	AA421492.1	EST_HUMAN	zu06h11.s1 Soares, testis, NHT Homo sapiens cDNA clone IMAGE:731109 3'
1238	10453	19611	2.68	7.0E-01	AB014514.1	NT	Homo sapiens mRNA for KIAA0614 protein, partial cds
1238	10453	19612	2.68	7.0E-01	AB014514.1	NT	Homo sapiens mRNA for KIAA0614 protein, partial cds
2412	11604	20825	1.49	7.0E-01	N62412.1	EST_HUMAN	yz73e07.s1 Soares, multiple sclerosis, 2NbHMSP Homo sapiens cDNA clone IMAGE:288708 3' similar to contains Alu repetitive element;
2412	11604	20826	1.49	7.0E-01	N62412.1	EST_HUMAN	yz73e07.s1 Soares, multiple sclerosis, 2NbHMSP Homo sapiens cDNA clone IMAGE:288708 3' similar to contains Alu repetitive element;
5088	14268		2.07	7.0E-01	AL163301.2	NT	Homo sapiens chromosome 21 segment HS21C101
5207	14382	23468	0.61	7.0E-01	AE003921.1	NT	Xyella fastidiosa, section 67 of 229 of the complete genome
5253	14426	23502	8.3	7.0E-01	T68328.1	EST_HUMAN	yc41103.s1 Strategene liver (#837224) Homo sapiens cDNA clone IMAGE:83285 3' similar to gb:K03020
6689	15785		9.8	7.0E-01	AE000253.1	NT	PHENYLALANINE-4-HYDROXYLASE (HUMAN);
7680	16879	26385	2.01	7.0E-01	AV763942.1	EST_HUMAN	Escherichia coli K-12 MG1655 section 143 of 400 of the complete genome
7680	16879	26386	2.01	7.0E-01	AV763942.1	EST_HUMAN	AV763942 MDS Homo sapiens cDNA clone MDSCH04 5'
977	10209	19364	11.39	6.9E-01	U69874.1	NT	AV763942 MDS Homo sapiens cDNA clone MDSCH04 5'
977	10209	19365	11.39	6.9E-01	U69874.1	NT	Candida albicans squalene epoxidase (CAERG1) gene, complete cds and translational regulator gene, partial cds
977	10209	19365	11.39	6.9E-01	U69874.1	NT	Candida albicans squalene epoxidase (CAERG1) gene, complete cds and translational regulator gene, partial cds

Page 25 of 382  
Table 4  
Single Exon Probes Expressed in HELA Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1317	10533	19695	2.41	6.9E-01	AA503530.1	EST_HUMAN	nm28a09.s1 NCI_CGAP_Gas1 Homo sapiens cDNA clone IMAGE:1085176 3'
3185	12420	21553	1.88	6.9E-01	AE002271.2	NT	Chlamydia muridarum, section 3 of 85 of the complete genome
5248	14419	23498	0.62	6.9E-01	BE782751.1	EST_HUMAN	601485594F1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3888943 5'
6455	15652	25120	3.94	6.9E-01	AL161573.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 69
6455	15652	25121	3.94	6.9E-01	AL161573.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 69
7810	17003	26516	2.35	6.9E-01	D89013.1	NT	Homo sapiens DAN gene, complete cds
7810	17003	26517	2.35	6.9E-01	D89013.1	NT	Homo sapiens DAN gene, complete cds
8278	18154		3.81	6.9E-01	Q89958	SWISSPROT	FORKHEAD BOX PROTEIN C2 (FORKHEAD-RELATED PROTEIN FKHL14) (MESENCHYME FORK HEAD PROTEIN 1) (MFH-1 PROTEIN) (TRANSCRIPTION FACTOR FKHL14)
984	10197	19352	0.92	6.8E-01	AF017784.1	NT	Giardia intestinalis carbamate kinase gene, complete cds
2834	11817		1.32	6.8E-01	D90917.1	NT	Synechocystis sp. PCC6803 complete genome, 27/27, 3418852-3573470
2781	10807	19983	1.28	6.8E-01	AA854475.1	EST_HUMAN	q75a05.s1 Soares_papillary_tumor_NbHPA Homo sapiens cDNA clone IMAGE:1402256 3' similar to gb:X56411_rna1 ALCOHOL DEHYDROGENASE CLASS II PI CHAIN (HUMAN);
4568	13763	22659	1.35	6.8E-01	J00782.1	NT	Rat(hooded) prolactin gene: exon iii and flanks
6878	18154	25626	3.23	6.8E-01	AB037766.1	NT	Homo sapiens mRNA for KIAA1345 protein, partial cds
7653	16853	26351	2.57	6.8E-01	AJ276875.1	NT	Stagonospora avenae bg11 gene for beta-glucosidase, exons 1-4
7653	16853	26352	2.57	6.8E-01	AJ276875.1	NT	Stagonospora avenae bg11 gene for beta-glucosidase, exons 1-4
7675	16874	26378	2.41	6.8E-01	AF038939.1	NT	Mus musculus zinc finger protein (Peg3) mRNA, complete cds
7675	16874	26380	2.41	6.8E-01	AF038939.1	NT	Mus musculus zinc finger protein (Peg3) mRNA, complete cds
7846	17037	26553	1.85	6.8E-01	AF164151.1	NT	Anopheles gambiae strain M2 translation initiation factor 4C (1A) (eIF-4C) mRNA, complete cds
303	9578	18709	27.9	6.7E-01	AF213884.1	NT	Homo sapiens nuclear factor of kappa light polypeptide gene enhancer in B-cells 1 (NFKB1) gene, complete cds
344	9612	18739	21.23	6.7E-01	AF213884.1	NT	Homo sapiens nuclear factor of kappa light polypeptide gene enhancer in B-cells 1 (NFKB1) gene, complete cds
1878	11083		1.07	6.7E-01	M12132.1	NT	Quail fast skeletal muscle troponin I gene, complete cds
2115	11314	20530	1.38	6.7E-01	AA451864.1	EST_HUMAN	2x12g12.s1 Soares_total_fetus_Nb2Hf8_9w Homo sapiens cDNA clone IMAGE:786310 3' similar to contains element TAR1 repetitive element;
2132	12011	20550	3.16	6.7E-01	AF186073.1	NT	Drosophila melanogaster Mst85C gene, complete cds; NMDMC isoform (Nmdmc) gene, complete cds, alternatively spliced; and transcription factor (Relish) gene, complete cds, alternatively spliced
2953	12191	21325	4.16	6.7E-01	6878580	NT	Mus musculus Wiskott-Aldrich syndrome protein (Wasp) mRNA
4447	13646	22742	0.8	6.7E-01	X74421.1	NT	S. tuberosum mRNA for glucose-6-phosphate dehydrogenase
4985	14172	23262	1.04	6.7E-01	AW079110.1	EST_HUMAN	x885g12.xt NCI_CGAP_Co17 Homo sapiens cDNA clone IMAGE:2574598 3'
6215	15398		4.48	6.7E-01	AE004608.1	NT	Pseudomonas aeruginosa PA01, section 167 of 529 of the complete genome

Page 26 of 382  
Table 4  
Single Exon Probes Expressed in HELA Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7527	16732	26222	2.56	6.7E-01	BF354640.1	EST_HUMAN	CM3-HT0769-010600-197-c03 HT0769 Homo sapiens cDNA
7694	16429	25916	3.48	6.7E-01	O14957	SWISSPROT	N-ACETYLGLUCOSAMINYL-PHOSPHATIDYLINOSITOL BIOSYNTHETIC PROTEIN GP11
2465	11656	20877	0.91	6.6E-01	AF075240.1	NT	Homo sapiens SLT1 protein (SLT2) mRNA, partial cds
2661	11842	21056	1.09	6.6E-01	AF199339.1	NT	Homo sapiens lens epithelium-derived growth factor gene, alternatively spliced, complete cds
3464	12689	21825	1.22	6.6E-01	4506880	NT	Homo sapiens sema domain, seven thrombospondin repeats (type 1 and type 1-like), transmembrane domain (TM) and short cytoplasmic domain, (semaphorin) 5A (SEMASA) mRNA
3638	12859	21978	3.96	6.6E-01	Y07669.1	NT	C albicans random DNA marker, 282bp
4087	13298						Human hereditary haemochromatosis region, histone 2A-like protein gene, hereditary haemochromatosis (HLA-H) gene, Rofet gene, and sodium phosphate transporter (NPT3) gene, complete cds
5803	15020	24421	1.19	6.6E-01	U91328.1	NT	Mus musculus kinesin light chain 2 (Klc2), mRNA
6369	15549	25005	4.35	6.6E-01	6890577	NT	Mus musculus GLC Homo sapiens cDNA clone GLCGID04 3'
629	9874	18985	3.49	6.6E-01	AV660506.1	EST_HUMAN	H. vulgaris Na,K-ATPase alpha subunit mRNA, complete cds
629	9874	18986	2.11	6.5E-01	M75140.1	NT	H. vulgaris Na,K-ATPase alpha subunit mRNA, complete cds
3411	12637	21768	5.25	6.5E-01	AB041225.1	NT	Mus musculus gene for Tab2, complete cds
4287	13470	22563	4.63	6.5E-01	AJ272265.1	NT	Homo sapiens SPP2 gene for secreted phosphoprotein 24 precursor, exons 1-8
4301	13502	22598	0.67	6.5E-01	AL161539.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 39
5095	14275	23358	1.84	6.5E-01	U28921.1	NT	Phaseolus vulgaris ATPase gamma subunit mRNA, nuclear gene encoding mitochondrial protein, partial cds
5413	18054	23773	2.09	6.5E-01	P18480	SWISSPROT	TRANSCRIPTION REGULATORY PROTEIN SNF5 (SWI/SNF COMPLEX COMPONENT SNF5)
7177	16354	25832	3.78	6.5E-01	AF119676.1	NT	Mus musculus small GTP-binding protein RAB25 (Rab25) gene, complete cds
7228	16449	25938	3.68	6.5E-01	H87583.1	EST_HUMAN	JW1706.1 Soares_placenta_8tobweeks_2NbhP8tobW Homo sapiens cDNA clone IMAGE:252515 5'
7278	16497	25989	4.84	6.5E-01	AA601287.1	EST_HUMAN	not5c07.st NCI CGAP_Phe1 Homo sapiens cDNA clone IMAGE:1100748 3'
7371	16587		4.71	6.5E-01	AU138078.1	EST_HUMAN	AU138078 PLACE1 Homo sapiens cDNA clone PLACE1007810 5'
8127	17261	28904	2.85	6.5E-01	AF014115.1	NT	Plasmodium berghei cytochrome c oxidase subunit III, cytochrome c oxidase subunit I, and cytochrome b genes, mitochondrial genes encoding mitochondrial proteins, complete cds
8700	17666		3.08	6.5E-01	BE465050.1	EST_HUMAN	h774a10.x1 NCI CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3179130 3'
8946	18098		1.75	6.5E-01	Z74145.1	NT	S. cerevisiae chromosome IV reading frame ORF YDL097c
256	9532	18663	8.75	6.4E-01	U48848.1	NT	Drosophila melanogaster 8kd dynein light chain mRNA, complete cds
3433	12658	21789	2.87	6.4E-01	U48854.2	NT	Mus musculus dystroglycan 1 (DAG1) gene, exons 1 and 2 and complete cds
4490	13688	22779	0.73	6.4E-01	Y12488.1	NT	M. musculus whn gene
4490	13688	22780	0.73	6.4E-01	Y12488.1	NT	M. musculus whn gene

Page 27 of 382  
Table 4  
Single Exon Probes Expressed in HELA Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7105	16282	25762	9.92	6.4E-01	U82628.1	NT	Homo sapiens ataxia telangiectasia (ATM) gene, complete cds
8816	17734		7.45	6.4E-01	AV759212.1	EST_HUMAN	AV759212 MDS Homo sapiens cDNA clone MDSGCG09 5'
440	9694	18833	4.65	6.3E-01	P05228	SWISSPROT	HISTIDINE-RICH PROTEIN PRECURSOR (CLONE PFHRP-III)
541	9792	18915	2.33	6.3E-01	U32689.1	NT	Haemophilus influenzae Rd section 4 of 163 of the complete genome
2128	11327	20545	2.37	6.3E-01	U81136.1	NT	Shigella flexneri multi-antibiotic resistance locus
2542	11730	20948	2.44	6.3E-01	U75331.1	NT	Gallus gallus bone morphogenetic protein 1 (BMP1) mRNA, partial cds
2542	11730	20949	2.44	6.3E-01	U75331.1	NT	Gallus gallus bone morphogenetic protein 1 (BMP1) mRNA, partial cds
2979	12218		0.69	6.3E-01	Y17275.1	NT	Lycopodium esculentum p69a gene, complete CDS
6886	16077	25545	4.49	6.3E-01	9827521	NT	Varicella virus, complete genome
6886	16077	25546	4.49	6.3E-01	9827521	NT	Varicella virus, complete genome
7627	16829	26326	1.96	6.3E-01	AA877715.1	EST_HUMAN	m09h08.s1 NCL CGAP_Co10 Homo sapiens cDNA clone IMAGE:1161371 3' similar to TR:002816 002816 HLAR.
7879	17087	26592	14.1	6.3E-01	A1904160.1	EST_HUMAN	CM-B7043-090288-046 BT043 Homo sapiens cDNA
7863	17142	26675	2.07	6.3E-01	P47003	SWISSPROT	HYPOTHETICAL 13.7 KD PROTEIN IN INO1-IDS2 INTERGENIC REGION
8116	17250	28780	1.95	6.3E-01	P36073	SWISSPROT	HYPOTHETICAL 15.3 KD PROTEIN IN VMA12-APN1 INTERGENIC REGION
8392	18320	23596	8.86	6.3E-01	9810283	NT	Mus musculus keratin complex 2, gene 6g (K12-6g), mRNA
8490	17534		1.48	6.3E-01	AF105227.1	NT	Homo sapiens 3'-phosphoadenosine 5'-phosphosulfate synthetase (PAPSS) mRNA, complete cds
8716	18230		2.12	6.3E-01	X83528.1	NT	C. limicola pscD gene
5600	14824	24200	1.94	6.2E-01	Q10135	SWISSPROT	HYPOTHETICAL 142.5 KD PROTEIN C23E2.02 IN CHROMOSOME I
6288	15469		2.85	6.2E-01	AF022253.1	NT	Mus musculus calcium-sensing receptor related protein 4 (Casr-r4) mRNA, partial cds
6561	15757	25220	6.38	6.2E-01	H72255.1	EST_HUMAN	ys01e08.s1 Soares fetal liver spleen 1NLS Homo sapiens cDNA clone IMAGE:213542 3'
6915	16103		3.47	6.2E-01	M24461.1	NT	Human pulmonary surfactant-associated protein SP-B (SFTPB) mRNA, complete cds
7100	16277	25757	10.3	6.2E-01	AL161511.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 23
7215	16392	25874	5.08	6.2E-01	P27410	SWISSPROT	NON-STRUCTURAL POLYPEPTIDE (CONTAINS: RNA-DIRECTED RNA POLYMERASE ; THIOL PROTEASE P3C ; HELICASE (2C LIKE PROTEIN); COAT PROTEIN)
7215	16392	25875	5.08	6.2E-01	P27410	SWISSPROT	NON-STRUCTURAL POLYPEPTIDE (CONTAINS: RNA-DIRECTED RNA POLYMERASE ; THIOL PROTEASE P3C ; HELICASE (2C LIKE PROTEIN); COAT PROTEIN)
2358	11551		6.54	6.1E-01	6876078	NT	Mus musculus secreted acidic cysteine rich glycoprotein (Spac), mRNA
6025	15233	24654	3.81	6.1E-01	M64733.1	NT	Rat TRPM-2 gene, complete cds
6025	15233	24655	3.81	6.1E-01	M64733.1	NT	Rat TRPM-2 gene, complete cds
6537	15733	25197	4.89	6.1E-01	AF033535.1	NT	Arabidopsis thaliana putative zinc transporter (ZIP1) mRNA, complete cds
6885	16076	25543	26.49	6.1E-01	AF236117.1	NT	Homo sapiens G-protein coupled receptor EDG-7 mRNA, complete cds
6885	16076	25544	26.49	6.1E-01	AF236117.1	NT	Homo sapiens G-protein coupled receptor EDG-7 mRNA, complete cds



Page 28 of 382  
Table 4  
Single Exon Probes Expressed in HELA Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8225	17355	26892	2.27	6.1E-01	S83182.1	NT	hyaluronan-binding protein=hepatocyte growth factor activator homolog [human, plasma, mRNA, 2408 nt]
8225	17355	26893	2.27	6.1E-01	S83182.1	NT	hyaluronan-binding protein=hepatocyte growth factor activator homolog [human, plasma, mRNA, 2408 nt]
8486	18116	23810	1.39	6.1E-01	AB041350.1	NT	Mus musculus Col4a5 mRNA for type IV collagen alpha 5 chain, complete cds
9150	17953		1.36	6.1E-01	X95287.1	NT	M.mazal orfA, orfB, and orfC of archaeal ABC-transporter system
501	9753	18881	0.83	6.0E-01	D87675.1	NT	Homo sapiens DNA for amyloid precursor protein, complete cds
568	9818		2.86	6.0E-01	5802999	NT	Homo sapiens adaptor-related protein complex 3, mu 2 subunit (CLA20), mRNA
1370	10584	19751	1.71	6.0E-01	AF065253.1	NT	Human respiratory syncytial virus strain CH89-53b attachment protein (G) gene, complete cds
3804	13022	22133	0.82	6.0E-01	AJ233386.1	NT	Viral hemorrhagic septicemia virus N, P, M, G, Nv, L genes, French strain 07-71
4011	13223	22324	1.39	6.0E-01	X16942.1	NT	Xenopus mRNA for desmin
4170	13374		1.31	6.0E-01	AF058895.1	NT	Homo sapiens Notch3 (NOTCH3) gene, exons 26, 27, and 28
5314	14546	23815	1.92	6.0E-01	P20288	SWISSPROT	D(2) DOPAMINE RECEPTOR
5412	14841	23772	2.63	6.0E-01	AW139713.1	EST_HUMAN	UI-H-B11-eeb-a-10-Q-UI.s1 NCI CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2718619 3'
5897	15114	24525	2.84	6.0E-01	U38813.1	NT	Musca domestica Insecticide-susceptible strain voltage-sensitive sodium channel mRNA, complete cds
6232	15413	24854	8.27	6.0E-01	AJ277661.1	NT	Homo sapiens partial LMO1 gene for LIM domain only 1 protein, exon 1
6500	15697	25161	5.08	6.0E-01	P02835	SWISSPROT	SEGMENTATION PROTEIN FUSHI TARAZU
6500	15697	25162	5.08	6.0E-01	P02835	SWISSPROT	SEGMENTATION PROTEIN FUSHI TARAZU
7019	16198	25672	2.66	6.0E-01	AB008193.1	NT	Homo sapiens genes for leukotriene B4 receptor BLT2, leukotriene B4 receptor BLT1, complete cds
7159	16336		2.39	6.0E-01	Q01497	SWISSPROT	PEROXISOMAL MEMBRANE PROTEIN PER9 (PEROXIN-3)
7824	16826	26323	1.98	6.0E-01	AJ131892.1	NT	Gallus gallus mRNA for Hyperion protein, 419 KD isoform
7824	16826	26324	1.98	6.0E-01	AJ131892.1	NT	Gallus gallus mRNA for Hyperion protein, 419 KD isoform
8085	17220	26756	2.66	6.0E-01	AJ420623.1	EST_HUMAN	ff08f07.x1 NCI CGAP_Pr28 Homo sapiens cDNA clone IMAGE:2095621 3'
8788	17715	23960	1.73	6.0E-01	11421863	NT	Homo sapiens nuclear factor (erythroid-derived 2)-like 3 (NFE2L3), mRNA
8896	17790		1.55	6.0E-01	AA706087.1	EST_HUMAN	498g05.s1 Soares_fetal_liver_spleen_INFLS_S1 Homo sapiens cDNA clone IMAGE:462776 3'
9052	18161		2.82	6.0E-01	5903136	NT	Homo sapiens RNA binding motif protein 3 (RBM3), mRNA
9083	18165	23755	1.87	6.0E-01	9055303	NT	Mus musculus cGMP-inhibited phosphodiesterase (Pde3a), mRNA
9121	18090		2.38	6.0E-01	BE157617.1	EST_HUMAN	RC1-HT0376-030500-015-c03 HT0375 Homo sapiens cDNA
1008	10239	19391	2.5	5.9E-01	U32701.1	NT	Haemophilus influenzae Rd section 16 of 163 of the complete genome
3237	12471	21602	5.43	5.9E-01	AL163267.2	NT	Homo sapiens chromosome 21 segment HS21C087
3237	12471	21603	5.43	5.9E-01	AL163267.2	NT	Homo sapiens chromosome 21 segment HS21C067
4205	13408		3.92	5.9E-01	AF162786.1	NT	Rattus norvegicus ctenexin 2 mRNA, partial cds

Page 29 of 382  
Table 4  
Single Exon Probes Expressed in HELA Cells

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5854	15072	24483	5.05	5.9E-01	AF065440.2	NT	Homo sapiens low density lipoprotein receptor-related protein II (LRP2) gene, exon 1 and partial cds
8195	15377	24817	1.64	5.9E-01	AB023486.1	NT	Homo sapiens gene for histamine H2 receptor, promoter region and complete cds
7130	16307	26787	2.2	5.9E-01	P56284	SWISSPROT	VASCULAR ENDOTHelial-CADHERIN PRECURSOR (VE-CADHERIN) (CADHERIN-5)
7264	16463	25976	3.21	5.9E-01	Q8X013	SWISSPROT	THYMIDYLATE KINASE (DTMP KINASE)
7269	16488	25978	1.75	5.9E-01	AF197944.1	NT	Xenopus laevis receptor protein tyrosine phosphatase delta (XPTP-D) mRNA, complete cds
7532	16737	26227	2.97	5.9E-01	AW93175.1	EST_HUMAN	PM1-DT0041-190100-002-003 DT0041 Homo sapiens cDNA
7748	16944	26456	2.23	5.9E-01	AF064626.1	NT	Mus spretus strain SPRET/Ei CD48 antigen (Cd48) gene, partial cds
8429	17495	24012	1.67	5.9E-01	L42320.1	NT	Oryctolagus cuniculus alpha 1 anti-trypsin (alpha 1 AT) gene, promoter region
8684	17653		1.53	5.9E-01	AB017705.1	NT	Aspergillus oryzae pyrG gene for orotidine-5'-phosphate decarboxylase, complete cds
8910	17799		6.21	5.9E-01	P34926	SWISSPROT	MICROTUBULE-ASSOCIATED PROTEIN 1A [CONTAINS: MAP1 LIGHT CHAIN LC2]
1873	11080	20270	0.93	5.8E-01	P40472	SWISSPROT	SIM1 PROTEIN
3982	13177	22280	0.95	5.8E-01	BF695738.1	EST_HUMAN	G01852474F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4076131 5'
4515	13711	22804	2.77	5.8E-01	AB009077.1	NT	Vigna radiata mRNA for protein pyrophosphatase, complete cds
4808	13987		1.44	5.8E-01	AF110846.1	NT	Megascella scalaris sex-lethal homolog (Meglxl) gene, partial cds, alternatively spliced products
6003	15285		2.43	5.8E-01	S65091.1	NT	cyclic AMP-regulated phosphoprotein [rats, mRNA, 1030 nt]
6525	15721	25185	2.9	5.8E-01	P14328	SWISSPROT	SPORE COAT PROTEIN SP86
6525	15721	25186	2.9	5.8E-01	P14328	SWISSPROT	SPORE COAT PROTEIN SP86
6741	15936	25397	12.15	5.8E-01	AJ270774.1	NT	Homo sapiens partial TCF-4 gene for T-cell transcription factor-4, exons 6-11
7581	16766	28257	9.84	5.8E-01	AJ243213.1	NT	Homo sapiens partial 5-HT4 receptor gene, exons 2 to 5
7608	16809		3.72	5.8E-01	BF700092.1	EST_HUMAN	G02127577F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4284403 5'
7701	16900		2.14	5.8E-01	BF700092.1	EST_HUMAN	G02127577F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4284403 5'
3008	12244		0.68	5.7E-01	6756253	NT	Mus musculus plasmacytoma variant translocation 1 (Pvt1), mRNA
3189	12424	21557	1.5	5.7E-01	Q8WTJ2	SWISSPROT	PUTATIVE TRANSCRIPTION FACTOR OVO-LIKE 1 (MOVOL1) (MOVOL1A)
3478	12702		3.08	5.7E-01	AB033503.1	NT	Populus euphratica peacs-2 mRNA for 1-aminocyclopropane-1-carboxylate synthase, complete cds
3881	13097	22214	1.81	5.7E-01	AF011581.1	NT	Homo sapiens T cell receptor beta chain (BV8S7*2-B11S1) mRNA, partial cds
5816	15033	24434	4.41	5.7E-01	BF035413.1	EST_HUMAN	G01454962F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3856590 5'
6400	15581	25038	2.26	5.7E-01	P00373	SWISSPROT	PYRROLINE-5-CARBOXYLATE REDUCTASE (P5CR) (P5C REDUCTASE)
8386	17467		1.31	5.7E-01	BE15051.1	EST_HUMAN	MR3-HT0736-180700-003-002 HT0736 Homo sapiens cDNA
3340	12569	21707	1.22	5.6E-01	AB018283.2	NT	Homo sapiens mRNA for KIAA0740 protein, partial cds
3340	12569	21708	1.22	5.6E-01	AB018283.2	NT	Homo sapiens mRNA for KIAA0740 protein, partial cds
6718	15913	26372	4.84	5.6E-01	AV684703.1	EST_HUMAN	AV684703 GKC Homo sapiens cDNA clone GKCF5F05 5'
6718	15913	25373	4.84	5.6E-01	AV684703.1	EST_HUMAN	AV684703 GKC Homo sapiens cDNA clone GKCF5F05 5'

Page 30 of 382  
Table 4  
Single Exon Probes Expressed in HELA Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8284	17400		2.94	5.8E-01	BE888280.1	EST_HUMAN	601514007F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3915457 5'
8401	17479	28595		5.8E-01	AA483535.1	EST_HUMAN	ng75g10.s1 NCL_CGAP_P16 Homo sapiens cDNA clone IMAGE:940874 similar to contains element PTR7 repetitive element:
8788	14494	23583	1.7	5.8E-01	AL161501.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 13
8812	17732		2.41	5.8E-01	P50505	SWISSPROT	HIGH AFFINITY POTASSIUM TRANSPORTER
9238	18010		4.08	5.8E-01	BF573829.1	EST_HUMAN	602132029F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4271334 5'
1219	10437	19593	1.49	5.5E-01	8393912	NT	[Rattus norvegicus] Protonyl Coenzyme A carboxylase, beta polypeptide (Pccb), mRNA
2882	11843	21057	2.75	5.5E-01	P03341	SWISSPROT	GAG POLYPEPTIDE [CONTAINS: INNER COAT PROTEIN P12; CORE PROTEIN P15; CORE SHELL PROTEIN P30; NUCLEOPROTEIN P10]
2882	11843	21058	2.75	5.5E-01	P03341	SWISSPROT	GAG POLYPEPTIDE [CONTAINS: INNER COAT PROTEIN P12; CORE PROTEIN P15; CORE SHELL PROTEIN P30; NUCLEOPROTEIN P10]
2889	12107	21236	1	5.5E-01	5902085	NT	Homo sapiens superkiller viralicidic activity 2 (S. cerevisiae homolog)-like (SKIV2L), mRNA
3030	12266		1.75	5.5E-01	H46219.1	EST_HUMAN	yo18a10.s1 Soares adult brain N2b5HB55Y Homo sapiens cDNA clone IMAGE:178268 3'
3200	12435	21570	3.16	5.5E-01	AF227240.1	NT	Rabbit oral papillomavirus, complete genome
3671	12892	22013	1.23	5.5E-01	P49755	SWISSPROT	FOS-RELATED ANTIGEN-1
5171	14350		1.05	5.5E-01	AF063866.1	NT	Melanoplus sanguinalipes entomopoxvirus, complete genome
142	9424	18557	10.17	5.4E-01	7657266	NT	Homo sapiens KIAA0928 protein Mx2 interacting nuclear target (MINT) homolog (KIAA0928), mRNA
142	9424	18558	10.17	5.4E-01	7657266	NT	Homo sapiens KIAA0928 protein Mx2 interacting nuclear target (MINT) homolog (KIAA0928), mRNA
592	9840	18559	1.64	5.4E-01	AF232006.1	NT	Pseudomonas syringae pv. tomato strain DC3000 AvrE (avrE), HrpW (hrpW), and Gsta (gsta) genes, complete cds; and unknown genes
592	9840	18560	1.64	5.4E-01	AF232006.1	NT	Pseudomonas syringae pv. tomato strain DC3000 AvrE (avrE), HrpW (hrpW), and Gsta (gsta) genes, complete cds; and unknown genes
1278	10493	19652	3.59	5.4E-01	AW896037.1	EST_HUMAN	QV4-NN0040-070400-180-c04 NN0040 Homo sapiens cDNA
2076	11276		2.48	5.4E-01	AE002247.2	NT	Chlamydomonas reinhardtii AR39, section 74 of 94 of the complete genome
2219	11416	20641	2.25	5.4E-01	AJ276682.1	NT	Drosophila melanogaster mRNA for 15,15' beta cerotene dioxygenase (beta-diox gene)
5260	14433		1.89	5.4E-01	X85973.1	NT	A.thaliana mRNA for phosphatidyl-specific phospholipase C
5514	14739	24104	1.87	5.4E-01	AW842327.1	EST_HUMAN	PM2-CN0030-030200-003-c10 CN0030 Homo sapiens cDNA
7070	16247		2.44	5.4E-01	BF572536.1	EST_HUMAN	602076545F1 NIH_MGC_62 Homo sapiens cDNA clone IMAGE:4243690 5'
7844	16844	28342	3.44	5.4E-01	P38858	SWISSPROT	NITRATE REDUCTASE [NADPH] (NR)
8141	17273	26817	6.26	5.4E-01	Q60875	SWISSPROT	LAMININ ALPHA-2 CHAIN PRECURSOR (LAMININ M CHAIN) (MEROSIN HEAVY CHAIN)
8141	17273	26818	6.26	5.4E-01	Q60875	SWISSPROT	LAMININ ALPHA-2 CHAIN PRECURSOR (LAMININ M CHAIN) (MEROSIN HEAVY CHAIN)

Page 31 of 382  
Table 4  
Single Exon Probes Expressed in HELA Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8348	17443		2.44	5.4E-01	A1858398.1	EST_HUMAN	w37g04.x1 NCL_CGAP_UH1 Homo sapiens cDNA clone IMAGE:2427128 3' similar to gb:M13452 LAMIN A (HUMAN);
522	9773	18898	1.4	5.3E-01	AF019413.1	NT	Homo sapiens HLA class III region containing tenascin X (tenascin-X) gene, partial cds; cytochrome P450 21-hydroxylase (CYP21B), complement component C4 (C4B) G11, helicase (SKI2W), RD, complement factor B (Bf), and complement component C2 (C2) genes, >
2737	11918	21129	7.07	5.3E-01	4506328	NT	Homo sapiens protein tyrosine phosphatase, receptor-type, zeta polypeptide 1 (PTPRZ1) mRNA
2737	11918	21130	7.07	5.3E-01	4506328	NT	Homo sapiens protein tyrosine phosphatase, receptor-type, zeta polypeptide 1 (PTPRZ1) mRNA
3209	12443	21575	3.37	5.3E-01	AF087658.1	NT	Homo sapiens secreted C-type lectin precursor (LSLCL) gene, complete cds
4194	13398		1.36	5.3E-01	U36887.1	NT	Mycoplasma genitalium section 9 of 51 of the complete genome
5423	14650	23785	1.82	5.3E-01	A1820921.1	EST_HUMAN	zu42h12.y5 Soares ovary tumor NbHOT Homo sapiens cDNA clone IMAGE:740711 5'
5423	14650	23788	1.82	5.3E-01	A1820921.1	EST_HUMAN	zu42h12.y5 Soares ovary tumor NbHOT Homo sapiens cDNA clone IMAGE:740711 5'
5510	14735	24097	2.05	5.3E-01	BE645620.1	EST_HUMAN	7e73c12.x1 NCL_CGAP_P28 Homo sapiens cDNA clone IMAGE:3288118 3' similar to gb:J02783 PROTEIN DISULFIDE ISOMERASE PRECURSOR (HUMAN);
5510	14735	24098	2.05	5.3E-01	BE645620.1	EST_HUMAN	7e73c12.x1 NCL_CGAP_P28 Homo sapiens cDNA clone IMAGE:3288118 3' similar to gb:J02783 PROTEIN DISULFIDE ISOMERASE PRECURSOR (HUMAN);
6745	15940		2.53	5.3E-01	L01950.2	NT	Roridula gorgonias ribulose 1,5-bisphosphate carboxylase (rbcl) gene, partial cds; chloroplast gene for chloroplast product
8095	17229	28787	6.26	5.3E-01	BE568291.1	EST_HUMAN	601339887F1 NIH_MGC_53 Homo sapiens cDNA clone IMAGE:3682168 5'
8277	18162		3.58	5.3E-01	AA916053.1	EST_HUMAN	og30e05.s1 NCL_CGAP_B17 Homo sapiens cDNA clone IMAGE:1441376 3' similar to gb:J02611 APOLIPOPROTEIN D PRECURSOR (HUMAN);
828	10084	19216	10.97	5.2E-01	L20770.1	NT	Drosophila melanogaster helix-loop-helix mRNA, complete cds
1172	10393	19545	11.35	5.2E-01	Q9WV30	SWISSPROT	NUCLEAR FACTOR OF ACTIVATED T CELLS 5 (T CELL TRANSCRIPTION FACTOR NFAT5) (NFAT5) (REL DOMAIN-CONTAINING TRANSCRIPTION FACTOR NFAT5)
1198	10419	19572	2.73	5.2E-01	AF224492.1	NT	Homo sapiens phospholipid scramblase 1 gene, complete cds
1851	11058		3.64	5.2E-01	AL163285.2	NT	Homo sapiens chromosome 21 segment HS21C085
2114	11313	20529	2.33	5.2E-01	AB018283.2	NT	Homo sapiens mRNA for KIAA0740 protein, partial cds
2461	11652	20873	10.39	5.2E-01	AF199339.1	NT	Homo sapiens lens epithelium-derived growth factor gene, alternatively spliced, complete cds
2461	11652	20874	10.39	5.2E-01	AF199339.1	NT	Homo sapiens lens epithelium-derived growth factor gene, alternatively spliced, complete cds
3083	12319	21440	1.91	5.2E-01	U65942.1	NT	Chlamydomonas reinhardtii S2838 POMP91A and POMP90A precursor, complete cds
3203	12438		0.77	5.2E-01	D73443.1	NT	Azotobacter vinelandii lcd gene for isocitrate dehydrogenase, complete cds
3383	12610		1.54	5.2E-01	AL116780.1	NT	Bacillus cereus strain T4 cDNA library under conditions of nitrogen deprivation
3421	12848	21776	2.28	5.2E-01	AA084165.1	EST_HUMAN	em77g05.s1 Stragelena schizos brain S11 Homo sapiens cDNA clone IMAGE:1616504 3'
3810	12831		0.6	5.2E-01	AF020289.1	NT	Medicago sativa chloroplast malate dehydrogenase precursor (p1mdh) mRNA, nuclear gene encoding chloroplast protein, complete cds

Page 32 of 382  
Table 4  
Single Exon Probes Expressed in HELA Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4482	13680		1.07	5.2E-01	AF093798.1	NT	Avian infectious bronchitis virus isolate variant 2 S1 spike glycoprotein gene, partial cds
4608	13802	22892	0.7	5.2E-01	6752947	NT	Mus musculus acetylcholine receptor beta (Acrb), mRNA
9206	17991		4.88	5.2E-01	P18516	SWISSPROT	RETINOIC ACID RECEPTOR GAMMA (RAR-GAMMA) (RETINOIC ACID RECEPTOR DELTA) (RAR-DELTA)
623	9868	18980	1.62	5.1E-01	M58509.1	NT	Human adrenodoxin reductase gene, exons 3 to 12
654	9800	19025	4.65	5.1E-01	AJ233944.1	NT	Polyomavirus vitellinum (strain PI vt1) 16S rRNA gene
654	9800	19026	4.65	5.1E-01	AJ233944.1	NT	Polyomavirus vitellinum (strain PI vt1) 16S rRNA gene
1992	11195		1.2	5.1E-01	BF683095.1	EST_HUMAN	602139319F1 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4298117 5'
4054	13284	22667	4.8	5.1E-01	A1858495.1	EST_HUMAN	w39b12.x1 NCI_CGAP_U11 Homo sapiens cDNA clone IMAGE:2427263 3'
4168	13372	22471	3.35	5.1E-01	P96380	SWISSPROT	TRANSCRIPTION-REPAIR COUPLING FACTOR (TRCF)
6049	15217	24637	1.74	5.1E-01	R80873.1	EST_HUMAN	y94409.x1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:146872 3'
6986	16164	25638	6.52	5.1E-01	J05412.1	NT	Human regenerating protein (reg) gene, complete cds
6987	16165	25637	4.7	5.1E-01	W22202.1	EST_HUMAN	6581 Human retina cDNA Tsp5091-cleaved sublibrary Homo sapiens cDNA not directional
8501	18084		3.24	5.1E-01	BF030207.1	EST_HUMAN	601556863F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:3826767 5'
8759	17700		2.09	5.1E-01	BF439982.1	EST_HUMAN	nac51f10.x1 NCI_CGAP_Bm23 Homo sapiens cDNA clone IMAGE:3406218 3' similar to contains element TAR1 repetitive element
2104	11304	20517	1.06	5.0E-01	4885552	NT	Homo sapiens postmeiotic segregation increased 2-like 9 (PMS2L9), mRNA
2104	11304	20518	1.06	5.0E-01	4885552	NT	Homo sapiens postmeiotic segregation increased 2-like 9 (PMS2L9), mRNA
2112	11311	20525	1.53	5.0E-01	AF008210.1	NT	Buchnera aphidicola genomic fragment containing (chaperone Hsp60) groEL, DNA biosynthesis initiating protein (dnaA), ATP operon (atpCDGAHFEB) and putative chromosome replication protein (gidA) genes, complete cds; and termination factor Rho (rho) gene>
2112	11311	20526	1.53	5.0E-01	AF008210.1	NT	Buchnera aphidicola genomic fragment containing (chaperone Hsp60) groEL, DNA biosynthesis initiating protein (dnaA), ATP operon (atpCDGAHFEB) and putative chromosome replication protein (gidA) genes, complete cds; and termination factor Rho (rho) gene>
3729	12948	22068	0.64	5.0E-01	U55574.1	NT	Mus musculus anti-DNA immunoglobulin light chain IgM mRNA, antibody 363p.138, partial cds
3854	13070	22184	3.27	5.0E-01	AB033010.1	NT	Homo sapiens mRNA for KIAA1184 protein, partial cds
6898	15604	25069	4.28	5.0E-01	BF317212.1	EST_HUMAN	601903871F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4136632 5'
8434	17500		1.92	5.0E-01	AF029215.1	NT	Mus musculus MRC OX-2 antigen homolog gene, exons 2-5, and complete cds
9174	17967		2.88	5.0E-01	AL163302.2	NT	Homo sapiens chromosome 21 segment HS21C102
9185	17976		3.84	5.0E-01	O13961	SWISSPROT	NUCLEAR ENVELOPE PROTEIN GUT11
789	10038	19189	2.7	4.9E-01	BF571462.1	EST_HUMAN	602076849F1 NIH_MGC_62 Homo sapiens cDNA clone IMAGE:4243860 5'
1635	10849	20027	2.96	4.9E-01	AJ243955.1	NT	Xenopus laevis mRNA for c-Jun protein, 1978 BP
1870	11077	20267	1.33	4.9E-01	U40869.1	NT	Cavia porcellus pulmonary surfactant protein A (SP-a) mRNA, complete cds
5677	14897	24289	3.1	4.9E-01	AF020931.1	NT	Homo sapiens diacylglycerol kinase 3 (DAGK3) gene, exon 10

Page 33 of 382  
Table 4  
Single Exon Probes Expressed in HELA Cells

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5677	14897	24280	3.1	4.9E-01	AF020831.1	NT	Homo sapiens diacylglycerol kinase 3 (DAGK3) gene, exon 10
6275	15455	24898	1.66	4.9E-01	AB040051.1	NT	Oryza sativa subsp. japonica mEF-G mRNA for mitochondrial elongation factor G, complete cds
6853	18389		2.73	4.9E-01	10948863	NT	Mus musculus unc13 homolog (C. elegans) 1 (Unc13h1), mRNA
8328	17429		1.61	4.9E-01	AF176912.1	NT	Homo sapiens neurotrophin-1/B-cell stimulating factor-3 gene, complete cds
9167	18354		4.8	4.9E-01	AA613562.1	EST_HUMAN	nc22e11.s1 NCI_CGAP_Co10 Homo sapiens cDNA clone IMAGE:1144652 3'
9249	18019		1.47	4.9E-01	11431438	NT	Homo sapiens eukaryotic translation initiation factor 4 gamma, 1 (EIF4G1), mRNA
3512	12736		0.98	4.8E-01	AA912842.1	EST_HUMAN	q32a09.s1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1525144 3'
4324	13525		0.69	4.8E-01	4504850	NT	Homo sapiens potassium channel, subfamily K, member 5 (TASK-2) (KCNK5) mRNA, and translated products
4678	13525		0.68	4.8E-01	4504850	NT	Homo sapiens potassium channel, subfamily K, member 5 (TASK-2) (KCNK5) mRNA, and translated products
5443	14869	23828	9.14	4.8E-01	J02987.1	NT	Saccharomyces cerevisiae sporulation protein (SPO11) gene required for meiotic recombination, complete cds
5961	15178		3.79	4.8E-01	AA659878.1	EST_HUMAN	nu85f09.s1 NCI_CGAP_A11 Homo sapiens cDNA clone IMAGE:1217513
6216	15397		2.3	4.8E-01	5031650	NT	Homo sapiens reproduction 8 (D8S2288E) mRNA
6399	15580	25036	3.91	4.8E-01	AL161492.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 4
6399	15580	25037	3.81	4.8E-01	AL161492.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 4
7316	16534		2.05	4.8E-01	X83502.1	NT	S.cerevisiae ORFs from chromosome X
8408	17483		1.26	4.8E-01	AL163227.2	NT	Homo sapiens chromosome 21 segment HS21C027
8645	18122		3.04	4.8E-01	AF227565.1	NT	Trypanosoma cruzi transposon VIP II SIRE repeat region
3039	12276		0.79	4.7E-01	AF192987.1	NT	Felis catus feline leukemia virus subgroup C receptor (FLVCR1) mRNA, complete cds
5882	15099	24510	8.23	4.7E-01	BF217173.1	EST_HUMAN	601883880F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4086387 5'
7424	16634		6.26	4.7E-01	AF102673.1	NT	Influenza A virus isolate hk51697 hemagglutinin (HA) gene, partial cds
7651	16851	26349	2.42	4.7E-01	U41069.1	NT	Human collagen alpha2(XI) (COL11A2) gene, exons 6 through 16, and partial cds
7915	17130	26660	2.99	4.7E-01	AW889448.1	EST_HUMAN	RC6-NT0029-240400-011-E08 NT0029 Homo sapiens cDNA
8667	17643		1.41	4.7E-01	AW341581.1	EST_HUMAN	hd11c08.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2809188 3'
3724	12944	22061	1.84	4.6E-01	BF683300.1	EST_HUMAN	602081103F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4245481 5'
3724	12944	22062	1.64	4.6E-01	BF683300.1	EST_HUMAN	602081103F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4245481 5'
5428	14655	23782	3.65	4.6E-01	Q90843	SWISSPROT	INTERFERON REGULATORY FACTOR 3 (IRF-3)
5428	14655	23793	3.65	4.6E-01	Q90843	SWISSPROT	INTERFERON REGULATORY FACTOR 3 (IRF-3)
5464	14690	24042	1.86	4.6E-01	BE734781.1	EST_HUMAN	qh59h02.x1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:3849637 5'
5473	14699	24052	1.88	4.6E-01	AI247679.1	EST_HUMAN	TR:015338 015338 BUTYRPHILIN.1

Page 34 of 382  
Table 4  
Single Exon Probes Expressed in HELA Cells

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5473	14699	24053	1.88	4.6E-01	A1247679.1	EST_HUMAN	qh59h02.x1 Soares_fetal_liver_spleen_INFLS_S1 Homo sapiens cDNA clone IMAGE:1849011 3' similar to TR:O15338 O15338 BUTYROPHILIN.;
5985	15287	24892	1.64	4.6E-01	U62332.1	NT	Emricella nidulans NEMPA (nempa) gene, mitochondrial gene encoding putative mitochondrial protein, complete cds
5985	15287	24893	1.64	4.6E-01	U62332.1	NT	Emricella nidulans NEMPA (nempa) gene, mitochondrial gene encoding putative mitochondrial protein, complete cds
6388	15568	25025	2.25	4.6E-01	AA493577.1	EST_HUMAN	nm04005.s1 NCI_CGAP_Thy1 Homo sapiens cDNA clone IMAGE:943353 similar to contains Alu repetitive element; contains element L1 repetitive element;
6568	15704	25228	21.67	4.6E-01	BF697399.1	EST_HUMAN	602130953F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4287828 5'
7063	16240	25713	3.37	4.6E-01	A1915634.1	EST_HUMAN	wg73e12.x1 Soares_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:2370768 3'
7063	16240	25714	3.37	4.6E-01	A1915634.1	EST_HUMAN	wg73e12.x1 Soares_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:2370768 3'
7563	16768		3.16	4.6E-01	P98163	SWISSPROT	PUTATIVE VITELLOGENIN RECEPTOR PRECURSOR (VL)
7571	16776	26268	3.63	4.6E-01	BE185449.1	EST_HUMAN	IL5-HT0730-100500-075-g05 HT0730 Homo sapiens cDNA
7571	16776	26269	3.63	4.6E-01	BE185449.1	EST_HUMAN	IL5-HT0730-100500-075-g05 HT0730 Homo sapiens cDNA
8007	16442	25930	5.97	4.6E-01	AF019369.1	NT	Human thiopurine methyltransferase (TPMT) gene, exon 10 and complete cds
8007	16442	25931	5.97	4.6E-01	AF019369.1	NT	Human thiopurine methyltransferase (TPMT) gene, exon 10 and complete cds
8588	17597		1.24	4.6E-01	D53316.1	EST_HUMAN	HUM105F03B Clontech human fetal brain poly(A+ mRNA (#8535) Homo sapiens cDNA clone GEN-105F03 5'
1875	11082	20272	1.17	4.5E-01	AE001931.1	NT	Deinococcus radiodurans R1 section 88 of 229 of the complete chromosome 1
1875	11082	20273	1.17	4.5E-01	AE001931.1	NT	Deinococcus radiodurans R1 section 88 of 229 of the complete chromosome 1
2822	12061	21184	5.61	4.5E-01	AA677086.1	EST_HUMAN	z55002.s1 Soares_fetal_liver_spleen_INFLS_S1 Homo sapiens cDNA clone IMAGE:454178 3'
3289	12520	21651	4.15	4.5E-01	Q05793	SWISSPROT	BASEMENT MEMBRANE-SPECIFIC HEPARAN SULFATE PROTEOGLYCAN CORE PROTEIN PRECURSOR (HSPG)(PERLECAN)(PLC)
3358	12584	21723	1.2	4.5E-01	AF126378.1	NT	Mus musculus DNA polymerase epsilon catalytic subunit (Pde) gene, exons 2 through 12
4006	13218		1.27	4.5E-01	Q28247	SWISSPROT	COLLAGEN ALPHA 5(V) CHAIN
4052	13262	22365	0.66	4.5E-01	A1708908.1	EST_HUMAN	es99e09.x1 Barstead aorta HPLR86 Homo sapiens cDNA clone IMAGE:2353480 3'
4157	14479		5.3	4.5E-01	AW873495.1	EST_HUMAN	hcd0g02.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:3041810 3'
4862	14149	23241	1.17	4.5E-01	BE963445.2	EST_HUMAN	601657225R1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3868023 3'
6340	15520	24967	2.51	4.5E-01	A1859849.1	EST_HUMAN	w32e02.x1 NCI_CGAP_U11 Homo sapiens cDNA clone IMAGE:2426618 3' similar to TR:Q92823 Q92823 SWI/ISF COMPLEX 170 KDA SUBUNIT.;
6602	15788	25255	4.3	4.5E-01	A1649598.1	EST_HUMAN	tz58g11.x1 NCI_CGAP_Ov35 Homo sapiens cDNA clone IMAGE:2282844 3'
6710	15905		2.22	4.5E-01	11444783	NT	Homo sapiens hypothetical protein DKFZp547G183 (DKFZp547G183), mRNA
7212	16389	25871	16.01	4.5E-01	M86006.1	EST_HUMAN	EST02531 Fetal brain, Strategene (cat#836206) Homo sapiens cDNA clone HFBCY17
7212	16389	25872	18.01	4.5E-01	M86006.1	EST_HUMAN	EST02531 Fetal brain, Strategene (cat#836206) Homo sapiens cDNA clone HFBCY17

Table 4

## Single Exon Probes Expressed in HELA Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7440	18648	26141	3.36	4.5E-01	AW691271.1	EST_HUMAN	x014h01.x1 NCL_CGAP_UK3 Homo sapiens cDNA clone IMAGE:2703985 3' similar to SW:INT6_MOUSE Q64252 VIRAL INTEGRATION SITE PROTEIN INT-6 [1]:
7804	18987		1.8	4.5E-01	AV719382.1	EST_HUMAN	AV719382 GLC Homo sapiens cDNA clone GLCCED12 5'
8036	17172	28711	2.23	4.5E-01	BE068472.1	EST_HUMAN	IRC3-BT0333-160300-016-503 BT0333 Homo sapiens cDNA
8286	18346		3.39	4.5E-01	BE871481.1	EST_HUMAN	601449201F1 NIH_MGC_85 Homo sapiens cDNA clone IMAGE:3852881 5'
8983	17854		1.42	4.5E-01	BF337531.1	EST_HUMAN	602035275F1 NCL_CGAP_Bm64 Homo sapiens cDNA clone IMAGE:4183280 5'
9067	17894		3.3	4.5E-01	11422099	NT	Homo sapiens testis-specific Kinase 2 (TESK2), mRNA
2004	11207		1.99	4.4E-01	6880503	NT	Mus musculus integral membrane-associated protein 1 (Itmap1), mRNA
2352	11545	20767	3.37	4.4E-01	P49765	SWISSPROT	VASCULAR ENDOTHELIAL GROWTH FACTOR B PRECURSOR (VEGF-B) (VEGF RELATED FACTOR)
3287	12518	21649	1.37	4.4E-01	AF058790.1	NT	Rattus norvegicus SynGAP-b mRNA, complete cds
3287	12518	21650	1.37	4.4E-01	AF058790.1	NT	Rattus norvegicus SynGAP-b mRNA, complete cds
3291	12522	21653	2.03	4.4E-01	BF058726.1	EST_HUMAN	791d02.y1 NCL_CGAP_Br16 Homo sapiens cDNA clone IMAGE:3393795 5'
4219	13422		1.4	4.4E-01	BE378707.1	EST_HUMAN	601237139F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3609393 5'
5242	14416		4.05	4.4E-01	Q11082	SWISSPROT	PROBABLE G PROTEIN-COUPLED RECEPTOR B0563.6
5770	14988	24389	1.93	4.4E-01	AW080795.1	EST_HUMAN	x027608.x1 NCL_CGAP_Co18 Homo sapiens cDNA clone IMAGE:2585510 3' similar to TR:O95154 O95154 AFLATOXIN B1-ALDEHYDE REDUCTASE.
6411	16608		10.38	4.4E-01	Z11879.1	NT	S. tuberculum mRNA for induced ablon lip protein (partial)
7058	18235		2.74	4.4E-01	P28922	SWISSPROT	GLYCOPROTEIN B PRECURSOR (GLYCOPROTEIN 14)
7110	16287	25768	4.94	4.4E-01	P35590	SWISSPROT	TYROSINE-PROTEIN KINASE RECEPTOR TIE-1 PRECURSOR
8570	17588	23998	3.41	4.4E-01	6677874	NT	Mus musculus sodium channel, type X, alpha polypeptide (Scn10a), mRNA
8581	18279		4.39	4.4E-01	AL163282.2	NT	Homo sapiens chromosome 21 segment HS21C082
9035	17879	23893	3.59	4.4E-01	P54725	SWISSPROT	Autographa californica nucleopolyhedrovirus, complete genome
9137	17945		1.88	4.4E-01	9627742	NT	UV EXCISION REPAIR PROTEIN PROTEIN RAD23 HOMOLOG A (HHR23A)
417	9670	18810	2.15	4.3E-01	AF155218.1	NT	Callithrix jacchus MW/LW opsin gene, upstream flanking region
417	9670	18811	2.15	4.3E-01	AF155218.1	NT	Callithrix jacchus MW/LW opsin gene, upstream flanking region
1583	10766	19873	0.92	4.3E-01	AW866550.1	EST_HUMAN	GV4-SN0024-200400-183-b01 SN0024 Homo sapiens cDNA
2824	12063		1.01	4.3E-01	AW935289.1	EST_HUMAN	CM2-DT0003-010200-077-c01 DT0003 Homo sapiens cDNA
3025	12261	21389	0.87	4.3E-01	AW999477.1	EST_HUMAN	MRO-BN0070-270300-008-g04 BN0070 Homo sapiens cDNA
4133	13339	22438	1.3	4.3E-01	J00306.1	NT	Human somatostatin 1 gene and flanks
4400	9670	18810	0.99	4.3E-01	AF155218.1	NT	Callithrix jacchus MW/LW opsin gene, upstream flanking region
4400	9670	18811	0.99	4.3E-01	AF155218.1	NT	Callithrix jacchus MW/LW opsin gene, upstream flanking region
5618	14841	24219	2.04	4.3E-01	AF179825.1	NT	Saimiri sciureus olfactory receptor (SSC188) gene, partial cds
5968	15183	24599	4.69	4.3E-01	AJ001678.1	NT	Coturnix coturnix japonica ifnG gene



Page 36 of 382  
Table 4  
Single Exon Probes Expressed in HELA Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6283	15444		1.94	4.3E-01	BF348001.1	EST_HUMAN	602023134F1 NCI_CGAP_Bm87 Homo sapiens cDNA clone IMAGE:4158286 5'
6609	15805		3.13	4.3E-01	U97040.1	NT	Methanococcus voltae flagella-related protein C-1 (flaC-fla) genes, complete cds
7505	15275	24705	2.79	4.3E-01	AF075629.1	NT	Equus caballus microsatellite LEX027
7757	16953	28460	1.8	4.3E-01	AW993658.1	EST_HUMAN	RC3-BN0034-280200-013-c12 BN0034 Homo sapiens cDNA
7757	16953	28461	1.8	4.3E-01	AW993658.1	EST_HUMAN	RC3-BN0034-280200-013-c12 BN0034 Homo sapiens cDNA
9238	18009		2.07	4.3E-01	AJ003022.1	NT	Streptomyces coelicolor whiH gene
1368	11992	19747	1.62	4.2E-01	Q39102	SWISSPROT	CELL DIVISION PROTEIN FTSH HOMOLOG PRECURSOR
1917	11122		0.89	4.2E-01	AA761653.1	EST_HUMAN	nc24a08 at NCI_CGAP_GCBT Homo sapiens cDNA clone IMAGE:1288896 3'
3587	12808	21930	5.31	4.2E-01	AE003947.1	NT	Xyella fastidiosa, section 93 of 229 of the complete genome
3618	12837	21958	1.03	4.2E-01	AI280338.1	EST_HUMAN	q94b01.x1 Soares_Nhi-MP_u_S1 Homo sapiens cDNA clone IMAGE:1879645 3'
3692	14478		0.8	4.2E-01	N81203.1	EST_HUMAN	788IE1 fetal brain cDNA Homo sapiens cDNA clone 788IE1-K similar to R07879, Z40498
3960	13175	22289	1.16	4.2E-01	Q04888	SWISSPROT	SOX-8 PROTEIN
4707	13898	22997	7.2	4.2E-01	AA534093.1	EST_HUMAN	ng69h01.s1 NCI_CGAP_P10 Homo sapiens cDNA clone IMAGE:987777 similar to gb:M33600 HLA CLASS III HISTOCOMPATIBILITY ANTIGEN, DR-1 BETA CHAIN (HUMAN);
4760	13979	23083	4.08	4.2E-01	R13467.1	EST_HUMAN	W77601.r1 Soares Infant brain 1N1B Homo sapiens cDNA clone IMAGE:28278 5'
6084	15254	24878	9.98	4.2E-01	AU158472.1	EST_HUMAN	AU158472 PLACE2 Homo sapiens cDNA clone PLACE2000470 3'
6084	15254	24879	9.98	4.2E-01	AU158472.1	EST_HUMAN	AU158472 PLACE2 Homo sapiens cDNA clone PLACE2000470 3'
6093	18071	24726	1.98	4.2E-01	S82504.1	NT	Brcal1=breast cancer gene [rata, WF, spleen, Genomic, 419 nt, segment 2 of 2]
6122	15308	24739	5.87	4.2E-01	AL161547.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 47
6461	15658	25129	5.45	4.2E-01	AW957448.1	EST_HUMAN	EST369413 MAGE resequences, MAGE Homo sapiens cDNA
6461	15658	25130	5.45	4.2E-01	AW957448.1	EST_HUMAN	EST369413 MAGE resequences, MAGE Homo sapiens cDNA
7612	16815	26311	2.08	4.2E-01	AB023489.1	NT	Oryzias latipes OIGC7 mRNA for membrane guanylyl cyclase, complete cds
7633	17073	26600	2.55	4.2E-01	BE968485.2	EST_HUMAN	601660352R1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3906085 3'
9179	17971		1.28	4.2E-01	AV731815.1	EST_HUMAN	AV731815 HTF Homo sapiens cDNA clone HTFBH05 5'
1102	10326	19476	1.44	4.1E-01	AI905481.1	EST_HUMAN	RC-BT091-210193-142 BT091 Homo sapiens cDNA
1111	10335	19485	0.85	4.1E-01	AV705243.1	EST_HUMAN	AV705243 ADB Homo sapiens cDNA clone ADBAHF08 5'
1111	10335	19488	0.85	4.1E-01	AV705243.1	EST_HUMAN	AV705243 ADB Homo sapiens cDNA clone ADBAHF08 5'
2671	11852	21068	1.14	4.1E-01	7705283	NT	Homo sapiens anaphase-promoting complex subunit 7 (APC7), mRNA
2891	12128	21261	2.32	4.1E-01	AL161536.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 38
3272	12505	21636	0.6	4.1E-01	AA906344.1	EST_HUMAN	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 38
3753	12972	22087	0.74	4.1E-01	AW961292.1	EST_HUMAN	EST373364 MAGE resequences, MAGG Homo sapiens cDNA
3753	12972	22088	0.74	4.1E-01	AW961292.1	EST_HUMAN	EST373364 MAGE resequences, MAGG Homo sapiens cDNA
4260	13463	22555	2.98	4.1E-01	AJ249207.1	NT	Rhodococcus sp. AD45 isoG, isoH, isoI, isoA, isoB, isoC, isoD, isoE and isoF genes

Page 37 of 382  
Table 4  
Single Exon Probes Expressed in HELA Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4292	13494		0.78	4.1E-01	AA099257.1	EST_HUMAN	cm33c02.s1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1542819 3'
4670	13864	22865	1.28	4.1E-01	AV747880.1	EST_HUMAN	AV747880 NPC Homo sapiens cDNA clone NPCBDF10 5'
5257	14430		0.85	4.1E-01	BF345483.1	EST_HUMAN	602019232F1 NCI_CGAP_Bim67 Homo sapiens cDNA clone IMAGE:4155102 5'
5650	14873	24260	4.51	4.1E-01	BF681393.1	EST_HUMAN	602156590F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4297319 5'
6285	15446	24985	2.7	4.1E-01	U67535.1	NT	Methanococcus jannaschii section 77 of 150 of the complete genome
7416	16628	26120	50.16	4.1E-01	X58700.1	NT	Zea mays ZMPMS2 gene for 19 kDa zein protein
7630	16406	25890	2.89	4.1E-01	Q09470	SWISSPROT	VOLTAGE-GATED POTASSIUM CHANNEL PROTEIN KV1.1 (HUK1) (HBK1)
8918	18325		1.75	4.1E-01	D87675.1	NT	Homo sapiens DNA for amyloid precursor protein, complete cds
138	11960		3.52	4.0E-01	AW847123.1	EST_HUMAN	RC2-CT0201-280999-012-d10 CT0201 Homo sapiens cDNA
1046	10271	19422	1.06	4.0E-01	8404856	NT	Laqueus rubellus mitochondrion, complete genome
1347	10562	19727	1.04	4.0E-01	AF203478.1	NT	Drosophila melanogaster Dalmatian (dm1) mRNA, complete cds
1478	10691		3.71	4.0E-01	6678258	NT	Mus musculus platelet derived growth factor receptor, beta polypeptide (Pdgfra), mRNA
1974	12007	20384	1.86	4.0E-01	Z96933.1	NT	Ascarobolus imnerus masc2 gene
1974	12007	20385	1.86	4.0E-01	Z96933.1	NT	Ascarobolus imnerus masc2 gene
2757	9421	18555	2.81	4.0E-01	6678190	NT	Mus musculus ubiquitin-protein ligase e3 component n-recogin (Ubr1), mRNA
2923	12161	21295	1.49	4.0E-01	AL163280.2	NT	Homo sapiens chromosome 21 segment HS21C080
2923	12161	21296	1.49	4.0E-01	AL163280.2	NT	Homo sapiens chromosome 21 segment HS21C080
							Streptococcus pneumoniae Y1C (y1C), Y1D (y1D), penicillin-binding protein 2x (pbp2x), and undecaprenyl-phosphate-UDP-MurNAc-pentapeptide phospho-MurNAc-pentapeptide transferase (mraY) genes, complete cds
3673	12894	22016	2.17	4.0E-01	AF068903.1	NT	Ovis aries partial JD2 gene for T cell receptor delta chain (TCRDJ2), exon 1
3817	13035	22146	3.33	4.0E-01	AJ277511.1	NT	Ovis aries partial JD2 gene for T cell receptor delta chain (TCRDJ2), exon 1
3817	13035	22147	3.33	4.0E-01	AJ277511.1	NT	NADH-PLASTOQUINONE OXIDOREDUCTASE CHAIN 5, CHLOROPLAST
4832	14021		9.93	4.0E-01	Q31849	SWISSPROT	Synechocystis sp. PCC 9413 transposase gene, complete cds
8212	17343		3.53	4.0E-01	L76080.1	NT	Homo sapiens chromosome 21 segment HS21C100
8587	18179		2.28	4.0E-01	AL163300.2	NT	HYPOTHETICAL 48.7 KD PROTEIN IN GIN2-STE3 INTERGENIC REGION
9138	17946		1.4	4.0E-01	P36049	SWISSPROT	Gorilla gorilla carboxyl-ester lipase (CEL) gene, complete cds
1384	10598	19765	1.52	3.9E-01	AF206618.1	NT	Homo sapiens mRNA for KIAA1193 protein, partial cds
2605	11789	21009	3.23	3.9E-01	AB033019.1	NT	H. sapiens B-myb gene
2666	11847	21061	4.39	3.9E-01	X82032.1	NT	H. sapiens B-myb gene
2666	11847	21062	4.39	3.9E-01	X82032.1	NT	Sinorhizobium meliloti egl, syB2, cya3 genes and orf3
3062	12298	21422	4.8	3.9E-01	AJ225896.1	NT	7f61401.x1 NCI_CGAP_Br16 Homo sapiens cDNA clone IMAGE:3339169 3'
4055	13265	22368	1.53	3.9E-01	BF592611.1	EST_HUMAN	601563948F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3833698 5'
5014	14201	23288	2.1	3.9E-01	BE728967.1	EST_HUMAN	601862362F1 NIH_MGC_53 Homo sapiens cDNA clone IMAGE:4082055 5'
9030	14854	24237	4.01	3.9E-01	BF208036.1	EST_HUMAN	

Page 38 of 382  
Table 4  
Single Exon Probes Expressed in HELA Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7032	16209	25686	3.45	3.9E-01	M19879.1	NT	Human clabindin 27 gene, exons 10 and 11, and L1 and Alu repeats
7397	16610		1.64	3.9E-01	AV695974.1	EST_HUMAN	AV695974 GKC Homo sapiens cDNA clone GKCBCQC11 5'
8352	18255		4.15	3.9E-01	AF304354.1	NT	Homo sapiens proteoglycan 3 (PRG3) gene, complete cds
8475	17528		2.15	3.9E-01	Q61670	SWISSPROT	HOMEOBOX PROTEIN HLX1
8561	17582	23987	1.37	3.9E-01	AE001811.1	NT	Thermotoga maritima section 123 of 136 of the complete genome
9011	17865		1.31	3.9E-01	11433335	NT	Homo sapiens hypothetical protein FLJ10583 (FLJ10583), mRNA
163	9445		16.12	3.8E-01	7019488	NT	Homo sapiens protein kinase PKNbeta (pknbeta), mRNA
512	9763		6.59	3.8E-01	AB029291.1	NT	Mus musculus pcm-1 mRNA for pericentriolar material-1, complete cds
1836	11044		1.28	3.8E-01	AE003870.1	NT	Xyella fastidiosa, section 18 of 229 of the complete genome
2535	11723	20940	3.41	3.8E-01	AF214117.1	NT	Arabidopsis thaliana putative c-myc-like transcription factor (MYB3R-3) mRNA, complete cds
2698	12021	21000	4.04	3.8E-01	6678002	NT	Mus musculus solute carrier family 1, member 8 (Slc1a8), mRNA
2861	12189		0.92	3.8E-01	AF251057.1	NT	Human immunodeficiency virus type 1 complete genome (isolate 88SE-MP1213)
3013	12249	21380	2.35	3.8E-01	AF043383.1	NT	Pleurocetes americanus aminopeptidase N (ampN) gene, partial cds
3458	12683	21817	9.08	3.8E-01	AL161518.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 30
3513	12737		0.75	3.8E-01	AF07219.1	EST_HUMAN	wf38b12.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2357855 3'
3528	12737		0.66	3.8E-01	AF07219.1	EST_HUMAN	wf38b12.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2357855 3'
3556	12779	21908	6.64	3.8E-01	AF109372.1	NT	Danio rerio blue-sensitive opsin (blups) mRNA, complete cds
3556	12779	21909	6.64	3.8E-01	AF109372.1	NT	Danio rerio blue-sensitive opsin (blups) mRNA, complete cds
3739	12959	22074	1.09	3.8E-01	BE154080.1	EST_HUMAN	PMO-HT0339-200400-010-G01 HT0339 Homo sapiens cDNA
3894	13110	22228	0.69	3.8E-01	6754095	NT	Mus musculus general transcription factor III (Gtf2l), mRNA
5079	14259	23344	1.14	3.8E-01	AF038833.1	NT	Homo sapiens Mpv17 protein (MPV17) gene, partial cds; and urocortin gene, complete cds
5221	14395	23480	4.31	3.8E-01	AF158635.1	NT	Tribolium ventriosum V6 (V6) gene, partial cds
5945	15161	24574	5.59	3.8E-01	BE072399.1	EST_HUMAN	QV3-BT0537-271289-049-e02 BT0537 Homo sapiens cDNA
5984	15266	24691	4.68	3.8E-01	AF374601.1	EST_HUMAN	ta54f11.x1 Soares_total_fetus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:2047917 3' similar to contains Alu repetitive element
6287	15478		4.51	3.8E-01	X61597.1	NT	M. musculus gene for kallikrein-binding protein
6641	15836	25297	3.65	3.8E-01	AB046851.1	NT	Homo sapiens mRNA for KIAA1631 protein, partial cds
6944	16088		7.37	3.8E-01	T95413.1	EST_HUMAN	ye43h06.r1 Soares fetal liver spleen 1NFS Homo sapiens cDNA clone IMAGE:120539 5' similar to contains Alu repetitive element
8065	17200		3.41	3.8E-01	BE719218.1	EST_HUMAN	RC0-HT0841-040800-032-b12 HT0841 Homo sapiens cDNA
8190	17322	26865	3.07	3.8E-01	R42550.1	EST_HUMAN	yf92h11.s1 Soares infant brain 1N1B Homo sapiens cDNA clone IMAGE:30289 3'
8190	17322	26866	3.07	3.8E-01	R42550.1	EST_HUMAN	yf92h11.s1 Soares infant brain 1N1B Homo sapiens cDNA clone IMAGE:30289 3'
8571	17589		2.97	3.8E-01	AE001124.1	NT	Borrelia burgdorferi (section 10 of 70) of the complete genome
8703	18276		1.58	3.8E-01	U94788.1	NT	Human p53 (TP53) gene, complete cds

Page 39 of 382  
Table 4  
Single Exon Probes Expressed in HELA Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8818	17738		1.91	3.8E-01	BE829258.1	EST_HUMAN	QV3-E T0063-190700-271-405 E T0063 Homo sapiens cDNA
9237	18251		1.26	3.8E-01	AF291483.1	NT	Mus musculus vomeronasal receptor V1RA4 (V1ra4) gene, complete cds
9255	18023	23852	1.24	3.8E-01	AF194972.1	NT	Mus musculus developmental control protein mRNA, partial cds
2443	11634	20854	8.52	3.7E-01	AB037831.1	NT	Homo sapiens mRNA for KIAA1410 protein, partial cds
3437	12882	21784	10.32	3.7E-01	AF056336.1	NT	Danio rerio bone morphogenetic protein 4 precursor (BMP4) gene, complete cds
3852	13088	22183	1	3.7E-01	AA319482.1	EST_HUMAN	EST21715 Adrenal gland tumor Homo sapiens cDNA 5' end
4214	13417	22513	8.6	3.7E-01	AI218707.1	EST_HUMAN	ok39cd07.x1 Scores_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA
4311	13512	22608	1.22	3.7E-01	AW878037.1	EST_HUMAN	MR3-OT0007-080300-104-b02 OT0007 Homo sapiens cDNA
4384	13585	22687	2.78	3.7E-01	AE002408.1	NT	Neisseria meningitidis serogroup B strain MC58 section 50 of 206 of the complete genome
5272	14474	23516	7.85	3.7E-01	BE865937.1	EST_HUMAN	601878239F1 NIH_MGC_53 Homo sapiens cDNA clone IMAGE:3961136 5'
6135	15319	24753	3.37	3.7E-01	11625843	NT	Homo sapiens tumor endothelial marker 7 precursor (TEM7), mRNA
6571	15767	25229	3.35	3.7E-01	11438739	NT	Homo sapiens chromosome 12 open reading frame 4 (C12ORF4), mRNA
6571	15767	25230	3.35	3.7E-01	11438739	NT	Homo sapiens chromosome 12 open reading frame 4 (C12ORF4), mRNA
7138	18315	25786	3.64	3.7E-01	AI336411.1	EST_HUMAN	q148b07.x1 Scores_fetal_lung_NHL19W Homo sapiens cDNA clone IMAGE:1950887 3'
7699	18802	26285	2.8	3.7E-01	AJ297357.1	NT	Homo sapiens partial LIMD1 gene for LIM domains containing protein 1 and KIAA0851 gene
7599	18802	26296	2.8	3.7E-01	AJ297357.1	NT	Homo sapiens partial LIMD1 gene for LIM domains containing protein 1 and KIAA0851 gene
7604	18807	26304	2.52	3.7E-01	AF149766.1	NT	Erythrocytic pata isolate #B289 decay-accelerating factor (CD55) gene, partial cds
8002	18437	25924	4.81	3.7E-01	X04122.1	NT	Bovine mRNA for terminal deoxynucleotidyltransferase (Tdt) (EC 2.7.7.31)
8239	17368		3.16	3.7E-01	6677678	NT	Mus musculus retinoblastoma 1 (Rb1), mRNA
8268	17916		1.53	3.7E-01	JD4882.1	NT	Human heart/skeletal muscle ATP/ADP translocator (ANT1) gene, complete cds
8441	17504		3.72	3.7E-01	AJ243525.1	NT	Chlamydomonas reinhardtii partial omp1 gene for outer membrane protein 1
8542	17567		2.37	3.7E-01	D86976.1	NT	Human mRNA for KIAA0223 gene, partial cds
8931	17813		1.89	3.7E-01	AL121154.1	EST_HUMAN	DKFZp762K075_r1 762 (synonym: hmel2) Homo sapiens cDNA clone DKFZp762K075 5'
9000	17860	23888	2.55	3.7E-01	Y18000.1	NT	Homo sapiens NF2 gene
9232	18210		1.23	3.7E-01	X91192.1	NT	H. sapiens PLC beta 3 gene (exon 1) and SOM172 gene (exon 1)
285	9540	18070	1.16	3.6E-01	AJ009609.1	NT	Brassica napus mRNA for MAP4K alpha2 protein
1003	10234		7.24	3.6E-01	U89241.1	NT	Human mlb gene, partial cds
1321	10536	19700	2.68	3.6E-01	T80255.1	EST_HUMAN	ydb3e05.r1 Scores infant brain 1N1B Homo sapiens cDNA clone IMAGE:24443 5'
1321	10536	19701	2.68	3.6E-01	T80255.1	EST_HUMAN	ydb3e05.r1 Scores infant brain 1N1B Homo sapiens cDNA clone IMAGE:24443 5'
1881	11088	20278	6.2	3.6E-01	AW590184.1	EST_HUMAN	hg33f02.x1 NCI_CGAP_G08 Homo sapiens cDNA clone IMAGE:2847419 3'
1881	11088	20279	6.2	3.6E-01	AW590184.1	EST_HUMAN	hg33f02.x1 NCI_CGAP_G08 Homo sapiens cDNA clone IMAGE:2847419 3'
1922	11126	20322	5.46	3.6E-01	AF216207.1	NT	Mus musculus ribosomal protein S19 (Rps19) gene, complete cds
2234	11429		1.19	3.6E-01	AB002321.1	NT	Human mRNA for KIAA0323 gene, partial cds
2353	11546		1.88	3.6E-01	X78725.1	NT	P. irregularis (P3804) gene for actin

Page 40 of 382  
Table 4  
Single Exon Probes Expressed in HELA Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2450	11841	20862	1.18	3.6E-01	AW812033.1	EST_HUMAN	RC5-ST0171-181089-011-g07 ST0171 Homo sapiens cDNA
2594	11780	20998	1.3	3.6E-01	P24208	SWISSPROT	PROTEIN-L-ISOASPARTATE O-METHYLTRANSFERASE (PROTEIN-BETA-ASPARTATE METHYLTRANSFERASE) (PIMT) (PROTEIN L-ISOASPARTYL METHYLTRANSFERASE) (L-ISOASPARTYL PROTEIN CARBOXYL METHYLTRANSFERASE)
2851	14476		9.22	3.6E-01	AF199485.1	NT	Drosophila melanogaster sugar transporter 3 (sut3) mRNA, complete cds
3448	12871	21805	2.86	3.6E-01	X78758.1	NT	H. sapiens serotonin transporter gene, exons 9 and 10
3448	12871	21806	2.88	3.6E-01	X78758.1	NT	H. sapiens serotonin transporter gene, exons 9 and 10
4402	13602	22702	1.01	3.6E-01	BE707893.1	EST_HUMAN	RC1-HT0545-150600-014-b12 HT0545 Homo sapiens cDNA
4700	13891	22891	0.94	3.6E-01	AJ009609.1	NT	Brassica napus mRNA for MAP4K alpha2 protein
4730	13821	23024	0.97	3.6E-01	AF071938.1	NT	Mus musculus protein tyrosine kinase Tec (Tec) gene, alternative exons 4 and 4a, exons 5 through 7 and Tec isoform, complete cds
4730	13821	23025	0.97	3.6E-01	AF071938.1	NT	Mus musculus protein tyrosine kinase Tec (Tec) gene, alternative exons 4 and 4a, exons 5 through 7 and Tec isoform, complete cds
4765	13954	23055	0.71	3.6E-01	Y11528.1	NT	Z. mays mRNA for casein kinase II alpha subunit
4802	13981	23099	5.79	3.6E-01	AJ228237.1	NT	Bacteria from anoxic bulk soil 16S rRNA gene (strain XB45)
5033	14218	23303	2.96	3.6E-01	AW339393.1	EST_HUMAN	ha02g04.x1 NCL CGAP_Lu24 Homo sapiens cDNA clone IMAGE:2872566 3'
5131	14309	23400	0.76	3.6E-01	BE087699.1	EST_HUMAN	MR4-BT0358-270300-005-c10 BT0358 Homo sapiens cDNA
5862	15080	24492	1.86	3.6E-01	Y10196.1	NT	Homo sapiens PHEX gene
6138	15322		4.03	3.6E-01	R94090.1	EST_HUMAN	y74a08.r1 Soares fetal liver spleen 1NLS Homo sapiens cDNA clone IMAGE:275987 5'
6202	15383	24825	1.81	3.6E-01	AW027174.1	EST_HUMAN	wt72c10.x1 Soares thymus NHFTh Homo sapiens cDNA clone IMAGE:2513010 3' similar to TR:O15117
6552	15748	25208	21.1	3.6E-01	AL181583.2	NT	O15117 FYN BINDING PROTEIN. [1]; Arabidopsis thaliana DNA chromosome 4, contig fragment No. 79
6765	15860	25415	5.02	3.6E-01	4504956	NT	Homo sapiens lysosomal-associated membrane protein 2 (LAMP2), transcript variant LAMP2A, mRNA
6765	15860	25418	5.02	3.6E-01	4504956	NT	Homo sapiens lysosomal-associated membrane protein 2 (LAMP2), transcript variant LAMP2A, mRNA
7027	18204	25681	24.7	3.6E-01	Q53194	SWISSPROT	PROBABLE PEPTIDE ABC TRANSPORTER ATP-BINDING PROTEIN Y4TS
7518	18723	26213	2.34	3.6E-01	BE602390.1	EST_HUMAN	601678418F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3958997 5'
7872	18871	26374	3.94	3.6E-01	AB004293.1	NT	Arabidopsis thaliana mRNA for SigB, complete cds
7980	18415	25902	3.79	3.6E-01	AE000856.1	NT	Methanobacterium thermoautotrophicum from bases 702375 to 714311 (section 62 of 148) of the complete genome
8305	18383		2.02	3.6E-01	Y18210.1	NT	Homo sapiens hrb5 gene for hair keratin, exons 1 to 9
8391	17472		5.38	3.6E-01	AE000335.1	NT	Escherichia coli K-12 MG1655 section 225 of 400 of the complete genome
8553	17576		3.86	3.6E-01	U68888.1	NT	Mus musculus Emv1 mRNA, complete cds

Page 41 of 382  
Table 4  
Single Exon Probes Expressed in HELA Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8937	17817		1.52	3.6E-01	11432598	NT	Homo sapiens myeloid/lymphoid or mixed-lineage leukemia (t(11q24;q24) translocation; translocated to, 10 (AF10), mRNA
9208	18327		2.18	3.6E-01	AW190229.1	EST_HUMAN	X60611.X1 NCI_CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2879116 3' similar to gb:K00558 TUBULIN
9259	18027		1.86	3.6E-01	L27208.1	NT	ALPHA-1 CHAIN (HUMAN);
115	9403	18532	0.79	3.5E-01	AL161536.2	NT	Oryza sativa root-specific RCc3 mRNA, complete cds
214	9494	18626	2.07	3.5E-01	6878933	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 36
684	9927	19058	1.16	3.5E-01	AL161581.2	NT	Mus musculus mannose receptor, C type 2 (Mrc2), mRNA
732	9973	19112	1.36	3.5E-01	7706136	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 77
732	9973	19113	1.36	3.5E-01	7706136	NT	Homo sapiens GAP-like protein (LOC51306), mRNA
789	10029	19178	3.99	3.5E-01	BF129798.1	EST_HUMAN	Homo sapiens GAP-like protein (LOC51306), mRNA
1917	10830	20005	1.84	3.5E-01	U35776.1	NT	601811060R1 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4053951 3'
2247	11442	20668	0.93	3.5E-01	P06798	SWISSPROT	Rattus norvegicus ADP-ribosylation factor-directed GTPase activating protein mRNA, complete cds
2567	12020	20972	2.03	3.5E-01	AA223252.1	EST_HUMAN	HOMEBOX PROTEIN HOX-A4 (HOX-1.4) (MH-3)
2957	12185	21329	0.76	3.5E-01	AA057691.1	EST_HUMAN	zr08a09.s1 Stragene NT2 neuronal precursor 937230 Homo sapiens cDNA clone IMAGE:650872 3'
3763	13011		1.23	3.5E-01	AA842138.1	EST_HUMAN	z94103.r1 Stragene corneal stroma (#937222) Homo sapiens cDNA clone IMAGE:512285 5'
4249	13452	22543	2.33	3.5E-01	AF071253.1	NT	nr60d03.s1 NCI_CGAP_Lym3 Homo sapiens cDNA clone IMAGE:1172357 3'
4953	14140	23234	4.58	3.5E-01	M18349.1	NT	Danio rerio homeobox protein (hoxb5b) gene, complete cds
5147	14326		3.22	3.5E-01	AA825140.1	EST_HUMAN	Rat leukocyte common antigen (L-Ca) gene, exons 1 through 5
5356	14586	23662	1.81	3.5E-01	Q96687	SWISSPROT	oe62b07.s1 NCI_CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1416181 3'
5356	14586	23663	1.81	3.5E-01	Q96687	SWISSPROT	EARLY E2A DNA-BINDING PROTEIN
6107	15201		3.66	3.5E-01	X98505.1	NT	EARLY E2A DNA-BINDING PROTEIN
6489	15888		3.28	3.5E-01	11448042	NT	S. cerevisiae mRNA for CD31 protein (PECAM-1)
7320	16337	26025	3.47	3.5E-01	X61084.1	NT	Homo sapiens tumor protein p53-binding protein, 2 (TP53BP2), mRNA
7592	16708	26289	2.15	3.5E-01	AJ243178.1	NT	C. griseus rhodopsin gene for opsin protein
7592	16708	26290	2.15	3.5E-01	AJ243178.1	NT	Gallus gallus SPARC gene for osteonectin, promoter and exon 1
8119	17253	26794	2.04	3.5E-01	N77597.1	EST_HUMAN	Gallus gallus SPARC gene for osteonectin, promoter and exon 1
8181	17313	26855	1.67	3.5E-01	L05145.1	NT	yz90h12.r1 Soares multiple sclerosis 2N5HMSP Homo sapiens cDNA clone IMAGE:290375 5'
8472	17525		2.16	3.5E-01	X64565.1	NT	Human glucokinase (GCK) gene, repeat polymorphism
8643	17628		1.55	3.5E-01	AE001774.1	NT	B. taurus atpA1 gene for F(0)F(1) ATP synthase alpha-subunit
9263	18227	23697	2.45	3.5E-01	H80814.1	EST_HUMAN	Thermoboga maritima section 86 of 138 of the complete genome
9263	18227	23698	2.45	3.5E-01	H80814.1	EST_HUMAN	ys84111.r1 Soares retina N2b4HR Homo sapiens cDNA clone IMAGE:219597 5'
9263	18227	23698	2.45	3.5E-01	H80814.1	EST_HUMAN	ys84111.r1 Soares retina N2b4HR Homo sapiens cDNA clone IMAGE:219597 5'

Page 42 of 382  
Table 4  
Single Exon Probes Expressed in HELA Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
714	9866		1.67	3.4E-01	AJ242956.1	NT	Homo sapiens partial N-myc (exon 3), HPV45 L2, HPV45 L1, HPV45 E8, HPV45 E7 and HPV45 E1 genes isolated from IC4 cervical carcinoma cell line
983	10214	19370	5.03	3.4E-01	Y09788.2	NT	Pseudomonas fluorescens colR, cds genes,orf222 and partial inaA gene
1334	10549	19713	1.61	3.4E-01	Y00554.1	NT	Azrobacter vinelandii nifA gene for NifA protein (positive regulatory element)
2366	11559	20781	2.41	3.4E-01	D90909.1	NT	Synechocystis sp. PCC6803 complete genome, 11/27, 1311235-1430418
2658	12197	21331	0.97	3.4E-01	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C010
2859	12197	21332	0.97	3.4E-01	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C010
3125	12360	21489	6.49	3.4E-01	U83905.1	NT	Genia familiaris rod photoreceptor cGMP-gated channel alpha-subunit (CNGC1) mRNA, complete cds
3317	12547	21880	0.94	3.4E-01	AF034862.1	NT	Homo sapiens pulmonary surfactant protein D, promoter region and exon 1
3505	12729	21886	4.93	3.4E-01	AF106835.1	NT	Methylovorus sp. strain SS1 putative GrpE (grpE), DnaK (dnaK), and putative DnaJ (dnaJ) genes, complete cds
3772	12990		1.4	3.4E-01	BF449010.1	EST_HUMAN	7r64e01.x1 NCI_CGAP_Ov18 Homo sapiens cDNA clone IMAGE:3572232 3' similar to TR:Q9UJ15
4029	13239		1.43	3.4E-01	AA594196.1	EST_HUMAN	not11b10.s1 NCI_CGAP_Phe1 Homo sapiens cDNA clone IMAGE:1100347 3'
4496	13694	22788	0.68	3.4E-01	AF168341.1	NT	Homo sapiens integrin alpha 8 (ITGA8) gene, exons 12 through 23
4645	13839	22929	2.14	3.4E-01	BE069912.1	EST_HUMAN	MR4-BT0403-230200-202-c01 BT0403 Homo sapiens cDNA
4971	14156		4.38	3.4E-01	AJ240973.1	EST_HUMAN	q95c05.x1 NCI_CGAP_Kid3 Homo sapiens cDNA clone IMAGE:1867208 3' similar to contains Alu repetitive element
5529	14753	24120	3.01	3.4E-01	AL161594.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 80
5577	14801		5.61	3.4E-01	AA085313.1	EST_HUMAN	zn12d11.s1 Stratagene hNT neuron (#837233) Homo sapiens cDNA clone IMAGE:547221 3'
5657	14880		1.94	3.4E-01	L02871.1	NT	Echovirus 22 1A, 1C, 1D, 2A, 2B, 2C, 3A, 3B, 3C, 3D proteins RNA, complete mature peptides and cds
5711	14930	24324	1.99	3.4E-01	AW204505.1	EST_HUMAN	UI-H-B11-ee1-e-12-0-UI.s1 NCI_CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2719582 3'
5788	14987	24387	1.86	3.4E-01	AL120544.1	EST_HUMAN	DKFZp761A249.1 761 (synonym: hamy2) Homo sapiens cDNA clone DKFZp761A249 5'
6831	16025	25490	5.51	3.4E-01	P28013	SWISSPROT	INTEGRIN BETA-8 PRECURSOR
6831	16025	25491	5.51	3.4E-01	P28013	SWISSPROT	INTEGRIN BETA-8 PRECURSOR
6892	15598	25063	8.46	3.4E-01	U19492.1	NT	Saccharomyces cerevisiae Maf1p (MAF1) gene, complete cds
6892	15598	25064	8.46	3.4E-01	U19492.1	NT	Saccharomyces cerevisiae Maf1p (MAF1) gene, complete cds
7037	16214	25691	3.24	3.4E-01	AJ225084.1	NT	Homo sapiens FAA gene, exon 16, 17 and 18
7586	16791		4.26	3.4E-01	AE000881.1	NT	Methanobacterium thermoautotrophicum from bases 1018444 to 1029212 (section 87 of 148) of the complete genome
7621	16824	26320	2.64	3.4E-01	P08925	SWISSPROT	PROBABLE E4 PROTEIN

Page 43 of 382  
Table 4  
Single Exon Probes Expressed in HELA Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7657	16857	26358	2.78	3.4E-01	AF045981.1	NT	Rutillus arcasii cytochrome b (cytb) gene, mitochondrial gene encoding mitochondrial protein, partial cds
7632	17024	26539	1.89	3.4E-01	M25856.1	NT	Human von Willebrand factor gene, exons 36 and 37
7632	17024	26540	1.89	3.4E-01	M25856.1	NT	Human von Willebrand factor gene, exons 36 and 37
8032	17169	26708	1.9	3.4E-01	AB035507.1	NT	Rattus norvegicus mRNA for e-gliadin/MUC18, complete cds
8058	17183	26731	4.69	3.4E-01	AL161515.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 27
8250	17378	26912	1.85	3.4E-01	BF061048.1	EST_HUMAN	7469d12.x1 NCI_CGAP_GC8 Homo sapiens cDNA clone IMAGE:3480646 3'
8282	17398		1.9	3.4E-01	U93604.1	NT	Citrus variegation virus putative replicase gene, partial cds
8394	17473		1.37	3.4E-01	Z21621.1	NT	S.cerevisiae RIB5 gene encoding Riboflavin synthase
8500	18118		1.58	3.4E-01	AF254351.1	NT	Schizosaccharomyces pombe Cwflp (cwf18) gene, complete cds
8623	17617		6.12	3.4E-01	L26339.1	NT	Human autotaxin mRNA, complete cds
8655	18149		2.98	3.4E-01	BE218652.1	EST_HUMAN	hva2h08.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3176127 3' similar to contains PTR5.13
8713	18252		1.9	3.4E-01	9838361	NT	PTR5 repetitive element
8825	17739	23931	1.98	3.4E-01	AJ297131.1	NT	Beta vulgaris mitochondrion, complete genome
						NT	Mus musculus SIL, MAP_17, CYP_a, SCL & CYP_b genes
9142	17948		2.16	3.4E-01	AF018413.1	NT	Homo sapiens HLA class III region containing tenascin X (tenascin-X) gene, partial cds; cytochrome P450 21-hydroxylase (CYP21B), complement component C4 (C4B) G11, helicase (SKI2W), RD, complement factor B (Bf), and complement component C2 (C2) genes, >
14	9310	18412	14.06	3.3E-01	X07990.1	NT	Rhizobium leguminosarum sym plasmid pRL5J nodX gene
105	9310	18412	5.73	3.3E-01	X07990.1	NT	Rhizobium leguminosarum sym plasmid pRL5J nodX gene
454	9707	18846	0.77	3.3E-01	AL161646.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 45
639	9885	18010	1.85	3.3E-01	7662485	NT	Homo sapiens KIAA1100 protein (KIAA1100), mRNA
1208	10427	19584	3.17	3.3E-01	Q12446	SWISSPROT	PROLINE-RICH PROTEIN LAS17
1314	10530	19692	3.14	3.3E-01	BF568880.1	EST_HUMAN	602184016T1 NIH_MGC_42 Homo sapiens cDNA clone IMAGE:4300251 3'
1585	10788	19974	1.04	3.3E-01	6753885	NT	Mus musculus disintegrin 5 (Dign5), mRNA
1710	10822		1.41	3.3E-01	AA332734.1	EST_HUMAN	EST38722 Embryo, 8 week 1 Homo sapiens cDNA 5' end
2369	11562		4.41	3.3E-01	4507834	NT	Homo sapiens uridine monophosphate synthetase (arotate phosphoribosyl transferase and orotidine-5'-decarboxylase) (UMPS) mRNA
2901	12139	21276	2.03	3.3E-01	AJ251605.1	NT	Bacteriophage phi-YeO3-12 complete genome
2877	12214		0.87	3.3E-01	O02743	SWISSPROT	INTERLEUKIN-12 ALPHA CHAIN PRECURSOR (IL-12A) (CYTOTOXIC LYMPHOCYTE MATURATION FACTOR 35 KD SUBUNIT) (CLMF P36)
3020	12256	21385	1.04	3.3E-01	AJ007932.2	NT	Streptomyces argillaceus mithramycin biosynthetic genes
3470	12695	21831	0.97	3.3E-01	AB012922.1	NT	Homo sapiens MTA1-L1 gene, complete cds
3783	13001	22116	0.6	3.3E-01	D14016.1	NT	Rat mRNA for cyclin E, complete cds



Table 4

## Single Exon Probes Expressed in HELA Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3787	13015	22128	2.2	3.3E-01	084645	SWISSPROT	EXODEOXYRIBONUCLEASE V BETA CHAIN
3808	13026	22136	1	3.3E-01	P22602	SWISSPROT	GENOME POLYPROTEIN [CONTAINS: N-TERMINAL PROTEIN (P1); HELPER COMPONENT PROTEINASE (HC-PRO); PROTEIN P3]
3942	13158	22275	1.97	3.3E-01	AL161498.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 10
3978	13192	22300	2.17	3.3E-01	AF200446.1	NT	Hypoxylon fragiforme chitin synthase gene, partial cds
4361	13563		2.43	3.3E-01	D31682.1	NT	Rattus norvegicus DNA for regucalcin, partial cds
4698	13887		1.58	3.3E-01	A1539114.1	EST_HUMAN	h78b12.x1 NCI_CGAP_U18 Homo sapiens cDNA clone IMAGE:2205407 3' similar to gb:X57522 ANTIGEN
4856	14044	23138	1.36	3.3E-01	D64003.1	NT	PEPTIDE TRANSPORTER 1 (HUMAN);
5222	14366	23481	1.51	3.3E-01	AW884409.1	EST_HUMAN	Synechocystis sp. PCC6803 complete genome, 22/27, 2755703-2868766
5348	14578	23654	2.48	3.3E-01	X89818.1	NT	QV3-OT0065-280300-137-g11 OT0065 Homo sapiens cDNA
5348	14578	23655	2.48	3.3E-01	X89818.1	NT	R. norvegicus mRNA for 3'UTR of ubiquitin-like protein
5636	14860	24244	1.76	3.3E-01	BE619650.1	EST_HUMAN	R. norvegicus mRNA for 3'UTR of ubiquitin-like protein
5636	14860	24245	1.76	3.3E-01	BE619650.1	EST_HUMAN	601472768T1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3875753 3'
5678	14898	24291	6.34	3.3E-01	P05691	SWISSPROT	601472768T1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3875753 3'
6035	15243	24684	4.91	3.3E-01	A1628131.1	EST_HUMAN	CIRCUMSPOROZOITE PROTEIN (CS)
6035	15243	24685	4.61	3.3E-01	A1628131.1	EST_HUMAN	ty64h01.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2265809 3' similar to contains Alu repetitive element; contains element L1 repetitive element;
6408	15589	25049	1.8	3.3E-01	N85146.1	EST_HUMAN	ty64h01.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2265809 3' similar to contains Alu repetitive element; contains element L1 repetitive element;
6642	15837	25298	14.61	3.3E-01	BF663954.1	EST_HUMAN	J2498F Human fetal heart, Lambda ZAP Express Homo sapiens cDNA clone J2498 5' similar to TEGT
6916	16104	25570	3.78	3.3E-01	N60866.1	EST_HUMAN	602140372F1 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4301800 5'
6935	16079	25549	3.25	3.3E-01	BF376745.1	EST_HUMAN	z667h01.s1 Soares_fetal_lung_NbHL19W Homo sapiens cDNA clone IMAGE:297649 3'
7309	16527	26017	2.71	3.3E-01	X63953.1	NT	RC4-TN0077-250800-011-g04 TN0077 Homo sapiens cDNA
7309	16527	26018	2.71	3.3E-01	X63953.1	NT	D.mauritiana Adh gene
7595	16798		1.89	3.3E-01	BF528499.1	EST_HUMAN	D.mauritiana Adh gene
7783	16878	26491	11.77	3.3E-01	BE219351.1	EST_HUMAN	602070802F1 NCI_CGAP_Bm84 Homo sapiens cDNA clone IMAGE:4213585 5'
							h51g02.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3176878 3'
							GALECTIN-3 (GALACTOSE-SPECIFIC LECTIN 3) (MAC-2 ANTIGEN) (IGE-BINDING PROTEIN) (35 KD LECTIN) (CARBOHYDRATE BINDING PROTEIN 35) (CBP 35) (LAMININ-BINDING PROTEIN) (LECTIN L-28) (CBP30)
7885	17101	26632	4.85	3.3E-01	P47953	SWISSPROT	
8209	17340		4.68	3.3E-01	AA806921.1	EST_HUMAN	6b71g02.s1 NCI_CGAP_GC81 Homo sapiens cDNA clone IMAGE:1336850 3'
8228	9310	18412	2.53	3.3E-01	X07900.1	NT	Rhizobium leguminosarum sym plasmid pRL5J1 nodX gene
8381	17465	26590	1.58	3.3E-01	6598319	NT	Homo sapiens aldehyde oxidase 1 (AOX1), mRNA

Page 45 of 382  
Table 4  
Single Exon Probes Expressed in HELA Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9131	17941		12.3	3.3E-01	AP000002.1	NT	Pyrococcus horikoshii OT3 genomic DNA, 287001-544000 nt, position (27)
463	9716		2.22	3.2E-01	AF018261.1	NT	Rattus norvegicus E1H domain binding protein Epsin mRNA, complete cds
725	9987		0.92	3.2E-01	AL191961.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 61
1170	10391	19543	18.32	3.2E-01	AF047013.1	NT	Fusarium roseum virus 1 RNA2 putative RNA dependent RNA polymerase gene, complete cds
1289	10504	19665	1.74	3.2E-01	Z50202.1	NT	P. vulgaris arc5-1 gene
1394	10608	19772	6.8	3.2E-01	Q48624	SWISSPROT	LACTOSE PERMEASE (LACTOSE-PROTON SYMPORT) (LACTOSE TRANSPORT PROTEIN)
1744	10956	20139	1.28	3.2E-01	Z36041.1	NT	S. cerevisiae chromosome II reading frame ORF YBR172e
1754	10966	20151	5.41	3.2E-01	AW957194.1	EST_HUMAN	EST389284 MAGE resequences, MAGD Homo sapiens cDNA
1754	10968	20152	5.41	3.2E-01	AW957194.1	EST_HUMAN	EST389284 MAGE resequences, MAGD Homo sapiens cDNA
1810	11019	20211	1.34	3.2E-01	AL111655.1	NT	Botrytis cinerea strain T4 cDNA library under conditions of nitrogen deprivation
2128	11325	20543	2.6	3.2E-01	BF20387.1	EST_HUMAN	601868804F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4111512 5'
2506	11694		2.24	3.2E-01	7710079	NT	Mus musculus Pbx/knotted 1 homeobox (Pbxox1), mRNA
2670	11851	21067	1.35	3.2E-01	AF050568.1	NT	Homo sapiens promyelocytic leukemia zinc finger protein (PLZF) gene, complete cds
3586	12807		0.67	3.2E-01	D10872.1	NT	Human h NAT allele 3-2 gene for arylamine N-acetyltransferase
4387	13588	22690	1.44	3.2E-01	M18818.1	NT	Rabbit beta-like globin gene cluster encoding the epsilon, gamma, delta (pseudogene) and beta globin polypeptides, complete cds
4501	13699	22783	1.34	3.2E-01	Q10268	SWISSPROT	HYPOTHETICAL 81.7 KD PROTEIN C13G7.04C IN CHROMOSOME 1 PRECURSOR
4749	13940		7.91	3.2E-01	BF693617.1	EST_HUMAN	602081972F1 NIH_MGC_91 Homo sapiens cDNA clone IMAGE:4246503 5'
4901	14089	23182	0.69	3.2E-01	Q57081	SWISSPROT	CYTADHERENCE HIGH MOLECULAR WEIGHT PROTEIN 3 (CYTADHERENCE ACCESSORY PROTEIN 3) (ACCESSORY ADHESIN PROTEIN 3) (P69)
5310	14541	23610	3.05	3.2E-01	BE173964.1	EST_HUMAN	CMO-HT0569-060300-269-f10 HT0569 Homo sapiens cDNA
6516	15712	25177	2.43	3.2E-01	M60266.1	NT	Rat ISO-alpha natriuretic factor gene, complete cds
6585	15781	25241	13.9	3.2E-01	X02508.1	NT	H. sapiens gene fragment for acetylcholine receptor (AChR) alpha subunit exons 8, 9 and 3' flanking region
6587	15783	25244	22.45	3.2E-01	BF311635.1	EST_HUMAN	601897107F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4126833 5'
6645	15840	25300	2.84	3.2E-01	AE002015.1	NT	Deinococcus radiodurans R1 section 152 of 229 of the complete chromosome 1
6766	15991		2.69	3.2E-01	M86511.1	NT	Human monocyte antigen CD14 (CD14) mRNA, complete cds
7071	16248	25721	2.71	3.2E-01	U44914.1	NT	Borrelia burgdorferi plasmid cp32-2, erpC and erpD genes, complete cds; and unknown genes
7170	16347		2.78	3.2E-01	AB011399.1	NT	Homo sapiens gene for AF-6, complete cds
7261	16480	25972	3.47	3.2E-01	T06813.1	EST_HUMAN	EST04702 Fetal brain, Stralagene (cat#938206) Homo sapiens cDNA clone HFB0221
8417	18278		2.4	3.2E-01	L07288.1	NT	Drosophila melanogaster laminin A (Lam-A) mRNA, complete cds
8968	17838		2.92	3.2E-01	O83217	SWISSPROT	ELONGATION FACTOR TU (EF-TU)
9111	17829		1.43	3.2E-01	L39874.1	NT	Homo sapiens deoxycytidylate deaminase gene, complete cds
9171	18319	23595	1.92	3.2E-01	BE385776.1	EST_HUMAN	601275460F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3616748 5'

Page 46 of 382  
Table 4  
Single Exon Probes Expressed in HELA Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2631	11814	21033	3.26	3.1E-01	R18051.1	EST_HUMAN	ye90h08.r1 Soares fetal liver spleen 1NLS Homo sapiens cDNA clone IMAGE:125051 5' similar to gb:M64241 QM PROTEIN (HUMAN);
2658	11955	21052	3.57	3.1E-01	7681971	NT	Homo sapiens KIAA0174 gene product (KIAA0174), mRNA
2658	11955	21053	3.57	3.1E-01	7681971	NT	Homo sapiens KIAA0174 gene product (KIAA0174), mRNA
2810	12050		1.15	3.1E-01	AW628036.1	EST_HUMAN	h46h08.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2875391 3'
3138	12373		3.8	3.1E-01	AB028089.1	NT	Mus musculus gene for Ser/Thr kinase KKIAMRE, exon 6
3885	13101	22218	1	3.1E-01	AJ251586.1	NT	Daucus carota mRNA for transcription factor E2F (E2F gene)
4983	14170	23260	0.89	3.1E-01	AE003984.1	NT	Xyella fastidiosa, section 130 of 229 of the complete genome
5430	14657	23795	9.75	3.1E-01	AF176111.1	NT	Homo sapiens hepatocyte nuclear factor-3 alpha (HNF3A) gene, exon 1
5561	14784	24154	2.13	3.1E-01	AF184122.1	NT	Homo sapiens filamin 2 (FLN2) gene, exons 10 through 22
6073	18048	23562	2.71	3.1E-01	BE737392.1	EST_HUMAN	60130812.F1 NIH_MGC_39 Homo sapiens cDNA clone IMAGE:3640420 5'
7119	16286	25778	2.92	3.1E-01	AJ244001.1	EST_HUMAN	q61611.x1 NCI_CGAP_Kid3 Homo sapiens cDNA clone IMAGE:1863980 3' similar to gb:S55700 HYDROXYMETHYLGUTARYL-COA LYASE PRECURSOR (HUMAN);
7414	16626	26119	1.86	3.1E-01	BF216117.1	EST_HUMAN	601883592.F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4095814 5'
8089	17204	26737	2.43	3.1E-01	7682281	NT	Homo sapiens KIAA0764 gene product (KIAA0764), mRNA
8551	17574		1.55	3.1E-01	AF204308.1	NT	Andis opalinus Isolate QS NADH dehydrogenase subunit 2 (ND2) gene, complete cds; mitochondrial gene for mitochondrial product
8590	17599		1.62	3.1E-01	AF304162.1	NT	Stizostedion vitreum 40S ribosomal protein S11 mRNA, partial cds
8740	17686		2.6	3.1E-01	AF195953.1	NT	Homo sapiens membrane-bound aminopeptidase P (XNPEP2) gene, complete cds
9116	17834		3.2	3.1E-01	AF198779.1	NT	Homo sapiens transcription factor IGHM enhancer 3, JM11 protein, JM4 protein, JM5 protein, T64 protein, JM10 protein, A4 differentiation-dependent protein, triple LIM domain protein 6, and synaptophysin genes, complete cds; and L-type calcium channel $\alpha$
9155	18314		1.52	3.1E-01	10946623	NT	Mus musculus peptidoglycan recognition protein-like (Polypr-pending), mRNA
72	11835	18494	1.46	3.0E-01	6755083	NT	Mus musculus protein kinase C, epsilon (Pkce), mRNA
258	9534	18665	8.66	3.0E-01	AJ271735.1	NT	Homo sapiens Xq pseudautosomal region, segment 1/2
1231	10449	19605	2.2	3.0E-01	AW300400.1	EST_HUMAN	xs63f08.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2774343 3'
1497	10710	19883	5.25	3.0E-01	AJ008755.1	NT	Balaenoptera physalus gene encoding atrial natriuretic peptide
3169	12404		0.94	3.0E-01	X83615.1	NT	S. pombe plc1 gene
3178	12413		1.29	3.0E-01	AB030491.1	NT	Corynebacterium sp. ALY-1 alyP gene for polyglutamate lyase, complete cds
3372	12600	21736	0.62	3.0E-01	P23825	SWISSPROT	GATA BINDING FACTOR-3 (TRANSCRIPTION FACTOR NF-E1C) (GATA-3)
3946	13063	22177	1.68	3.0E-01	AW817785.1	EST_HUMAN	PM1-ST0262-281199-001-g01 ST0262 Homo sapiens cDNA
3951	13168	22280	1.08	3.0E-01	AJ271736.1	NT	Homo sapiens Xq pseudautosomal region, segment 2/2
4514	13710	22803	1.88	3.0E-01	AJ006755.1	NT	Balaenoptera physalus gene encoding atrial natriuretic peptide
5180	12600	21736	0.63	3.0E-01	P23825	SWISSPROT	GATA BINDING FACTOR-3 (TRANSCRIPTION FACTOR NF-E1C) (GATA-3)

Page 47 of 382  
Table 4  
Single Exon Probes Expressed in HELA Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5366	14596	23673	5.64	3.0E-01	BE741629.1	EST_HUMAN	601594960F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3948734 5'
5441	14667	23822	3.77	3.0E-01	BE693575.1	EST_HUMAN	RC3-BT0333-180700-111-e03 BT0333 Homo sapiens cDNA
5441	14667	23823	3.77	3.0E-01	BE693575.1	EST_HUMAN	RC3-BT0333-180700-111-e03 BT0333 Homo sapiens cDNA
5462	14688	24039	4.58	3.0E-01	U01247.1	NT	Mus musculus 120/sv Clara cell 10 kd protein (mCC10) gene, complete cds
6011	15261	24685	2.89	3.0E-01	D16313.1	NT	Mouse cybkeratin 15 gene, complete cds
8221	15402	24843	3.34	3.0E-01	10947007	NT	Mus musculus midnolin (Midn-pending), mRNA
8290	15471	24912	1.75	3.0E-01	AF071810.1	NT	Streptococcus pneumoniae strain DBL5 PspA (pspA) gene, partial cds
8588	15784		4.69	3.0E-01	9910161	NT	Mus musculus C-type (calcium dependent, carbohydrate recognition domain) lectin, superfamily member 9 (Clec3f), mRNA
6620	15816	25275	2.36	3.0E-01	BE56083.1	EST_HUMAN	601339079F1 NIH_MGC_53 Homo sapiens cDNA clone IMAGE:3681594 5'
7186	16363	25843	2.79	3.0E-01	AB030231.1	NT	Aspergillus oryzae bpa gene for ER chaperone BIP, complete cds
8240	17369	26904	3.04	3.0E-01	H51029.1	EST_HUMAN	yp84b10.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:194107 5'
8240	17369	26905	3.04	3.0E-01	H51029.1	EST_HUMAN	yp84b10.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:194107 5'
8852	18261		1.68	3.0E-01	AJ297631.1	NT	Rattus norvegicus mRNA for glyceraldehyde-3-phosphate dehydrogenase type 2 (gapdh-2 gene)
8149	18311		3.57	3.0E-01	6677766	NT	Mus musculus ribose 5-phosphate isomerase A (Rplp), mRNA
1706	10918		1.72	2.9E-01	AJ249895.1	NT	Mus musculus mas proto-oncogene and Igf2r gene for insulin-like growth factor type 2 and L41ps and Au76 pseudogenes
1993	11196	20405	1.33	2.9E-01	AE000736.1	NT	Aquifex aeolicus section 68 of 109 of the complete genome
3217	12451	21583	1.76	2.9E-01	AW754239.1	EST_HUMAN	PM1-CT0328-171289-001-f12 CT0328 Homo sapiens cDNA
3217	12451	21584	1.76	2.9E-01	AW754239.1	EST_HUMAN	PM1-CT0328-171289-001-f12 CT0328 Homo sapiens cDNA
4048	13258	22360	0.66	2.9E-01	AB016426.1	NT	Cavia porcellus mRNA for glutathione s-transferase, complete cds
4061	13272		0.66	2.9E-01	AW002802.1	EST_HUMAN	wr02f10.x1 NCI_CGAP_GC8 Homo sapiens cDNA clone IMAGE:2480395 3'
4483	13681	22770	1.18	2.9E-01	AA284488.1	EST_HUMAN	zs57d12.r1 NCI_CGAP_GC81 Homo sapiens cDNA clone IMAGE:701591 5' similar to contains Alu repetitive element
4852	14041	23134	4.7	2.9E-01	AB018028.1	NT	Mus musculus gene, complete cds, similar to EXLM1
5144	14323		1.21	2.9E-01	AI670899.1	EST_HUMAN	wa0803.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2287309 3' similar to contains L1.12 L1 repetitive element
5557	14781	24149	5.09	2.9E-01	X56098.1	NT	B subtilis levansucrase operon levD, levE, levF, levG and sacC (partial) genes for fructose phosphotransferase
5557	14781	24150	5.09	2.9E-01	X56098.1	NT	B subtilis levansucrase operon levD, levE, levF, levG and sacC (partial) genes for fructose phosphotransferase
5563	14787	24158	6.3	2.9E-01	5679662	NT	system polypeptides P16,18,28,30 and levansucrase
5769	15016	24419	2.5	2.9E-01	U03420.1	NT	Mus musculus Eph receptor A8 (Epha8), mRNA
6123	15307	24740	3.4	2.9E-01	Q04399	SWISSPROT	Bos taurus myosin I mRNA, complete cds

Page 48 of 382  
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7470	16878	26160	2.13	2.9E-01	AF128843.1	NT	Tyrosinase cruzi stage-specific surface glycoprotein gp82 (gp82) mRNA, partial cds
7721	16820	26427	2.67	2.9E-01	V01394.1	NT	Torpedo californica mRNA encoding acetylcholine receptor gamma subunit
7721	16820	26428	2.67	2.9E-01	V01394.1	NT	Torpedo californica mRNA encoding acetylcholine receptor gamma subunit
8111	17245	26785	2.54	2.9E-01	AA835373.1	EST_HUMAN	ny95h02.s1 NCI_CGAP_P12 Homo sapiens cDNA clone IMAGE:1273779 similar to contains LTR&2 LTR8 repetitive element;
8114	17248	26788	4.72	2.9E-01	AL139078.2	NT	Campylobacter jejuni NCTC11168 complete genome; segment 5/6
8802	17727	23928	1.34	2.9E-01	AW005671.1	EST_HUMAN	wz88f05.x1 NCI_CGAP_Bn25 Homo sapiens cDNA clone IMAGE:2565921 3' similar to contains element
8893	17787	23920	3.11	2.9E-01	AF092453.1	NT	MER29 repetitive element;
9202	17987	23860	1.57	2.9E-01	Y08837.1	NT	Homo sapiens TNF- $\alpha$ -inducible RNA binding protein (TIRP) gene, complete cds
9202	17987	23861	1.57	2.9E-01	Y08837.1	NT	Chlamydomonas reinhardtii mRNA for nitrite reductase structural locus
575	9825		1.73	2.8E-01	U67136.1	NT	Chlamydomonas reinhardtii mRNA for nitrite reductase structural locus
580	9829		0.76	2.8E-01	L28145.1	NT	Rattus norvegicus A-kinase anchoring protein AKAP150 mRNA, complete cds
1091	10315	19469	3.05	2.8E-01	AF188050.1	NT	Prune dwarf virus movement protein, complete cds; coat protein, complete cds
1284	10499	19659	1.07	2.8E-01	BE313442.1	EST_HUMAN	Guir guira oocyte maturation factor Mos (c-mos) gene, partial cds
1284	10499	19660	1.07	2.8E-01	BE313442.1	EST_HUMAN	601148733F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3163688 5'
1298	10513	19671	0.88	2.8E-01	D86550.1	NT	601148733F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3163688 5'
1702	10914	20102	1.41	2.8E-01	AW860020.1	EST_HUMAN	Human mRNA for serine/threonine protein kinase, complete cds
1880	11184	20392	1.49	2.8E-01	AL047620.1	EST_HUMAN	QV1-CT0384-120200-065-505 CT0384 Homo sapiens cDNA
2101	11301	20515	1.13	2.8E-01	AW511195.1	EST_HUMAN	DKFZp586i2321.1 586 (synonym: hute1) Homo sapiens cDNA clone DKFZp586i2321
2435	11626	20848	2.08	2.8E-01	AE000494.1	NT	hd44b03.x1 Soares_NFL_I_GBC_S1 Homo sapiens cDNA clone IMAGE:2912333 3'
2435	11626	20849	2.08	2.8E-01	AE000494.1	NT	Escherichia coli K-12 MG1655 section 384 of 400 of the complete genome
2512	11701		1.46	2.8E-01	AL161565.2	NT	Escherichia coli K-12 MG1655 section 384 of 400 of the complete genome
2825	12163		1.56	2.8E-01	AF178480.1	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 65
2828	12164	21288	1.96	2.8E-01	Z14037.1	NT	Toxoplasma gondii 90kDa heat-shock protein (HSP90) mRNA, partial cds
2828	12164	21289	1.96	2.8E-01	Z14037.1	NT	B. taunus microsatellite (ETH121)
3357	12585	21724	1.07	2.8E-01	AP000004.1	NT	B. taunus microsatellite (ETH121)
3973	13187	22295	2.91	2.8E-01	AE001180.1	NT	Pyrococcus horikoshii OT3 genomic DNA, 777001-994000 nt position (4/7)
4104	13311		0.75	2.8E-01	AE004450.1	NT	Borrelia burgdorferi (section 66 of 70) of the complete genome
4180	13384		2.26	2.8E-01	AI090968.1	EST_HUMAN	Pseudomonas aeruginosa PAO1, section 11 of 529 of the complete genome
4454	13652	22747	2.77	2.8E-01	P19615	SWISSPROT	ov44g10.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1640228 3' similar to contains Alu repetitive element; contains element MER22 repetitive element;
4792	13981	23085	1.17	2.8E-01	D15050.1	NT	RNA POLYMERASE BETA SUBUNIT (LARGE STRUCTURAL PROTEIN)(L PROTEIN)
4792	13981	23086	1.17	2.8E-01	D15050.1	NT	Human mRNA for transcription factor AREB6, complete cds
4792	13981	23086	1.17	2.8E-01	D15050.1	NT	Human mRNA for transcription factor AREB6, complete cds

Page 49 of 382  
Table 4  
Single Exon Probes Expressed in HELA Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4839	14028	23120	0.95	2.8E-01	AF075238.1	NT	Hepatitis G virus isolate 60 (SZNAE12) polyprotein precursor, gene, partial cds
4846	14035	23128	2.98	2.8E-01	AF030154.1	NT	Bovine adenovirus 3 complete genome
4877	14065	23160	1.52	2.8E-01	BF528188.1	EST_HUMAN	602042601F1 NCL_CGAP_Bim67 Homo sapiens cDNA clone IMAGE:4180128 5'
4906	14094	23187	2.89	2.8E-01	AI272669.1	EST_HUMAN	ql59c11.x1 Soares_NhhMPu_S1 Homo sapiens cDNA clone IMAGE:1876828 3' similar to contains Alu repetitive element; contains element LTR5 repetitive element
5209	14384	23468	1.85	2.8E-01	AW608625.1	EST_HUMAN	MR1-ST0111-111199-010-g07 ST0111 Homo sapiens cDNA
5240	14414	23494	0.79	2.8E-01	U65949.1	NT	Mus musculus hepatocyte growth factor-like protein receptor (Rcn) gene, complete cds
5291	14462	23530	0.68	2.8E-01	6878616	NT	Mus musculus Yarnaguchi sarcoma viral (v-yes) oncogene homolog (Yes), mRNA
5338	18051	23843	22.74	2.8E-01	AA349987.1	EST_HUMAN	EST57072 Infant brain Homo sapiens cDNA 5' and
5494	14720	24077	2.89	2.8E-01	AB016625.1	NT	Homo sapiens OCTN2 gene, complete cds
5976	15190	24607	7.37	2.8E-01	BF511215.1	EST_HUMAN	UHH-B14-act-f-04-0-UI s1 NCL_CGAP_Sub88 Homo sapiens cDNA clone IMAGE:3085182 3'
6531	15727	25182	3.85	2.8E-01	U51688.1	NT	Homo sapiens lanosterol 14-alpha demethylase cytochrome P450 (CYP51) gene, exon 5
6851	15848		8.12	2.8E-01	BF347847.1	EST_HUMAN	602022887F1 NCL_CGAP_Bim67 Homo sapiens cDNA clone IMAGE:4188525 5'
7095	16272	25749	4.31	2.8E-01	7706163	NT	Homo sapiens hypothetical protein (LOC51319), mRNA
7328	16545	26034	2.35	2.8E-01	BF241082.1	EST_HUMAN	601880784F1 NIH_MGC_35 Homo sapiens cDNA clone IMAGE:4109350 5'
7329	16545	26035	2.35	2.8E-01	BF241082.1	EST_HUMAN	601880784F1 NIH_MGC_35 Homo sapiens cDNA clone IMAGE:4109350 5'
7354	16570	26061	3.21	2.8E-01	BF695970.1	EST_HUMAN	601852148F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4076026 5'
7457	16665	26154	2.95	2.8E-01	AF051682.1	NT	Drosophila heteronema fruitless (fru) gene, alternative splice products, 5' flanking region, exons 1 through 7 and complete cds
7827	17019		4.12	2.8E-01	BF674023.1	EST_HUMAN	602137418F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4273853 5'
8840	17749		7.9	2.8E-01	D83329.1	NT	Mus musculus DNA for prostaglandin D2 synthase, complete cds
8952	17826	23905	4.34	2.8E-01	BE178699.1	EST_HUMAN	PMA-HT0606-030400-001-a07 HT0606 Homo sapiens cDNA
8980	17847	23915	1.23	2.8E-01	BE900116.1	EST_HUMAN	601673020F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3955998 5'
9139	18268		2.15	2.8E-01	11433629	NT	Homo sapiens CDC42-binding protein kinase beta (DMPK-like) (CDC42BPB), mRNA
483	9735	18868	3.37	2.7E-01	Y17324.1	NT	Rattus norvegicus CDK104 mRNA
619	9864	18984	3.09	2.7E-01	AA450061.1	EST_HUMAN	zc99b10.s1 Soares_total_fetus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:788827 3' similar to contains Alu repetitive element
1288	10483	19842	1.39	2.7E-01	AB004906.1	NT	Ipomoea purpurea transposable element T1p100 gene for transposase, complete cds
1598	10812		1.78	2.7E-01	X70815.1	NT	G lambdla SR2 gene
1704	10916	20103	3.76	2.7E-01	W58097.1	EST_HUMAN	zd22h10.r1 Soares_fetal_heart_NbHH19W Homo sapiens cDNA clone IMAGE:341443 5'
1746	10958	20141	1.35	2.7E-01	P03341	SWISSPROT	GAG POLYPROTEIN [CONTAINS: INNER COAT PROTEIN P12; CORE PROTEIN P15; CORE SHELL PROTEIN P30; NUCLEOPROTEIN P10]
2105	12010		2.25	2.7E-01	AF047575.1	NT	Rattus norvegicus vesicular monoamine transporter type 2, promoter region and exon 1
2335	11528	20749	7.56	2.7E-01	Y13668.1	NT	Feline immunodeficiency virus env gene, isolate ITTO088PIU (M88), partial

Page 50 of 382  
Table 4  
Single Exon Probes Expressed in HELA Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2418	11609	20831	3.29	2.7E-01	AJ310858.1	EST_HUMAN	ta43c11.x2 NCI_CGAP_Lu26 Homo sapiens cDNA clone IMAGE:20468336 3' similar to contains element L1 repetitive element
2841	12179		0.66	2.7E-01	BF088284.1	EST_HUMAN	CM1-HT0875-060800-385-e05 HT0875 Homo sapiens cDNA
3987	13201	22309	1.66	2.7E-01	AJ928015.1	EST_HUMAN	wc92e11.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2462828 3'
4001	13214	22318	0.77	2.7E-01	AF216214.1	NT	Drosophila buzzatii alpha-esterase 5 (aE5) gene, partial cds
4001	13214	22319	0.77	2.7E-01	AF216214.1	NT	Drosophila buzzatii alpha-esterase 5 (aE5) gene, partial cds
4007	13219	22322	2.21	2.7E-01	L77569.1	NT	Homo sapiens DGeorge syndrome critical region, telomeric end
4914	14102	23185	1.12	2.7E-01	L27516.1	NT	Triticum aestivum (Wcs68) gene, complete cds
5068	14248		2.97	2.7E-01	AW856131.1	EST_HUMAN	RC1-CT0266-230200-016-e03 CT0266 Homo sapiens cDNA
5308	14539	23544	2.45	2.7E-01	P17277	SWISSPROT	HOMEOBOX PROTEIN HOX-A4 (CHOX-1.4)
5991	16273	24702	2.12	2.7E-01	Q81554	SWISSPROT	FIBRILLIN 1 PRECURSOR
6234	15415	24858	1.66	2.7E-01	Q11079	SWISSPROT	HYPOPHYSICAL 20.9 KD PROTEIN B0563.3 IN CHROMOSOME X
6371	15551	25007	1.99	2.7E-01	AF248054.1	NT	Bos taurus micromolar calcium activated neutral protease 1 (CAPN1) gene, exons 11-20, and partial cds
6371	15551	25008	1.99	2.7E-01	AF248054.1	NT	Bos taurus micromolar calcium activated neutral protease 1 (CAPN1) gene, exons 11-20, and partial cds
6862	16052	25519	3.3	2.7E-01	O83909	SWISSPROT	THREONYL-TRNA SYNTHETASE (THREONINE-TRNA LIGASE) (THRRS)
6862	16052	25520	3.3	2.7E-01	O83909	SWISSPROT	THREONYL-TRNA SYNTHETASE (THREONINE-TRNA LIGASE) (THRRS)
7117	16284	25776	3.68	2.7E-01	AF087434.1	NT	Mus musculus transcription factor NF-ATc isoform a (NF-ATc) mRNA, complete cds
7389	16603	26091	2.21	2.7E-01	AV705043.1	EST_HUMAN	AV705043 ADB Homo sapiens cDNA clone ADBCOD05 5'
7389	16603	26092	2.21	2.7E-01	AV705043.1	EST_HUMAN	AV705043 ADB Homo sapiens cDNA clone ADBCOD05 5'
7399	16612	26102	4.34	2.7E-01	AJ133269.1	NT	Homo sapiens caveolin-1/2 locus, Contig1, D7S522, genes CAV2 (exons 1, 2a, and 2b), CAV1 (exons 1 and 2)
8861	17638		1.41	2.7E-01	AJ012482.1	NT	Rattus norvegicus mRNA for phosphatidylinositol 3-kinase, catalytic subunit, beta isoform
9023	17874		1.5	2.7E-01	Q63627	SWISSPROT	CTD-BINDING SR-LIKE PROTEIN RA4
9122	17937		2.34	2.7E-01	AF217491.1	NT	Homo sapiens fragile 16D oxidoreductase (FOR) gene, exon 8
476	11983	18861	1.68	2.6E-01	P78411	SWISSPROT	IRQUOIS-CLASS HOMEODOMAIN PROTEIN IRX-2
487	9740		0.93	2.6E-01	D16459.1	NT	Bos taurus mRNA for mb-1, complete cds
1397	10611	19775	1.44	2.6E-01	BE885087.1	EST_HUMAN	601510838F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3912345 5'
1438	10652	19825	0.97	2.6E-01	AB013260.1	NT	Glycine max pseudogene for B4 30K
1861	11088	20258	6.36	2.6E-01	AL161472.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 2
1861	11088	20259	6.36	2.6E-01	AL161472.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 2

Single Exon Probes Expressed in HELA Cells

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2062	11263		10.1	2.8E-01	AW733152.1	EST_HUMAN	bb04d10.x1 NIH_MGC_14 Homo sapiens cDNA clone IMAGE:2958451 3' similar to gb:M36072.60S
2121	11320	20538	1.03	2.8E-01	M11844.1	NT	RIBOSOMAL PROTEIN L7A (HUMAN); gb:M14689_cds1 Mouse surfact locus surfact 3 protein gene (MOUSE);
2436	11627		1.48	2.8E-01	Y12896.1	NT	Human prealbumin gene, complete cds
2511	11700		9.82	2.8E-01	BE272440.1	EST_HUMAN	B.martinius fcdL gene
3057	12293		1.03	2.8E-01	AW974531.1	EST_HUMAN	801126016F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:2890043 5'
3557	12780	21910	1.04	2.8E-01	M22342.1	NT	EST386635 IMAGE resequences, MAGM Homo sapiens cDNA
3622	12843	21663	1.94	2.8E-01	AF229118.1	NT	Bacteriophage T2 DNA-(adenine-N6)methyltransferase (dam) gene, complete cds
3634	13150	22265	0.96	2.8E-01	AJ012174.2	NT	Homo sapiens acetylcholinesterase collagen-like tail subunit (COLQ) gene, exons 1A, 2, 3, 4, and 5
3634	13150	22266	0.96	2.8E-01	AJ012174.2	NT	Chlamydomonas reinhardtii partial mpb gene for RNase P RNA subunit
4077	13287	22385	0.8	2.8E-01	AW895910.1	EST_HUMAN	Chlamydomonas reinhardtii partial mpb gene for RNase P RNA subunit
4136	13342	22443	17.81	2.8E-01	BE080598.1	EST_HUMAN	EST371580 IMAGE resequences, MAGF Homo sapiens cDNA
4350	13552	22647	1.15	2.8E-01	AF175283.1	NT	QV1-BT0630-040400-132-403 B.T0630 Homo sapiens cDNA
4494	13692	22785	0.83	2.8E-01	AB021180.1	NT	Enterococcus faecium strain N97-330 vanD glycopeptide resistance gene cluster, complete cds; and unknown gene
4494	13692	22786	0.83	2.8E-01	AB021180.1	NT	Gallus gallus mRNA for skeletal myosin heavy chain, complete cds
4545	13740	22840	1.51	2.8E-01	AA457617.1	EST_HUMAN	Gallus gallus mRNA for skeletal myosin heavy chain, complete cds
4648	13842	22832	1.45	2.8E-01	U01103.1	NT	aa88d07.r1 Stratiotea fatal retina 937202 Homo sapiens cDNA clone IMAGE:838477 5'
4726	13917	23018	1.39	2.8E-01	AF142703.1	NT	Arabidopsis thaliana PSI type III chlorophyll a/b-binding protein (Lhca3*) mRNA, complete cds
4991	14178	23269	4.02	2.8E-01	H04856.1	EST_HUMAN	Ophrestia radicata maturase-like protein (matK) gene, complete cds; chloroplast gene for chloroplast product
5066	14248		0.59	2.8E-01	AA884825.1	EST_HUMAN	y51605.r1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:152288 5'
5203	14378	23465	1.24	2.8E-01	AA985392.1	EST_HUMAN	am33b11.s1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1468605 3'
5699	18386		2.32	2.8E-01	AE001811.1	NT	am81g11.s1 Stratiotea schizobrain S11 Homo sapiens cDNA clone IMAGE:1629572 3' similar to contains L1.12 L1 repetitive element;
5764	14973	24371	2.17	2.8E-01	AI582557.1	EST_HUMAN	Thermotoga maritima section 123 of 136 of the complete genome
5754	14973	24372	2.17	2.8E-01	AI582557.1	EST_HUMAN	ts02a12.x1 NCI_CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2227438 3' similar to SW:NDF1_RAT
6575	15771	25233	2.72	2.8E-01	BF343588.1	EST_HUMAN	Q64289 NEUROGENIC DIFFERENTIATION FACTOR 1 ; contains element LTR1 repetitive element ;



Page 52 of 382  
Table 4  
Single Exon Probes Expressed in HELA Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6679	15874	25332	2.87	2.6E-01	BE830339.1	EST_HUMAN	RC5-ET0082-310500-021-F10 ET0082 Homo sapiens cDNA
6678	15874	25333	2.87	2.6E-01	BE830339.1	EST_HUMAN	RC5-ET0082-310500-021-F10 ET0082 Homo sapiens cDNA
7860	17089	26628	1.99	2.6E-01	P49280	SWISSPROT	CELL DIVISION PROTEIN FTSW HOMOLOG
8058	17191		25.68	2.6E-01	X51755.1	NT	Human lambda-immunoglobulin constant region complex (gamma line)
8400	17478		2.5	2.6E-01	10190655	NT	Mus musculus jerky (Jrk), mRNA
8803	18269		2.25	2.6E-01	BE883491.1	EST_HUMAN	601511052F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3912612 5'
8872	17647	23978	2.83	2.6E-01	AF316896.1	NT	Homo sapiens Na/K-ATPase gamma subunit (FXD02) gene, complete cds, alternatively spliced
9017	17669		1.39	2.6E-01	D88425.1	NT	Cavia cobaya mRNA for serine/threonine kinase, complete cds
9145	17950		1.29	2.6E-01	AF141325.2	NT	Homo sapiens insulin polyphosphate 1-phosphatase (NPP1) gene, complete cds
9184	17975		1.27	2.6E-01	P47285	SWISSPROT	HYPOTHETICAL PROTEIN MG039
245	9523	18653	2.05	2.5E-01	4502286	NT	Homo sapiens ATP synthase, H+ transporting, mitochondrial F1 complex, delta subunit (ATP5D), nuclear gene encoding mitochondrial protein, mRNA
246	9523	18653	2.52	2.5E-01	4502286	NT	Homo sapiens ATP synthase, H+ transporting, mitochondrial F1 complex, delta subunit (ATP5D), nuclear gene encoding mitochondrial protein, mRNA
259	9535		7.15	2.5E-01	M26501.1	NT	Starfish (P. ochraceus) cytoplasmic actin gene, complete cds
842	10079	19237	1.27	2.5E-01	U09864.1	NT	Mus musculus ICR/Swiss glyceraldehyde 3-phosphate dehydrogenase (Gapd-S) gene, complete cds
1067	10283		0.95	2.5E-01	AE002156.1	NT	Ureaplasma urealyticum section 57 of 59 of the complete genome
1129	10353	19505	9.34	2.5E-01	T88837.1	EST_HUMAN	ye11g07.r1 Stragene lung (H837210) Homo sapiens cDNA clone IMAGE:117468 5'
1385	10599		2.16	2.5E-01	AB025343.1	NT	Olea europaea OEW mRNA for lupeol synthase, complete cds
1703	10915		5.2	2.5E-01	4885406	NT	Homo sapiens hyperpolarization activated cyclic nucleotide-gated potassium channel 4 (HCN4) mRNA
1848	12004	20246	1	2.5E-01	BE696604.1	EST_HUMAN	PM4-CT0400-310700-005-408 CT0400 Homo sapiens cDNA
1848	12004	20247	1	2.5E-01	BE696604.1	EST_HUMAN	PM4-CT0400-310700-005-408 CT0400 Homo sapiens cDNA
2371	11564		5.84	2.5E-01	AE000875.1	NT	Aquifex aeolicus section 7 of 109 of the complete genome
2459	11650		1.02	2.5E-01	AA281987.1	EST_HUMAN	zs11a12.r1 NCI CGAP_GCB1 Homo sapiens cDNA clone IMAGE:684862 5'
3390	12617		4.31	2.5E-01	AW973471.1	EST_HUMAN	EST385464 MAGE resequences, MAGM Homo sapiens cDNA
3508	12732	21870	0.77	2.5E-01	AF233875.1	NT	Danio rerio peptide YY precursor gene, complete cds
3524	12748	21879	8.77	2.5E-01	AL161517.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 29
4045	13255		0.9	2.5E-01	P32323	SWISSPROT	A-AGGLUTININ ATTACHMENT SUBUNIT PRECURSOR
4308	13510		0.85	2.5E-01	Q03314	SWISSPROT	RHIB PROTEIN
4761	13952		1.18	2.5E-01	Q27225	SWISSPROT	MOL-T-INHIBITING HORMONE PRECURSOR (MIH)
4767	13958	23057	4.65	2.5E-01	AF007768.1	NT	Choristoneura fumiferana diapause associated protein 2 (DAP2) mRNA, complete cds
4791	13980	23084	2.54	2.5E-01	AE004416.1	NT	Vibrio cholerae chromosome II, section 73 of 93 of the complete chromosome

Page 53 of 382  
Table 4  
Single Exon Probes Expressed in HELA Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4816	14005		3.4	2.5E-01	AJ230113.1	NT	Mus musculus annexin V gene, intron 4 segment containing 5' LTR and gag portion of MuERV-L (murine endogenous retrovirus) element
5074	14254	23337	0.61	2.5E-01	AW873588.1	EST_HUMAN	h02f11.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:3041997 3' similar to WP:Y71F9A_294.D CE22858
5349	14578	23658	12.94	2.5E-01	S83390.1	NT	T3 receptor-associated cofactor-1 [human, fetal liver, mRNA, 2830 nt]
6349	15529	24979	4.91	2.5E-01	AL183282.2	NT	Homo sapiens chromosome 21 segment HS21C082
6538	15732	25186	3.18	2.5E-01	BF038595.1	EST_HUMAN	601459238F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3862809 5'
6668	15881	25320	4.29	2.5E-01	H53238.1	EST_HUMAN	y08407.r1 Soares fetal liver spleen 1NLS Homo sapiens cDNA clone IMAGE:202501 5'
6920	16113	25578	29.84	2.5E-01	U89651.2	NT	Homo sapiens matrix metalloproteinase MMP Rasi-1 gene, promoter region
6920	16113	25578	29.84	2.5E-01	U89651.2	NT	Homo sapiens matrix metalloproteinase MMP Rasi-1 gene, promoter region
7111	16288	25769	2.7	2.5E-01	AW581997.1	EST_HUMAN	RC3-ST0186-130100-015-407 ST0186 Homo sapiens cDNA
7217	16394	25878	2.22	2.5E-01	X58491.1	NT	Mouse L1Md LINE DNA
7643	16843	26341	3.62	2.5E-01	D50914.1	NT	Human mRNA for KIAA0124 gene, partial cds
8335	17433	26938	4.13	2.5E-01	AF200528.1	NT	Zea mays cellulose synthase-4 (Cesa-4) mRNA, complete cds
8364	18350		6.92	2.5E-01	AL191541.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 41
8848	18192	23761	1.28	2.5E-01	AF170072.1	NT	Spodoptera frugiperda CALNUC mRNA, complete cds
8892	18113		1.37	2.5E-01	AV692543.1	EST_HUMAN	AV692543 GKC Homo sapiens cDNA clone GKCZF10 5'
560	9810	18933	1.07	2.4E-01	AA696316.1	EST_HUMAN	en70d04.s1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1562023 3'
858	10094	19257	2.17	2.4E-01	BF576124.1	EST_HUMAN	602132442F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4271578 5'
1311	10527	19687	11.61	2.4E-01	AJ289880.1	NT	Homo sapiens KIAA0851 gene (partial), XT3 gene and LZTFL1 gene
1311	10527	19688	11.61	2.4E-01	AJ289880.1	NT	Homo sapiens KIAA0851 gene (partial), XT3 gene and LZTFL1 gene
1818	11028		21.38	2.4E-01	AF267753.1	NT	Mesembryanthemum crystallinum putative potassium channel protein Mktip mRNA, complete cds
1884	11071	20262	1.38	2.4E-01	AF251708.1	NT	Zoocys dhumnades fructose-1,6-bisphosphatase mRNA, complete cds
2107	11308	20520	1.03	2.4E-01	AF111168.2	NT	Homo sapiens serine palmitoyl transferase, subunit II gene, complete cds; and unknown genes
2134	11332		1.04	2.4E-01	P45384	SWISSPROT	IMMUNOGLOBULIN A1 PROTEASE PRECURSOR (IGA1 PROTEASE)
2227	11423	20849	1.67	2.4E-01	AE000680.1	NT	Aquifex aeolicus section 12 of 109 of the complete genome
2349	11542	20765	1.01	2.4E-01	BF002171.1	EST_HUMAN	7h23d04.x1 NCI_CGAP_Cot16 Homo sapiens cDNA clone IMAGE:3316807 3' similar to SW:PRSB_XENLA
2502	11591	20911	1.59	2.4E-01	Z36534.1	NT	O42568 26S PROTEASE REGULATORY SUBUNIT 6A ;
2717	11886	21113	5.18	2.4E-01	X71783.1	NT	D discoideum (AX3-K) parA gene
2739	11918	21132	4.61	2.4E-01	AF030154.1	NT	S. pombe swi6 gene
						NT	Bovine adenovirus 3 complete genome
3097	12333		3.32	2.4E-01	U72726.1	NT	Oryza longistaminata receptor kinase-like protein, family member D, and retrofit (gag/pol) genes, complete cds
3643	12664	21682	1	2.4E-01	AF169793.1	NT	Podospora anserina HET-C protein (Het-c) gene, complete cds

Page 54 of 382  
Table 4  
Single Exon Probes Expressed in HELA Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3743	12683	22078	0.69	2.4E-01	AE000312.1	NT	Escherichia coli K-12 MG1655 section 202 of 400 of the complete genome
4008	13220		0.9	2.4E-01	D29860.1	NT	Rattus norvegicus mRNA for alphaB crystallin-related protein, complete cds
5512	14737	24101	9.26	2.4E-01	AF091216.1	NT	Mus musculus Wrm protein (Wrm) gene, complete cds
5512	14737	24102	9.26	2.4E-01	AF091216.1	NT	Mus musculus Wrm protein (Wrm) gene, complete cds
							754404.x1 NCL CGAP_Br16 Homo sapiens cDNA clone IMAGE:3338503 3' similar to SW_SFR4_HUMAN
							Q08170 SPLICING FACTOR, ARGININE/SERINE-RICH 4; contains element TAR1 TAR1 repetitive element
5612	14836	24211	2.4	2.4E-01	BF592336.1	EST_HUMAN	
5648	14871	24258	2.63	2.4E-01	AF035546.1	NT	Drosophila melanogaster p38a MAP kinase gene, complete cds
5703	14922	24315	2.49	2.4E-01	766180.1	NT	Homo sapiens HSPC142 protein (HSPC142), mRNA
							wc62c11.x1 NCL CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2323220 3' similar to gb.J03464
5894	15111	24523	1.92	2.4E-01	AI698989.1	EST_HUMAN	PROCOLLAGEN ALPHA 2(I) CHAIN PRECURSOR (HUMAN);
6228	15409	24851	8.53	2.4E-01	L43001.1	NT	Bos taurus guanylyl cyclase-activating protein 2 (guca2) mRNA, complete cds
6945	16089	25556	6.01	2.4E-01	AI693515.1	EST_HUMAN	wd43e02.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2330906 3' similar to contains
7191	16368	25847	2.4	2.4E-01	Q03692	SWISSPROT	MER22.b1 TAR1 repetitive element;
7351	16567	26057	3.3	2.4E-01	AL161494.2	NT	COLLAGEN ALPHA 1(X) CHAIN PRECURSOR
7412	16624	26118	2.68	2.4E-01	AF030199.1	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 6
7754	16950		2.26	2.4E-01	Z21647.1	NT	Mus musculus type 1 sigma receptor gene, complete cds
8291	17404	26931	1.22	2.4E-01	AF217491.1	NT	P. asiatica mosaic virus genomic RNA
8426	18136		1.93	2.4E-01	AF004213.1	NT	Homo sapiens fragile 18D oxidoreductase (FOR) gene, exon 6
8482	17535		2.37	2.4E-01	AJ278191.1	NT	Arabidopsis thaliana ethylene-insensitive3-like1 (EIL1) mRNA, complete cds
8720	18120		2.21	2.4E-01	V01507.1	NT	Mus musculus mRNA for putative mc7 protein (mc7 gene)
9180	17972		3.78	2.4E-01	AL163281.2	NT	Gallus gallus gene coding for e-actin
9222	18001		2.34	2.4E-01	L20422.1	NT	Homo sapiens chromosome 21 segment HS21C081
394	9649	18784	1.02	2.3E-01	S75988.1	NT	Human 14-3-3n protein mRNA, complete cds
643	8889		3.82	2.3E-01	U39713.1	NT	aromatase [Poephila guttata=zebra finches, ovary, mRNA, 3188 nt]
673	9818	19047	23.98	2.3E-01	U67596.1	NT	Mycoplasma genitalium section 35 of 51 of the complete genome
942	10175	19328	4.61	2.3E-01	BE311893.1	EST_HUMAN	Methanococcus jannaschii section 138 of 150 of the complete genome
1499	10712	19884	0.92	2.3E-01	6677980	NT	601142073F1 NIH_MGC_14 Homo sapiens cDNA clone IMAGE:3505818 5'
1609	10822	19998	3.69	2.3E-01	Y10887.2	NT	Mus musculus vacuolar protein sorting 4b (yeast) (Vps4b), mRNA
2012	11214		1.15	2.3E-01	AJ235353.1	NT	Mus musculus cdh5 gene, exon 1, partial
2409	11601	20821	1.57	2.3E-01	BE297718.1	EST_HUMAN	Homo sapiens partial intron 3 of the wild type AF-4/FEL gene
2776	10608	19770	2	2.3E-01	AB015033.1	NT	601175562F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3531015 5'
							Marinibacteria agarivorans gyrB gene for DNA gyrase subunit B, partial cds, strain:IFO 14957

670

Page 55 of 382  
Table 4  
Single Exon Probes Expressed in HELA Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2818	12156	21281	0.96	2.3E-01	AA601379.1	EST_HUMAN	nc16d06.s1 NCI_CGAP_Phe1 Homo sapiens cDNA clone IMAGE:1100843 3' similar to contains Alu repetitive element; contains element THR repetitive element;
3049	12285		7	2.3E-01	R21732.1	EST_HUMAN	yt21b07.s1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:130357 3'
3349	12577	21718	1.24	2.3E-01	H69836.1	EST_HUMAN	yt97h10.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:213283 5'
3909	13125		5.19	2.3E-01	7662133	NT	Homo sapiens KIAA0450 gene product (KIAA0450), mRNA
4343	13545	22636	1.08	2.3E-01	R82252.1	EST_HUMAN	yt17f01.r1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:149017 5'
4394	13595		1.97	2.3E-01	L78789.1	NT	Mus musculus renin (Ren-1c) gene, promoter region
4445	13644	22739	1.16	2.3E-01	D90899.1	NT	Synechocystis sp. PCC6803 complete genome, 1/27, 1-133859
4485	13693	22773	2.23	2.3E-01	AF082535.1	NT	Homo sapiens mitogen-activated protein kinase p38delta (PRKM13) mRNA, complete cds
4551	13746	22846	5.67	2.3E-01	5031984	NT	Homo sapiens nuclear transport factor 2 (placental protein 15) (PP15) mRNA
5075	14255	23338	0.64	2.3E-01	AB032400.1	NT	Mus musculus tulip 1 mRNA, complete cds
5252	14425		1.08	2.3E-01	AF080322.1	NT	Bos taurus NAD(+) isocitrate dehydrogenase subunit 1 IDH1-B precursor (IDH) mRNA, nuclear gene encoding mitochondrial protein, complete cds
5332	14563	23637	2.38	2.3E-01	AB040945.1	NT	Homo sapiens mRNA for KIAA1512 protein, partial cds
5407	14635	23763	2.13	2.3E-01	BF058381.1	EST_HUMAN	7k30b06.x1 NCI_CGAP_Ov18 Homo sapiens cDNA clone IMAGE:3476699 3' similar to SW:GAG_SMSAV P03330 GAG POLYPROTEIN [CONTAINS: CORE PROTEIN P15; INNER COAT PROTEIN P12; CORE SHELL PROTEIN P30; NUCLEOPROTEIN P10];
5456	14682	24032	4.76	2.3E-01	X95687.1	NT	C.familiaris rom1 gene
5633	14857	24239	2.26	2.3E-01	AI708840.1	EST_HUMAN	as27e12.x1 Barslead aorta HPLRB6 Homo sapiens cDNA clone IMAGE:2318446 3' similar to gb:X13238 CYTOCHROME C OXIDASE POLYPEPTIDE VIC PRECURSOR (HUMAN);
5633	14857	24240	2.26	2.3E-01	AI708840.1	EST_HUMAN	as27e12.x1 Barslead aorta HPLRB6 Homo sapiens cDNA clone IMAGE:2318446 3' similar to gb:X13238 CYTOCHROME C OXIDASE POLYPEPTIDE VIC PRECURSOR (HUMAN);
6032	15240	24662	4.01	2.3E-01	AI718148.1	EST_HUMAN	as42f12.x1 Barslead aorta HPLRB6 Homo sapiens cDNA clone IMAGE:2319887 3' similar to contains Alu repetitive element;
6257	15438	24878	2.77	2.3E-01	AF175389.1	NT	Glycine max resistance protein LM17 precursor RNA, partial cds
6339	15519		3.64	2.3E-01	8754779	NT	Mus musculus myosin XV (Myo15), mRNA
6398	15579		2.64	2.3E-01	N80983.1	EST_HUMAN	za12e08.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:292358 5'
6462	15659	25131	2.45	2.3E-01	M69831.1	NT	Oxytricha nova macronuclear telomere-binding protein alpha subunit (tel-alpha alanine version) gene, complete cds
7049	16228	25701	3.31	2.3E-01	BE173060.1	EST_HUMAN	MR0-HT0559-240400-014-g11 HT0559 Homo sapiens cDNA
7199	16376		5.86	2.3E-01	BF133577.1	EST_HUMAN	601646155R2 NIH_MGC_59 Homo sapiens cDNA clone IMAGE:4102092 3'
7744	16940	28450	1.81	2.3E-01	AJ250189.1	NT	Mus musculus partial mRNA for muscle protein 534 (mg534 gene)
7744	16940	28451	1.81	2.3E-01	AJ250189.1	NT	Mus musculus partial mRNA for muscle protein 534 (mg534 gene)
7891	17107	26637	2.22	2.3E-01	AE002167.2	NT	Chlamydomonas reinhardtii AR39, section 4 of 64 of the complete genome

Page 56 of 382  
Table 4  
Single Exon Probes Expressed in HELA Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8410	17485		3.16	2.3E-01	U45426.1	NT	Borrelia burgdorferi 2.9-6 locus, ORF-A-D genes, complete cds and REP+ gene, partial cds
8503	17642		25.49	2.3E-01	T27231.1	EST_HUMAN	HCOEST44 HT29M6 Homo sapiens cDNA clone HCC44 5'
8527	18083		1.36	2.3E-01	AA089819.1	EST_HUMAN	chm1424 seq.F Human fetal heart, Lambda ZAP Express Homo sapiens cDNA 5'
8536	17561		1.46	2.3E-01	AW863940.1	EST_HUMAN	PM4-SN0012-030400-001-008 SN0012 Homo sapiens cDNA
8598	18281	23681	3.26	2.3E-01	AW303623.1	EST_HUMAN	xv21d07.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2813773 3' similar to TR:Q8Z175
8635	18331	23603	5.25	2.3E-01	BE892484.1	EST_HUMAN	Q8Z175 LYSYL OXIDASE-RELATED PROTEIN 2, contains PTR5 b2 TAR1 repetitive element;
8687	17656		1.79	2.3E-01	BF663319.1	EST_HUMAN	601507202F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3908689 5'
8739	17685		2.68	2.3E-01	AJ006519.1	NT	602144459F1 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4297719 5'
8834	17744		1.32	2.3E-01	U49645.1	NT	Rattus norvegicus mRNA for acid gated ion channel
9102	17825		3.77	2.3E-01	BF475611.1	EST_HUMAN	Pleurodeles waltl distal-less like protein PwDlx-3 (PwDlx-3) mRNA, complete cds
9261	18242	23708	1.26	2.3E-01	M60675.1	NT	nac39h12.x1 Lupski_sciatic_nerve Homo sapiens cDNA clone IMAGE:3395950 3' similar to contains element
89	9382	18512	0.82	2.2E-01	AJ052190.1	EST_HUMAN	Human von Willebrand factor gene, exons 23 through 34
1547	10761	18935	2.55	2.2E-01	AF187850.1	NT	oz14a10.x1 Soares_fetal_liver_spleen_INFLS_S1 Homo sapiens cDNA clone IMAGE:1875280 3' similar to
1988	11189		0.99	2.2E-01	AF171901.1	NT	TR:Q13040 Q13040 ATP-BINDING CASSETTE PROTEIN;
2058	11259	20474	2.57	2.2E-01	M34640.1	NT	Homo sapiens PPAR delta gene, promoter region
2367	11560	20782	5.34	2.2E-01	BF677538.1	EST_HUMAN	Trimeresurus malabaricus cytb gene, partial cds; mitochondrial gene for mitochondrial product
2548	11736	20953	1.67	2.2E-01	BE618258.1	EST_HUMAN	Fresh-water sponge Emf1 alpha collagen (COLF1) gene
2548	11736	20954	1.67	2.2E-01	BE618258.1	EST_HUMAN	602085608F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4249969 5'
2835	12074	21186	5.33	2.2E-01	BE155625.1	EST_HUMAN	601462629F1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3866180 5'
2835	12074	21197	5.33	2.2E-01	BE155625.1	EST_HUMAN	601462629F1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3866180 5'
2871	12109		1.67	2.2E-01	AF020503.1	NT	PM2-HT0353-281298-003-a12 HT0353 Homo sapiens cDNA
3363	12597		2.58	2.2E-01	AL161562.2	NT	PM2-HT0353-281298-003-a12 HT0353 Homo sapiens cDNA
3735	12955	22071	0.61	2.2E-01	AL163265.2	NT	Homo sapiens FRA3B common fragile region, diadenosine triphosphate hydrolase (FHIT) gene, exon 5
3803	13021		1.59	2.2E-01	AF155728.1	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 62
4073	13283	22382	0.59	2.2E-01	AF213391.1	NT	Homo sapiens chromosome 21 segment HS21C085
4106	13313		0.61	2.2E-01	U68174.1	NT	Xiphophorus maculatus truncated Rax1 retrotransposon reverse transcriptase (RT) pseudogene
4195	13399		1.05	2.2E-01	AF119102.1	NT	Mus musculus ATP-binding cassette protein (Abcb8) mRNA, partial cds
4203	13406	22501	6.45	2.2E-01	AF155142.1	NT	Mus musculus breast/ovarian cancer susceptibility protein (BRCA1) mRNA, complete cds
							Mus musculus melanogaster UNC-119 (unc-119) gene, complete cds
							Drosophila melanogaster UNC-119 (unc-119) gene, complete cds
							Mus musculus mixed lineage kinase 3 (Mlk3) and two pore domain K+ channel subunit (Kcnk6) genes, complete cds

Table 4  
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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4250	13453	22544	2.81	2.2E-01	AF117340.1	NT	Mus musculus MAP kinase kinase kinase 1 (Mekk1) mRNA, complete cds
4250	13453	22545	2.81	2.2E-01	AF117340.1	NT	Mus musculus MAP kinase kinase kinase 1 (Mekk1) mRNA, complete cds
4349	13551	22845	1.25	2.2E-01	U01307.1	NT	Human scRNA (BC200 beta) pseudogene
4349	13551	22846	1.25	2.2E-01	U01307.1	NT	Human scRNA (BC200 beta) pseudogene
4842	14031		1.18	2.2E-01	D50604.1	NT	Human beta-cytoplasmic actin (ACTBP9) pseudogene
4848	14037	23130	2.94	2.2E-01	AA211216.1	EST_HUMAN	z87c05.r1 Stratagene HNT neuron (#837233) Homo sapiens cDNA clone IMAGE:848868 5'
5069	14249		1.22	2.2E-01	L13289.1	NT	Mus musculus vinculin gene, exon 3
5549	14773	24141	1.96	2.2E-01	5803002	NT	Homo sapiens diaphanous (Drosophila, homolog) 2 (DIAPH2), transcript variant 156, mRNA
5553	14777		4.03	2.2E-01	D64000.1	NT	Synechocystis sp. PCC6803 complete genome, 1927, 2392729-2538999
6097	15297	24729	8.28	2.2E-01	AV756238.1	EST_HUMAN	AV756238 BM Homo sapiens cDNA clone BMFAHC06 5'
6204	15385	24827	1.82	2.2E-01	M24136.1	NT	Human glycophorin B gene, exon 4
6204	15385	24828	1.82	2.2E-01	M24136.1	NT	Human glycophorin B gene, exon 4
6470	15667		2.59	2.2E-01	AF155143.1	NT	Mus musculus nm23-M1 gene, promoter region
6742	15937	25398	2.32	2.2E-01	AE001713.1	NT	Thermotoga maritima section 25 of 136 of the complete genome
6771	15966		2.88	2.2E-01	AW855039.1	EST_HUMAN	PM3-CT0263-241299-009-b07 CT0263 Homo sapiens cDNA
6811	16006	25487	2.22	2.2E-01	8393247	NT	Mus musculus deformed epidermal autoregulatory factor 1 (Drosophila) (Dera1), mRNA
6828	16022	25488	3.06	2.2E-01	BF378354.1	EST_HUMAN	MR1-TN0045-110900-008-c02 TN0045 Homo sapiens cDNA
6857	16109	25575	22.93	2.2E-01	P48634	SWISSPROT	LARGE PROLINE-RICH PROTEIN BAT2 (HLA-B-ASSOCIATED TRANSCRIPT 2)
7016	16193	25667	3.82	2.2E-01	AF197941.1	NT	Funaria hygrometrica chloroplast-localized small heat shock protein (CP-sHSP21) mRNA, complete cds; nuclear gene for chloroplast product
7055	16232	25707	2.67	2.2E-01	BF206507.1	EST_HUMAN	601869724F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4100189 5'
7859	17098	26628	5.39	2.2E-01	X01918.1	NT	Drosophila 68C glue gene cluster
7896	16431	25918	2.96	2.2E-01	7706215	NT	Homo sapiens H-2K binding factor-2 (LOC51580), mRNA
8336	17436		2.96	2.2E-01	BE870959.1	EST_HUMAN	601446957F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3850670 5'
8447	18342		3.58	2.2E-01	U82671.2	NT	Homo sapiens chromosome Xq28 melanoma antigen family A2a (MAGEA2A), melanoma antigen family A12 (MAGEA12), melanoma antigen family A2b (MAGEA2B), melanoma antigen family A3 (MAGEA3), caltractin (CALT), NAD(P)H dehydrogenase-like protein (NSDHL), and L1>
8539	17564		2.37	2.2E-01	AF188843.1	NT	Vitis vinifera cultivar Pinot Noir plasma membrane aquaporin (PIP1a) mRNA, complete cds
8656	14496	23584	3.17	2.2E-01	AV1361098.1	EST_HUMAN	RC1-CT0249-141199-021-q04 CT0249 Homo sapiens cDNA
9192	18336		2.87	2.2E-01	AV694801.1	EST_HUMAN	AV694801 GK Homo sapiens cDNA clone GKCAHB02 5'
9273	18036	23843	1.35	2.2E-01	BF243095.1	EST_HUMAN	AV1876452F1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:4104986 5'
9284	18283	23682	1.57	2.2E-01	AL161576.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 74
978	10210	19366	1.69	2.1E-01	AA569289.1	EST_HUMAN	nm31e11.s1 NCI_CGAP_Lip2 Homo sapiens cDNA clone IMAGE:1061804
981	10212	19368	1.69	2.1E-01	AL161504.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 16

Table 4  
Single Exon Probes Expressed in HELA Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1132	10355		3.44	2.1E-01	AE002314.2	NT	Chlamydia muridarum, section 45 of 85 of the complete genome
1206	10425	19580	1.31	2.1E-01	6754299	NT	Mus musculus interferon (alpha and beta) receptor 2 (Ifnar2), mRNA
1206	10425	19581	1.31	2.1E-01	6754299	NT	Mus musculus interferon (alpha and beta) receptor 2 (Ifnar2), mRNA
1878	11085	20275	1.91	2.1E-01	AA908824.1	EST_HUMAN	ak73e02.s1 NCI CGAP_G04 Homo sapiens cDNA clone IMAGE:1518610 3' similar to gb:K02765
2124	11323	20541	4.13	2.1E-01	BF685073.1	EST_HUMAN	COMPLEMENT C3 PRECURSOR (HUMAN);
2875	12113	21241	2.07	2.1E-01	6812445	NT	602083129F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4247503 5'
2917	12155	21290	1.12	2.1E-01	U72145.1	NT	Homo sapiens potassium voltage-gated channel, subfamily H (eag-related), member 4 (KCNH4), mRNA
3794	13012	22345	6.61	2.1E-01	9838361	NT	Campylobacter jejuni 3-hydroxy-3-methylglutaryl coenzyme A reductase (hmgl3) mRNA, complete cds
4031	13241	22345	1.17	2.1E-01	P11675	SWISSPROT	Beta vulgaris mitochondrion, complete genome
4031	13241	22346	1.17	2.1E-01	P11675	SWISSPROT	IMMEDIATE-EARLY PROTEIN IE180
4236	13439		2.87	2.1E-01	AF124526.1	NT	IMMEDIATE-EARLY PROTEIN IE180
4370	13572		1.53	2.1E-01	AB033041.1	NT	Orchestia cavimana calcium-binding protein BP23 precursor (BP23) gene, complete cds
4574	13768	22863	1.99	2.1E-01	AB010273.1	NT	Homo sapiens mRNA for KIAA1215 protein, partial cds
5290	14461	23529	1.2	2.1E-01	AE001173.1	NT	Homo sapiens pshsp47 gene, complete cds
5329	14581	23633	6	2.1E-01	BF672895.1	EST_HUMAN	Borrelia burgdorferi (section 59 of 70) of the complete genome
6258	15439		2.04	2.1E-01	AF000949.1	NT	602152001F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4283001 5'
6378	15558	25014	1.82	2.1E-01	AF000949.1	NT	Archaeoglobus fulgidus section 135 of 172 of the complete genome
6776	15971	25427	5.83	2.1E-01	Z35786.1	NT	Canis familiaris keratin (KRT9) gene, complete cds
6818	16111	25577	4.67	2.1E-01	X97378.1	NT	S. cerevisiae chromosome II reading frame ORF YBL025w
7182	16359	25838	2.49	2.1E-01	P52824	SWISSPROT	A. thaliana mRNA for AtRanBP1b protein
8098	17232		2.2	2.1E-01	11038647	NT	DIACYLGLYCEROL KINASE, DELTA (DIGLYCERIDE KINASE) (DGK-DELTA) (DAG KINASE DELTA)
8109	17243	26784	2.2	2.1E-01	BE180422.1	EST_HUMAN	(80 KD) DIACYLGLYCEROL KINASE
8810	17731		1.54	2.1E-01	AF217490.1	NT	Homo sapiens pancreatic polypeptide 2 (PPY2), mRNA
9034	18247		1.28	2.1E-01	L32588.1	NT	RC3-HT0822-040500-013-b11 HT0822 Homo sapiens cDNA
9228	18004	23848	1.66	2.1E-01	BE672330.1	EST_HUMAN	Homo sapiens fragile 16D oddo reductase (FOR) gene, exons 8, 9, and partial cds
205	9485	18619	4.22	2.0E-01	AB017437.1	NT	Human granulosa gene
540	9781		2.28	2.0E-01	7705601	NT	7a59602.X1 NCI CGAP_G08 Homo sapiens cDNA clone IMAGE:3223034 3'
708	9943	19084	0.93	2.0E-01	M77085.1	NT	Gallus gallus mRNA for avian, complete cds
820	10058	19211	1.88	2.0E-01	AF027865.1	NT	Homo sapiens germine IgH heavy chain V-H pseudogene, alictype VH42
1019	10247	19398	0.76	2.0E-01	D90905.1	NT	O. cuniculus Major Histocompatibility Locus class II region
							Mus musculus Major Histocompatibility Locus class II region
							Synechocystis sp. PCC6803 complete genome, 7/27, 781449-820815

Table 4  
Single Exon Probes Expressed in HELA Cells

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1133	10356	19507	3.48	2.0E-01	AL163213.2	NT	Homo sapiens chromosome 21 segment HS21C013
1261	10476	19638	1.65	2.0E-01	AJ132695.5	NT	Homo sapiens rac1 gene
1315	10531	19693	1.37	2.0E-01	AW384937.1	EST_HUMAN	PM1-HT0422-291298-002-c08 HT0422 Homo sapiens cDNA
1480	10693	19868	12.02	2.0E-01	4503408	NT	Homo sapiens dystrobrevin, alpha (DTNA), mRNA
1537	10760	19923	4.33	2.0E-01	AB007974.1	NT	Homo sapiens mRNA, chromosome 1 specific transcript KIA0505
1542	10755	19929	1.25	2.0E-01	AF260700.1	NT	Homo sapiens sodium iodide symporter mRNA, partial cds
1672	10885	20069	2.02	2.0E-01	U22346.1	NT	Human bradykinin B1 receptor (bradyb1) gene, complete cds
1692	10904		2.15	2.0E-01	AF111170.3	NT	Homo sapiens 14q32 Jagged2 gene, complete cds; and unknown gene
1729	10941		3.16	2.0E-01	U67625.1	NT	Methanococcus jannaschii section 67 of 150 of the complete genome
1855	11092	20252	4.96	2.0E-01	BE871330.1	EST_HUMAN	801449441F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:38533330 5'
1855	11092	20253	4.96	2.0E-01	BE871330.1	EST_HUMAN	801449441F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:38533330 5'
2316	11510		1.87	2.0E-01	X82877.1	NT	H.sapiens Nat-D-glucose cotransport regulator gene
3482	12897	21823	1.8	2.0E-01	P46607	SWISSPROT	HOMEBOX PROTEIN GLABRA2 (HOMEBOX-LEUCINE ZIPPER PROTEIN ATHB-10) (HD-ZIP PROTEIN ATHB-10)
3544	12767		0.7	2.0E-01	AW238005.1	EST_HUMAN	xp15602.x1 NCI_CGAP_HNG Homo sapiens cDNA clone IMAGE:2740385 3' similar to contains element MER21 repetitive element ;
3696	12907	22027	0.99	2.0E-01	P34641	SWISSPROT	CED-11 PROTEIN
3691	12912		0.65	2.0E-01	6680797	NT	Mus musculus bone morphogenetic protein 6 (Bmp6), mRNA
3831	13147	22264	0.71	2.0E-01	Z46906.1	NT	Sus scrofa
4423	13623	22718	0.6	2.0E-01	AF242431.1	NT	Mus musculus neuronal apoptosis inhibitory protein 6 (Naip6) gene, complete cds; and Naip3 gene, exons 2-9 and 11-16
4563	13757		9.02	2.0E-01	BE828165.1	EST_HUMAN	QV4-EN0032-190500-223-c03 EN0032 Homo sapiens cDNA
5065	14245	23332	5.68	2.0E-01	8822080	NT	Homo sapiens hypothetical protein ASH1 (ASH1), mRNA
5135	14313	23405	1.02	2.0E-01	Y19216.1	NT	Homo sapiens putative psihHbD pseudogene for hair keratin, exons 1 to 9
5232	14408	23489	1.4	2.0E-01	M59257.1	NT	Human carcinoembryonic antigen (CEA) gene, exon 4
5415	14643	23775	2.42	2.0E-01	X56600.1	NT	Rat SOD-2 gene for manganese-containing superoxide dismutase
5547	14771	24138	2.26	2.0E-01	11432540	NT	Homo sapiens dual oxidase-like domains 2 (DUOX2), mRNA
5693	14913	24307	5.85	2.0E-01	U15300.1	NT	Saccharomyces cerevisiae Hal5p (HAL5) mRNA, complete cds
5842	15059	24467	3.26	2.0E-01	X61033.1	NT	M.auratus mu class glutathione transferase gene
5891	15108	24519	4.07	2.0E-01	AW360865.1	EST_HUMAN	PM1-CT0247-141099-001-g06 CT0247 Homo sapiens cDNA
6443	15640		8.48	2.0E-01	AF028028.1	NT	Andes virus strain OJ23133 glycoprotein G1 and G2 precursor, gene, partial cds
6529	15725	25180	4.35	2.0E-01	X91151.1	NT	M.musculus scp2 gene exon 14
6839	16083		4.41	2.0E-01	AE001278.1	NT	Chlamydia trachomatis section 5 of 87 of the complete genome
7038	16215		2.78	2.0E-01	AF146892.1	NT	Homo sapiens filamin 2 (FLN2) mRNA, complete cds



Page 60 of 382  
Table 4

## Single Exon Probes Expressed in HELA Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7417	18629	26121	2.97	2.0E-01	D89088.1	NT	Salvelinus pluvius mRNA for transferrin, complete cds
7417	18629	26122	2.97	2.0E-01	D89088.1	NT	Salvelinus pluvius mRNA for transferrin, complete cds
9051	17823	23874	2.36	2.0E-01	AI023592.1	EST_HUMAN	ov60a10.s1 Scores_testis_NHT Homo sapiens cDNA clone IMAGE:1843810 3'
9074	17800		7.52	2.0E-01	AF078164.2	NT	Homo sapiens Ku70-binding protein (KUB3) mRNA, partial cds
9218	17997	23866	1.9	2.0E-01	11528495	NT	Mus musculus fructosamine 3 kinase (Fn3k), mRNA
110	8398		9.7	1.9E-01	7549743	NT	Rattus norvegicus Aryl hydrocarbon receptor nuclear translocator 1 (Ahr1), mRNA
357	9925	18755	7.17	1.9E-01	AF004353.1	NT	Mus musculus pale ear (ep) gene, wild type allele, 3' region, partial cds
662	9908	18036	1.12	1.9E-01	U32581.2	NT	Homo sapiens lambda/delta protein kinase C-interacting protein mRNA, complete cds
662	9908	19037	1.12	1.9E-01	U32581.2	NT	Homo sapiens lambda/delta protein kinase C-interacting protein mRNA, complete cds
669	9915	19044	5.78	1.9E-01	BE070801.1	EST_HUMAN	RC3-BT0502-251189-011-d01 BT0502 Homo sapiens cDNA
670	9915	19044	6.13	1.9E-01	BE070801.1	EST_HUMAN	RC3-BT0502-251189-011-d01 BT0502 Homo sapiens cDNA
683	10224		1.39	1.9E-01	7305180	NT	Mus musculus interleukin 2 receptor, gamma chain (Il2rg), mRNA
1112	10336	19487	13.08	1.9E-01	AA358813.1	EST_HUMAN	EST187784 Fetal lung II Homo sapiens cDNA 5' end
1378	10562	19756	2.31	1.9E-01	AF061282.1	NT	Sorghum bicolor 22 kDa kafirin cluster
1437	10651		3.35	1.9E-01	AF184623.1	NT	Plasmodium vivax reticulocyte binding protein-2 (rbp-2) gene, complete cds
2348	11541	20764	5.01	1.9E-01	8922533	NT	Homo sapiens hypothetical protein FLJ10581 (FLJ10581), mRNA
2873	12111	21239	4.06	1.9E-01	U66086.1	NT	Sigmoidon hispidus p53 gene, partial cds
2889	12126		6.97	1.9E-01	J00922.1	NT	Gallus gallus ovalbumin (Y) gene, complete cds
2960	12198	21333	1.11	1.9E-01	U25148.1	NT	Rattus norvegicus brush border myosin-I (BBMI) mRNA, partial cds
3373	12801	21737	4.46	1.9E-01	D13197.1	NT	Mouse gene for immunoglobulin diversity region D1
3455	12680	21815	5.59	1.9E-01	R16487.1	EST_HUMAN	yf42f10.r1 Scores fetal liver spleen 1NFSL Homo sapiens cDNA clone IMAGE:128547 5'
3792	13010	22125	0.72	1.9E-01	AF264017.1	NT	Rattus norvegicus arylacetamide deacetylase gene, complete cds
3970	13185	22294	3.62	1.9E-01	AB006784.1	NT	Schizosaccharomyces pombe DNA for cytoplasmic dynein heavy chain, complete cds
4059	13270	22372	1.63	1.9E-01	AW754108.1	EST_HUMAN	CM3-C10315-271193-045-b11 CT0315 Homo sapiens cDNA
4218	13419	22514	1.02	1.9E-01	BE834943.1	EST_HUMAN	MR1-FN0010-280700-007-404 FN0010 Homo sapiens cDNA
4465	13683	22756	0.59	1.9E-01	AL161493.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 6
4783	13972	23075	0.78	1.9E-01	Z93780.1	NT	Fugu rubripes genes encoding carboxyl phosphatase III, myosin light chain, MAP2
5035	14220		1.08	1.9E-01	AF223642.1	NT	Rattus norvegicus chemokine receptor CXCR3 mRNA, complete cds
5243	14480		3.78	1.9E-01	AE004594.1	NT	Pseudomonas aeruginosa PA01, section 155 of 528 of the complete genome
							xf28a07.x1 NCI CGAP_U11 Homo sapiens cDNA clone IMAGE:2619444 3' similar to gb:M73779 RETINOIC
							ACID RECEPTOR ALPHA-1 (HUMAN)
5492	14718		4.47	1.9E-01	AW130148.1	EST_HUMAN	Homo sapiens DNA polymerase epsilon catalytic subunit protein (POLE1) gene, exon 1a
5509	14734	24086	7.78	1.9E-01	AF127937.1	NT	Homo sapiens DNA polymerase epsilon catalytic subunit protein (POLE1) gene, exon 1a
5607	14831		2.28	1.9E-01	AU133116.1	EST_HUMAN	AU133116 NT2RP4 Homo sapiens cDNA clone NT2RP4001328 5'
6306	15487	24832	2.74	1.9E-01	AF072724.1	NT	Zea mays starch branching enzyme I (sbe1) gene, complete cds

Table 4

## Single Exon Probes Expressed in HELA Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6875	15870	25329	15.9	1.8E-01	AB033024.1	NT	Homo sapiens mRNA for KIAA1198 protein, partial cds
7237	18458	25946	1.98	1.9E-01	AL161503.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 15
7237	18458	25947	1.98	1.8E-01	AL161503.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 15
7340	16558	26044	2.08	1.9E-01	AF223391.1	NT	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced
8215	17346	26888	2.81	1.8E-01	AJ243213.1	NT	Homo sapiens partial 5-HT4 receptor gene, exons 2 to 5
9239	18175		1.52	1.9E-01	7524759	NT	Chlorella vulgaris chloroplast, complete genome
33	9329	18434	3.28	1.8E-01	U73200.1	NT	Mus musculus p116Rip mRNA, complete cds
264	11984	18669	2.47	1.8E-01	AB022090.1	NT	Mus musculus Cctg gene for chaperonin containing TCP-1 gamma subunit, partial cds
375	9841	18778	1.41	1.8E-01	4502532	NT	Homo sapiens calcium channel, voltage-dependent, beta 2 subunit (CACNB2) mRNA, and translated products
754	9895	19140	0.78	1.8E-01	AB021490.2	NT	Oryza latipes gene for membrane guanylyl cyclase OIGC1, complete cds
989	10220	19374	0.88	1.8E-01	A912212.1	EST_HUMAN	wf1102.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:2337051 3'
1058	10322	19473	3.09	1.8E-01	AF000580.1	NT	Dictyostelium discoideum plasmid Ddp5, complete genome
1295	10510	19870	8.42	1.8E-01	AL117189.1	NT	Yersinia pestis plasmid pCD1
1814	11022		1.71	1.8E-01	4505038	NT	Homo sapiens latent transforming growth factor beta binding protein 4 (LTBP4) mRNA
1832	11040		1.82	1.8E-01	A1733708.1	EST_HUMAN	qg22d10.x5 NCI_CGAP_Kid3 Homo sapiens cDNA clone IMAGE:1761811 3' similar to TR:075938 O75938 GAMMA BUTYROBETAINE HYDROXYLASE
1880	11087	20277	1.52	1.8E-01	AB051897.1	NT	Mus musculus Scyl6, Scyl6, Scyl6 genes for small inducible cytokine A6 precursor, small inducible cytokine A9 precursor, Scyl6 pseudogene, small inducible cytokine A5 precursor, complete cds
2652	11835		2.24	1.8E-01	AW935728.1	EST_HUMAN	QV3-DT0018-081289-036-g04 DT0018 Homo sapiens cDNA
2850	12089		1.85	1.8E-01	AF184588.1	NT	Jonopsidium acule LEAFY protein (LEAFY2) gene, partial cds
2855	12093	21223	1.11	1.8E-01	AW182300.1	EST_HUMAN	X41a03.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2659756 3'
3088	12324	21446	1.88	1.8E-01	AW995178.1	EST_HUMAN	QV0-BN0041-070300-147-c04 BN0041 Homo sapiens cDNA
3344	12572	21711	0.8	1.8E-01	BF183582.1	EST_HUMAN	601809723R1 NIH_MGC_18 Homo sapiens cDNA clone IMAGE:4040821 3'
3600	12821	21942	0.97	1.8E-01	H03369.1	EST_HUMAN	y45e01.s1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:151704 3' similar to contains Alu repetitive element
3600	12821	21943	0.97	1.8E-01	H03369.1	EST_HUMAN	y45e01.s1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:151704 3' similar to contains Alu repetitive element
4325	13526		1.2	1.8E-01	D37954.1	NT	Bovine NB25 mRNA for MHC class II (BoLA-DOB), complete cds
4553	13748	22847	5.71	1.8E-01	AL161556.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 56

Table 4

## Single Exon Probes Expressed in HELA Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4784	13973	23076	2.53	1.8E-01	AB051897.1	NT	Mus musculus Scya6, Scya6, Scya18-ps, Scya5 genes for small inducible cytokine A6 precursor, small inducible cytokine A6 precursor, Scya18 pseudogene, small inducible cytokine A5 precursor, complete cds
5072	14252	23335	2.38	1.8E-01	AW814270.1	EST_HUMAN	MRS-ST0203-151289-112-g06 ST0203 Homo sapiens cDNA
5091	14271	23355	4.94	1.8E-01	AF792382.1	EST_HUMAN	an28g07.y5 Gessler Wilms tumor Homo sapiens cDNA clone IMAGE:1700028 5'
5126	14305	23395	7.48	1.8E-01	AF181258.1	NT	Mesocricetus auratus Na-taurocholate cotransporting polypeptide mRNA, partial cds
5143	14322	23414	1.28	1.8E-01	AF143988.1	EST_HUMAN	mesocricetus auratus Na-taurocholate cotransporting polypeptide mRNA, partial cds
5254	14427	23503	11.75	1.8E-01	AW809402.1	EST_HUMAN	MR4-ST0121-041189-019-b01 ST0121 Homo sapiens cDNA
5904	15121		2.11	1.8E-01	N94853.1	EST_HUMAN	Y62H02.r1 Soares multiple sclerosis 2NHMSP Homo sapiens cDNA clone IMAGE:278163 5'
7231	16452	25942	2.63	1.8E-01	X77338.1	NT	A thaliana mRNA for ribonucleotide reductase R2
7270	16489	25978	7.41	1.8E-01	U38906.1	NT	Bacteriophage r11 integrase, repressor protein (ro), dUTPase, holin and lysin genes, complete cds
7322	15288	24721	2.94	1.8E-01	AB018561.1	NT	Citullus lanatus mRNA for wsus, complete cds
7322	15288	24722	2.94	1.8E-01	AB018561.1	NT	Citullus lanatus mRNA for wsus, complete cds
7323	16539	26028	4.55	1.8E-01	AF019107.1	NT	Dictyostelium discoideum unknown (DG1041) gene, complete cds
7588	16782	26284	1.69	1.8E-01	M59257.1	NT	Human carcinoembryonic antigen (CEA) gene, exon 4
7898	16433	25921	4.57	1.8E-01	X57033.1	NT	B. taurus mRNA for potassium channel
8236	17385	26903	2.48	1.8E-01		NT	Rattus norvegicus Thromboxane receptor (Tbx2r), mRNA
8371	17458		1.24	1.8E-01	8394421	NT	Bovine ephemeral fever virus, complete genome
8433	17498	24014	1.38	1.8E-01	BF348623.1	EST_HUMAN	602019928F1 NC1 CGAP_Bn67 Homo sapiens cDNA clone IMAGE:4155318 5'
8919	17805		2.59	1.8E-01	Q96682	SWISSPROT	DNA TERMINAL PROTEIN (BELLETT PROTEIN) (PTP PROTEIN)
9042	17884		9.36	1.8E-01	R24494.1	EST_HUMAN	Yn48h10.r1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:133027 5'
9084	17906		1.98	1.8E-01	Y11114.1	NT	E. dispar mRNA for hexokinase (hck1)
584	8833	18951	1.41	1.7E-01	BE385184.1	EST_HUMAN	601274604FT NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3615768 5'
815	10053	19207	2.22	1.7E-01	X53330.1	NT	P. dumerilii histone gene cluster for core histones H2A, H2B, H3 and H4
868	10201		1.93	1.7E-01	P35616	SWISSPROT	NEUROFILAMENT TRIPLET L PROTEIN (NEUROFILAMENT LIGHT POLYPEPTIDE) (NF-L)
1065	10291	19441	0.82	1.7E-01	AF081810.1	NT	Lymnaea dispar nucleopolydnavirus, complete genome
1065	10291	19442	0.82	1.7E-01	AF081810.1	NT	Lymnaea dispar nucleopolydnavirus, complete genome
1786	10986	20192	1.31	1.7E-01	AL161573.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 69
1950	11154		3.02	1.7E-01	AF255051.1	NT	Homo sapiens BNIP3H (BNIP3H) gene, complete cds, nuclear gene for mitochondrial product
2812	12052	21173	1.8	1.7E-01	AF000716.1	NT	Vibrio cholerae hypoxanthine phosphoribosyltransferase (hpt) gene, partial cds, hemagglutinin/protease regulatory protein (hapR) gene, complete cds, and YRAL VIBCO gene, partial cds

Page 63 of 382  
Table 4  
Single Exon Probes Expressed in HELA Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2812	12052	21174	1.9	1.7E-01	AF000716.1	NT	Vibrio cholerae hypoxanthine phosphoribosyltransferase (hpt) gene, partial cds, hemagglutinin/protease regulatory protein (hapR) gene, complete cds, and YRAL VIBCO gene, partial cds
2877	12115	21244	1.75	1.7E-01	AA338808.1	EST_HUMAN	EST41651 Endometrial tumor Homo sapiens cDNA 5' end
2954	12192	21328	1.34	1.7E-01	AJ238736.1	NT	Naja naja atra cdx-1 gene, exons 1-3
2954	12192	21327	1.34	1.7E-01	AJ238736.1	NT	Naja naja atra cdx-1 gene, exons 1-3
3089	12305	21427	1.82	1.7E-01	AF081514.1	NT	Toxus canadensis geranylgeranyl diphosphate synthase mRNA, complete cds
3343	12571	21710	0.87	1.7E-01	N55763.1	EST_HUMAN	J2348F Human fetal heart, Lambda ZAP Express Homo sapiens cDNA clone J2348 5'
3423	12848	21778	1.51	1.7E-01	AJ269505.1	NT	Anabaena sp. ORF4 (partial), ORF3, ORF2, ORF1, adpA gene, adpB gene, adpC gene, adpD gene, adpE gene and adpF gene
3605	12826		0.66	1.7E-01	5031886	NT	Homo sapiens LIM domain-containing preferred translocation partner in lipoma (LPP) mRNA
3912	13128	22245	5.85	1.7E-01	AJ235377.1	NT	Homo sapiens derivative 11 breakpoint fragment: partial intron 10 of the ALL-1/MLL/HRX gene fused to intron 5 of the AF-4/FEL gene
4453	12052	21173	3.09	1.7E-01	AF000716.1	NT	Vibrio cholerae hypoxanthine phosphoribosyltransferase (hpt) gene, partial cds, hemagglutinin/protease regulatory protein (hapR) gene, complete cds, and YRAL VIBCO gene, partial cds
4453	12052	21174	3.09	1.7E-01	AF000716.1	NT	Vibrio cholerae hypoxanthine phosphoribosyltransferase (hpt) gene, partial cds, hemagglutinin/protease regulatory protein (hapR) gene, complete cds, and YRAL VIBCO gene, partial cds
4558	13752		1.93	1.7E-01	X52836.1	NT	Schistosoma gregaria alpha repetitive DNA
4773	13882	23064	0.73	1.7E-01	AF217490.1	NT	Homo sapiens fragile 16D oxidoreductase (FOR) gene, exons 8, 9, and partial cds
4857	14045	23139	1.13	1.7E-01	AJ247635.1	EST_HUMAN	q157c09.x1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:1848808 3' similar to contains ORF.b1 ORF repetitive element
5154	14333		1.49	1.7E-01	AF072725.1	NT	Zea mays starch branching enzyme 1b (ae) gene, complete cds
5801	15018	24420	11.05	1.7E-01	H72118.1	EST_HUMAN	ys02q06.s1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:213658 3'
6033	15241		2.09	1.7E-01	AF028552.3	NT	Mesocricetus auratus oviductin precursor (OVI) gene, complete cds
6205	15386	24828	8.82	1.7E-01	BE734179.1	EST_HUMAN	601569022F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3843964 5'
6551	15747	25207	5.6	1.7E-01	7708426	NT	Homo sapiens cleavage and polyadenylation specificity factor 3, 73kD subunit (CPSF3), mRNA
6551	15747	25208	5.8	1.7E-01	7708426	NT	Homo sapiens cleavage and polyadenylation specificity factor 3, 73kD subunit (CPSF3), mRNA
6689	15884	25344	3.97	1.7E-01	D00384.1	NT	Rat (SHR strain) SX1 gene
6956	16134	25604	11.14	1.7E-01	AP001508.1	NT	Bacillus halodurans genomic DNA, section 2/14
6995	16173	25644	2.61	1.7E-01	U16288.1	NT	Human class IV alcohol dehydrogenase (ADH7) gene, exon 3
7143	16320		3.39	1.7E-01	AL163284.2	NT	Homo sapiens chromosome 21 segment HS21C084
7272	16491	25692	9.77	1.7E-01	BE390835.1	EST_HUMAN	601286547F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3613258 5'

Table 4

## Single Exon Probes Expressed in HELA Cells

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7384	16598	26086	3.22	1.7E-01	AA814617.1	EST_HUMAN	of43a03.s1 NCI CGAP CNS1 Homo sapiens cDNA clone IMAGE:1426924 3'
7873	16872	26375	8.77	1.7E-01	7106300	NT	Mus musculus adenomatosis polyposis coli binding protein Eb1 (Eb1), mRNA
7873	16872	26376	8.77	1.7E-01	7106300	NT	Mus musculus adenomatosis polyposis coli binding protein Eb1 (Eb1), mRNA
8202	17334		1.84	1.7E-01	P15272	SWISSPROT	AMP NUCLEOSIDASE
8270	17618		1.34	1.7E-01	AJ272584.1	NT	Blaibella aurantiacea mitochondrial partial COII gene for cytochrome c oxidase subunit II
8274	17355	26928	3.52	1.7E-01	11418157	NT	Homo sapiens calcium channel, voltage-dependent, alpha 1I subunit (CACNA1I), mRNA
8404	18282		1.48	1.7E-01	AL163278.2	NT	Homo sapiens chromosome 21 segment HS21C078
8701	18124		1.59	1.7E-01	AI824404.1	EST_HUMAN	h89g05.x1 NCI CGAP U11 Homo sapiens cDNA clone IMAGE:2274872 3' similar to gb:M73779 RETINOIC ACID RECEPTOR ALPHA-1 (HUMAN);
9005	17883	23889	9.13	1.7E-01	U01317.1	NT	Human beta globin region on chromosome 11
124	9409	18543	1.74	1.6E-01	AF217532.1	NT	Homo sapiens mevalonate kinase gene, exon 6 and 7
886	11941	19060	1.2	1.6E-01	R31497.1	EST_HUMAN	y75f12.1 Soares placenta ND2IP Homo sapiens cDNA clone IMAGE:135589 5'
1509	10722	19884	3.18	1.6E-01	AF288117.1	NT	Homo sapiens homeobox protein OTX2 gene, complete cds
1892	11099	20280	1.84	1.6E-01	P22063	SWISSPROT	AXONIN-1 PRECURSOR (AXONAL GLYCOPROTEIN TAG-1)
1953	11157		1.12	1.6E-01	U10334.1	NT	Crassostrea gigas RNA polymerase II largest subunit mRNA, partial cds
2456	11647	20968	1.25	1.6E-01	AB037726.1	NT	Homo sapiens mRNA for KIAA1308 protein, partial cds
2844	12083	21209	11.43	1.6E-01	AF185589.1	NT	Homo sapiens cytochrome P450 3A4 (CYP3A4) gene, promoter region
2844	12083	21210	11.43	1.6E-01	AF185589.1	NT	Homo sapiens cytochrome P450 3A4 (CYP3A4) gene, promoter region
2968	12206	21342	1.77	1.6E-01	AE001862.1	NT	Deinococcus radiodurans R1 section 1 of 2 of the complete chromosome 2
3611	12832	21952	1.23	1.6E-01	AJ003165.1	NT	Populus trichocarpa cv. Trichobol ABI3 gene
3611	12832	21953	1.23	1.6E-01	AJ003165.1	NT	Populus trichocarpa cv. Trichobol ABI3 gene
3754	12973	22089	0.73	1.6E-01	AE000882.1	NT	Archaeoglobus fulgidus section 145 of 172 of the complete genome
3977	13181		2.81	1.6E-01	AE004413.1	NT	Vibrio cholerae chromosome II, section 70 of 93 of the complete chromosome
4320	13521	22616	11.43	1.6E-01	AF179880.1	NT	Homo sapiens apelin gene, complete cds
4450	13848		3.4	1.6E-01	AW968601.1	EST_HUMAN	EST380677 MAGE resequences, MAGJ Homo sapiens cDNA
4459	13657		4.67	1.6E-01	6753319	NT	Mus musculus chaperonin subunit 3 (gamma) (Cct3), mRNA
4945	14132	23227	0.79	1.6E-01	P40631	SWISSPROT	MICRONUCLEAR LINKER HISTONE POLYPROTEIN (MIC LH) [CONTAINS: LINKER HISTONE PROTEINS ALPHA, BETA, DELTA AND GAMMA]
4984	14151	23242	1.37	1.6E-01	AA088343.1	EST_HUMAN	z84h09.s1 Stratiagene colon (8837204) Homo sapiens cDNA clone IMAGE:511361 3' similar to TR:E221855
4988	14175	23265	1.3	1.6E-01	AJ006356.1	NT	E221955 38,855 BP SEGMENT OF CHROMOSOME XIV ;
4988	14175	23266	1.3	1.6E-01	AJ006356.1	NT	Lycopodium obscurum RsaI fragment 2, satellite region
5451	14677	23836	3	1.6E-01	AW197496.1	EST_HUMAN	Lycopodium obscurum RsaI fragment 2, satellite region xmi4301.x1 NCI CGAP_G08 Homo sapiens cDNA clone IMAGE:2686959 3' similar to TR:O75984 O75984 HYPOTHETICAL 127.6 KD PROTEIN ;

Table 4

## Single Exon Probes Expressed in HELA Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5451	14677	23837	3	1.6E-01	AW197498.1	EST_HUMAN	nm4301.x1 NCI_CGAP_GC8 Homo sapiens cDNA clone IMAGE:2686969 3' similar to TR.O75684 O75684
5459	14685	24035	2.4	1.6E-01	AF034716.1	NT	HYPOTHETICAL 127.6 KD PROTEIN ;
5841	15058	24465	2	1.6E-01	AL161588.2	NT	Rattus norvegicus CCAT1/enhancer binding protein epsilon (cbtpe) gene, complete cds
5841	15058	24466	2	1.6E-01	AL161588.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 84
6069	14516	23558	4.34	1.6E-01	AW281215.1	EST_HUMAN	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 84
6417	15814	25078	2.81	1.6E-01	L49349.1	NT	UI-H-BI2-agt-b-08-0-UI.s1 NCI_CGAP_Sub4 Homo sapiens cDNA clone IMAGE:2724418 3'
6979	16157	25629	3.08	1.6E-01	Z49501.1	NT	Gorilla gorilla androgen receptor gene, partial exon
7250	16470	25962	3.11	1.6E-01	AW850853.1	EST_HUMAN	S.cerevisiae chromosome X reading frame ORF YJR001W
7678	16875	26619	8.9	1.6E-01	AF106064.1	NT	IL3-CT0220-111189-028-G01 CT0220 Homo sapiens cDNA
7680	17089	26619	11.94	1.6E-01	6671552	NT	Plasmodium falciparum calcium-dependent protein kinase-3 (cdpk3) gene, complete cds
8286	18298	26596	1.58	1.6E-01	6879468	NT	Mus musculus adaptor-related protein complex AP-1, beta 1 subunit (Ap1b1), mRNA
8408	17482	26596	3.99	1.6E-01	AV719585.1	EST_HUMAN	Mus musculus protein kinase, cGMP-dependent, type II (Ptkg2), mRNA
8854	18100		8.77	1.6E-01	AB045310.1	NT	AV719585 GLC Homo sapiens cDNA clone GLCEMF07 5'
9029	17877		3.54	1.6E-01	AK024498.1	NT	Cucumis sativus KS mRNA for anti-leucine synthase, complete cds
9117	17935		2.51	1.6E-01	AF287344.1	NT	Homo sapiens mRNA for FLJ00104 protein, partial cds
9141	17947	23882	1.7	1.6E-01	9506522	NT	Fuchsia hybrid cultivar Qiu 94208 ribosomal protein S10 gene, partial cds; nuclear gene for mitochondrial product
252	9528	18656	1.25	1.5E-01	BE710087.1	EST_HUMAN	Rattus norvegicus chondroitin sulfate proteoglycan 5 (neuroglycan C) (Cspg5), mRNA
252	9528	18659	1.25	1.5E-01	BE710087.1	EST_HUMAN	IL3-HT0619-040700-197-E05 HT0619 Homo sapiens cDNA
594	11940		1.58	1.5E-01	AV711698.1	EST_HUMAN	IL3-HT0619-040700-197-E05 HT0619 Homo sapiens cDNA
792	10032	19181	1.17	1.5E-01	AL16284.2	NT	AV711698 DCA Homo sapiens cDNA clone DCAADH08 5'
1100	10324	19475	0.79	1.5E-01	AJ009735.1	NT	Homo sapiens chromosome 21 segment HS21C084
1105	10329	19479	2.27	1.5E-01	AJ251885.1	NT	Cyprinus carpio mRNA for EGGS22 myosin heavy chain, 3'UTR
1121	10345		1.4	1.5E-01	L36125.1	NT	Homo sapiens partial SLC22A2 gene for organic cation transporter (OCT2), exon 1
1224	10442	19597	0.77	1.5E-01	AW195616.1	EST_HUMAN	Rattus norvegicus insulin-responsive glucose transporter (GLUT4) gene, 5' end
1282	10497	19656	3.74	1.5E-01	D26535.1	NT	nm394111.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2696085 3'
1282	10497	19657	3.74	1.5E-01	D26535.1	NT	Human gene for dihydropyrimidinase succinyltransferase, complete cds (exon 1-15)
1475	10688	19885	1.29	1.5E-01	AF117340.1	NT	Human gene for dihydropyrimidinase succinyltransferase, complete cds (exon 1-15)
1872	11079	20269	1.34	1.5E-01	AW444451.1	EST_HUMAN	Mus musculus MAP kinase kinase kinase 1 (Mekkk1) mRNA, complete cds
2931	12189	21301	1.26	1.5E-01	AF208066.1	NT	UI-H-BI3-akt-b-09-0-UI.s1 NCI_CGAP_Sub5 Homo sapiens cDNA clone IMAGE:2733641 3'
2931	12189	21302	1.26	1.5E-01	AF208066.1	NT	Murine hepatitis virus strain Penn 97-1, complete genome
3326	12555	21692	4.94	1.5E-01	AA035049.1	EST_HUMAN	Murine hepatitis virus strain Penn 97-1, complete genome
							cc68405.s1 NCI_CGAP_GC4 Homo sapiens cDNA clone IMAGE:1571337 3' similar to gb:M11433
							RETINOL-BINDING PROTEIN I, CELLULAR (HUMAN);

Page 66 of 382  
Table 4  
Single Exon Probes Expressed in HELA Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3347	12575	21715	0.77	1.5E-01	Z23104.1	NT	L. stagnalis mRNA for G protein-coupled receptor
3347	12575	21716	0.77	1.5E-01	Z23104.1	NT	L. stagnalis mRNA for G protein-coupled receptor
3738	12958	22073	1.82	1.5E-01	U09964.1	NT	Mus musculus ICR/Swiss glyceraldehyde 3-phosphate dehydrogenase (Gapd-S) gene, complete cds
3751	12970	22085	0.59	1.5E-01	7108358	NT	Homo sapiens pyruvate dehydrogenase kinase, isoenzyme 1 (PDK1), nuclear gene encoding mitochondrial protein, mRNA
3764	12982	22086	0.63	1.5E-01	M87882.1	NT	XYNA; Thermoplasma volcanium; xyna; 4182 base-pairs
3848	13065	22179	2.72	1.5E-01	AW85983.1	EST_HUMAN	h10706.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2881411 3'
4027	13238	22343	0.92	1.5E-01	AW36659.1	EST_HUMAN	RC2-HT0149-191099-012-c09 HT0149 Homo sapiens cDNA
4164	13368	22467	10.65	1.5E-01	AL163284.2	NT	Homo sapiens chromosome 21 segment HS21C084
4484	13682	22771	0.77	1.5E-01	BE781253.1	EST_HUMAN	601583988F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3938345 5'
4484	13682	22772	0.77	1.5E-01	BE781253.1	EST_HUMAN	601583988F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3938345 5'
4737	13928	23032	1.55	1.5E-01	BF687685.1	EST_HUMAN	602067192F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4068223 5'
4762	11853	21089	2.25	1.5E-01	BF69381.1	EST_HUMAN	602067192F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4247537 5'
4800	13989	23098	0.97	1.5E-01	BE173796.1	EST_HUMAN	602083269F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4068223 5'
4800	13989	23097	0.97	1.5E-01	BE173796.1	EST_HUMAN	602083269F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4068223 5'
5023	14210	23283	1.25	1.5E-01	AL161580.2	EST_HUMAN	CM0-HT0565-280200-245-b10 HT0565 Homo sapiens cDNA
5304	14536	23540	2.13	1.5E-01	P07986	SWISSPROT	CM0-HT0565-280200-245-b10 HT0565 Homo sapiens cDNA
5351	14581		7.98	1.5E-01	P15186	SWISSPROT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 60
5461	14687	24038	4.08	1.5E-01	AW850754.1	EST_HUMAN	THROMBOSPONDIN 1 PRECURSOR
5480	14707	24081	6.8	1.5E-01	U85016.1	NT	SEX HORMONE-BINDING GLOBULIN PRECURSOR (SHBG) (SEX STEROID-BINDING PROTEIN) (SBP) (TESTIS-SPECIFIC ANDROGEN-BINDING PROTEIN) (ABP)
5480	14707	24082	6.8	1.5E-01	U85016.1	NT	IL3-CT0219-160200-064-F10 CT0219 Homo sapiens cDNA
5655	14878	24267	1.86	1.5E-01	6753659	NT	Mus musculus transforming growth factor alpha (TGfa) mRNA, complete cds
5655	14878	24268	1.86	1.5E-01	6753659	NT	Mus musculus transforming growth factor alpha (TGfa) mRNA, complete cds
5683	14903	24296	2.11	1.5E-01	AJ276505.1	NT	Mus musculus DNA methyltransferase 2 (Dnm12), mRNA
5752	14971	24369	27.85	1.5E-01	BE727658.1	EST_HUMAN	Mus musculus genomic fragment, 279 Kb, chromosome 7
5771	14989		1.88	1.5E-01	4506396	NT	601564322F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3833081 5'
5808	15025	24425	1.73	1.5E-01	AF134807.1	NT	Homo sapiens RAD54 (S cerevisiae)-like (RAD54L) mRNA
5876	18065	24507	2.13	1.5E-01	AE001039.1	NT	Influenza B virus (B/Nanchang/480/94) NB protein gene, complete cds; and neuraminidase gene, partial cds
5892	15109	24520	5.01	1.5E-01	11417238	NT	Archaeoglobus fulgidus section 98 of 172 of the complete genome
5899	15116	24528	1.64	1.5E-01	P48508	SWISSPROT	Homo sapiens chromosome 5 open reading frame 3 (C5ORF3), mRNA
							GLUTAMATE-CYSTEINE LIGASE REGULATORY SUBUNIT (GAMMA-GLUTAMYL-CYSTEINE SYNTHETASE) (GAMMA-ECS) (GCS LIGHT CHAIN)

Page 67 of 382  
Table 4  
Single Exon Probes Expressed in HELA Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5926	15142	24553	2.25	1.5E-01	Q28462	SWISSPROT	AMELOGENIN
5970	15185	24602	1.71	1.5E-01	P30143	SWISSPROT	HYPOTHETICAL 51.7 KD PROTEIN IN THRC-TALB INTERGENIC REGION (ORF8)
6078	14524	23566	5.92	1.5E-01	AW970295.1	EST_HUMAN	EST382376 MAGE resequences, MAGK Homo sapiens cDNA
6172	15354		2.42	1.5E-01	AF210842.1	NT	Homo sapiens HARP (HARP) gene, exon 17 and complete cds
6252	15433	24872	1.72	1.5E-01	AB73157.1	EST_HUMAN	wf52c08.x1 NCL CGAP_U11 Homo sapiens cDNA clone IMAGE:2491310.3
6332	15513	24959	1.92	1.5E-01	AW500611.1	EST_HUMAN	UIHF-BNO-alk-4-05-0-U1.1 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3077409.5
6332	15513	24960	1.92	1.5E-01	AW500611.1	EST_HUMAN	UIHF-BNO-alk-4-05-0-U1.1 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3077409.5
6600	15796		19.61	1.5E-01	C16800.1	EST_HUMAN	C16800 Clontech human aorta polyA+ mRNA (#6572) Homo sapiens cDNA clone GEN-529H09.5
6808	16003	25483	2.46	1.5E-01	N74228.1	EST_HUMAN	z859e06.s1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:296866.3 similar to PIR-S44443 S44443 RAD23 protein homolog2 - human
6829	16023		3.09	1.5E-01	AV754818.1	EST_HUMAN	AV754818 TP Homo sapiens cDNA clone TPAAHB12.5
6896	16601	25067	7.62	1.5E-01	U00455.1	NT	Acipenser transmontano vitellogenin mRNA, partial cds
7044	16221	25698	6.88	1.5E-01	AF007570.1	NT	Aplysia californica carboxypeptidase D mRNA, complete cds
7044	16221	25697	6.88	1.5E-01	AF007570.1	NT	Aplysia californica carboxypeptidase D mRNA, complete cds
7135	16312	25763	4.56	1.5E-01	X98952.1	NT	P. lantulus mRNA for integrin beta subunit
7169	16346	25826	4.07	1.5E-01	AB14046.1	EST_HUMAN	wk53h12.x1 NCL CGAP_P122 Homo sapiens cDNA clone IMAGE:2419175.3 similar to gb:M27508 BETA GALACTOSIDASE-RELATED PROTEIN PRECURSOR (HUMAN);
7169	16346	25827	4.07	1.5E-01	AB14046.1	EST_HUMAN	wk53h12.x1 NCL CGAP_P122 Homo sapiens cDNA clone IMAGE:2419175.3 similar to gb:M27508 BETA GALACTOSIDASE-RELATED PROTEIN PRECURSOR (HUMAN);
7401	16614	26103	6.47	1.5E-01	AL163280.2	NT	Homo sapiens chromosome 21 segment HS21C080
7401	16614	26104	6.47	1.5E-01	AL163280.2	NT	Homo sapiens chromosome 21 segment HS21C080
7548	16753		1.84	1.5E-01	AB042975.1	NT	Sus scrofa CYP51 gene for lanosterol 14 alpha-demethylase, exon 1
7642	16842	26340	1.8	1.5E-01	AW841915.1	EST_HUMAN	IL5-CN0024-030300-025-D04 CN0024 Homo sapiens cDNA
7725	15433	24872	2.9	1.5E-01	AB73157.1	EST_HUMAN	wf52c08.x1 NCL CGAP_U11 Homo sapiens cDNA clone IMAGE:2491310.3
8363	18157		31.79	1.5E-01	BF700582.1	EST_HUMAN	602128753F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4285549.5
8755	17696		1.5	1.5E-01	AF030358.2	NT	Rattus norvegicus chemokine CX3C mRNA, complete cds
8756	17696		1.22	1.5E-01	AJ238332.1	NT	Mus musculus mRNA for death inducer-obliterant-1 (Dio-1)
8819	18177		6.75	1.5E-01	RB3077.1	EST_HUMAN	ys87e04.1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:194430.5
8916	18200		2.3	1.5E-01	AV741272.1	EST_HUMAN	AV741272 CB Homo sapiens cDNA clone CBDAAGD04.5
9027	18103	23808	6.2	1.5E-01	AL139074.2	NT	Campylobacter jejuni NCTC11168 complete genome, segment 1/8
9251	18020	23851	3.72	1.5E-01	AJ276242.1	NT	Sus scrofa mRNA for sodium iodide symporter
304	9577		1.45	1.4E-01	AF009663.1	NT	Homo sapiens T cell receptor beta locus, TCRBV/SSP to TCRBV/21S2A2 region
920	10155		3.95	1.4E-01	DF6638.1	NT	Xenopus laevis mRNA for DNA (cytosine-5)-methyltransferase, complete cds
1266	10481		2.73	1.4E-01	T91864.1	EST_HUMAN	yf54c01.s1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:112032.3



Page 68 of 382  
Table 4  
Single Exon Probes Expressed in HELA Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1720	10932		1.43	1.4E-01	6878980	NT	Mus musculus growth differentiation factor 5 (Gdf5), mRNA
1723	10935	20118	1.65	1.4E-01	AE001710.1	NT	Thermotoga maritima section 22 of 136 of the complete genome
1869	11078		0.92	1.4E-01	AW135741.1	EST_HUMAN	UI-H-B1-act-a-09-Q-UI.s1 NCI_CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2714009 3'
1954	11158		10.51	1.4E-01	AA720615.1	EST_HUMAN	ny72d07.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1283821 3'
2745	11924	21139	4.09	1.4E-01	A933496.1	EST_HUMAN	wm74d01.x1 NCI_CGAP_UI2 Homo sapiens cDNA clone IMAGE:2441685 3'
4165	13361	22461	11.2	1.4E-01	A1698094.1	EST_HUMAN	b56c02.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:2273570 3'
4165	13361	22462	11.2	1.4E-01	A1698094.1	EST_HUMAN	b56c02.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:2273570 3'
4222	13426	22518	3.52	1.4E-01	AE001710.1	NT	Thermotoga maritima section 22 of 136 of the complete genome
4680	13873	22973	0.61	1.4E-01		NT	Homo sapiens phosphodiesterase 4A, cAMP-specific (dunce (Drosophila))-homolog phosphodiesterase E2 (PDE4A), mRNA
5334	14565	23639	4.95	1.4E-01	T80677.1	EST_HUMAN	ye15c11.s1 Stratagene lung (#937210) Homo sapiens cDNA clone IMAGE:117812 3'
5352	14582	23657	4.24	1.4E-01	AB004556.1	NT	Candida tropicalis DNA for mitochondrial NADP-linked isocitrate dehydrogenase, complete cds
5352	14582	23658	4.24	1.4E-01	AB004556.1	NT	Candida tropicalis DNA for mitochondrial NADP-linked isocitrate dehydrogenase, complete cds
5787	15004	24408	2.98	1.4E-01	BE326891.1	EST_HUMAN	hr67c02.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:3133538 3'
5865	15083	24498	4.8	1.4E-01	AU117147.1	EST_HUMAN	AU117147 HEMBA1 Homo sapiens cDNA clone HEMBA1000769 5'
5865	15083	24497	4.8	1.4E-01	AU117147.1	EST_HUMAN	AU117147 HEMBA1 Homo sapiens cDNA clone HEMBA1000769 5'
5911	15128	24537	3.7	1.4E-01	AW082796.1	EST_HUMAN	xb71d12.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2581751 3'
5923	15140		1.65	1.4E-01	BE266536.1	EST_HUMAN	601183523F1 NIH_MGC 7 Homo sapiens cDNA clone IMAGE:3537581 5'
5935	15151	24581	2.2	1.4E-01	BF378533.1	EST_HUMAN	QV1-UM0038-080300-103-409 UM0036 Homo sapiens cDNA
6280	15431		1.78	1.4E-01	AW015373.1	EST_HUMAN	UI-H-B10-aat-c-09-Q-UI.s1 NCI_CGAP_Sub1 Homo sapiens cDNA clone IMAGE:2710289 3'
6749	15944	25404	7.58	1.4E-01	AA307073.1	EST_HUMAN	EST1178192 Colon carcinoma (HCC) cell line Homo sapiens cDNA 5' end
6825	16019	25484	9.29	1.4E-01	BF310959.1	EST_HUMAN	601895465F1 NIH_MGC 19 Homo sapiens cDNA clone IMAGE:4124824 5'
6867	16057	25524	2.65	1.4E-01	Y10198.1	NT	Homo sapiens PHEX gene
6867	16057	25525	2.65	1.4E-01	Y10198.1	NT	Homo sapiens PHEX gene
7287	16516		1.91	1.4E-01	AA811480.1	EST_HUMAN	oe99a03.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1320384 3'
7419	16631	26123	3.5	1.4E-01	RG3400.1	EST_HUMAN	yf70c05.r1 Soares breast 2NbrHst Homo sapiens cDNA clone IMAGE:154088 5'
7840	17032	26547	2.07	1.4E-01	X66092.1	NT	C.perfringens ORF for putative membrane transport protein
7874	15431		1.74	1.4E-01	AW015373.1	EST_HUMAN	UI-H-B10-aat-c-09-Q-UI.s1 NCI_CGAP_Sub1 Homo sapiens cDNA clone IMAGE:2710289 3'
8005	16440	25928	2.41	1.4E-01	U28780.1	NT	Borrelia burgdorferi glyceraldehyde-3-phosphate dehydrogenase (GAPDH), phosphoglycerate kinase (PGK), triosephosphate isomerase (TPI) genes, complete cds
8057	17192		1.63	1.4E-01	X52102.1	NT	M.musculus p18K gene for 16 kDa protein
8642	18128	23814	1.29	1.4E-01	AB000890.1	NT	Ephydra fluviatilis mRNA for aldolase, partial cds
8684	17682	23946	2.39	1.4E-01	X74773.1	NT	P.salina plastid gene secY
8708	17670		2.27	1.4E-01	11988117	NT	Rattus norvegicus desmin (Des), mRNA

Page 69 of 382  
Table 4  
Single Exon Probes Expressed in HELA Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8753	18355		1.65	1.4E-01	BE513802.1	EST_HUMAN	601315838F1 NIH_MGC 8 Homo sapiens cDNA clone IMAGE:3634329 5'
8949	17758		3.74	1.4E-01	AF083221.1	NT	Fugu rubripes putative neurotransmitter receptors, YDR140w homolog, and glycineamide ribonucleotide transferase (GART) genes, complete cds
8961	17764		2.08	1.4E-01	D64004.1	NT	Synechocystis sp. PCC6803 complete genome, 23127, 2868767-3002855
8943	18374		3.7	1.4E-01	P10447	SWISSPROT	TYROSINE-PROTEIN KINASE TRANSFORMING PROTEIN ABL
9166	18178		3.76	1.4E-01	D82983.1	NT	Mus musculus mRNA for prolidase, complete cds
9245	18016		1.74	1.4E-01	AW377898.1	EST_HUMAN	MRO-HT0208-221209-204-008 HT0208 Homo sapiens cDNA
327	9598	18727	5.19	1.3E-01	4758467	NT	Homo sapiens G protein-coupled receptor 50 (GPR50) mRNA
327	9598	18728	5.19	1.3E-01	4758467	NT	Homo sapiens G protein-coupled receptor 50 (GPR50) mRNA
535	9786	18909	1.61	1.3E-01	AB013139.1	NT	Homo sapiens gene for NBS1, complete cds
642	9888	19013	1.32	1.3E-01	AJ277606.1	NT	Human calicivirus HUNLV/Girlington/93/UK RNA for capsid protein (ORF2), strain HUNLV/Girlington/93/UK
642	9888	19014	1.32	1.3E-01	AJ277606.1	NT	Human calicivirus HUNLV/Girlington/93/UK RNA for capsid protein (ORF2), strain HUNLV/Girlington/93/UK
854	10090	19252	0.8	1.3E-01	X53330.1	NT	P. dumerilii histone gene cluster for core histones H2A, H2B, H3 and H4
904	10139	19301	1.77	1.3E-01	AF139518.1	NT	Rattus norvegicus A-kinase anchor protein mRNA, complete cds
1034	10260	19410	1.42	1.3E-01	AL117078.1	NT	Botrytis cinerea strain T4 cDNA library under conditions of nitrogen deprivation
1135	10358		2.11	1.3E-01	AL115285.1	NT	Botrytis cinerea strain T4 cDNA library under conditions of nitrogen deprivation
1223	10441	18596	1.48	1.3E-01	AV712467.1	EST_HUMAN	AV712467 DCA Homo sapiens cDNA clone DCAAF05 5'
1445	10658		0.83	1.3E-01	AF146277.1	NT	Homo sapiens adapter protein GMS mRNA, complete cds
1825	11033	20228	7.72	1.3E-01	6680957	NT	Mus musculus proclolagen, type XI, alpha 1 (Col11a1), mRNA
1829	11133	20328	2.16	1.3E-01	AL117078.1	NT	Botrytis cinerea strain T4 cDNA library under conditions of nitrogen deprivation
2136	11334		0.97	1.3E-01	AJ243578.1	NT	Rhodopseudomonas acidophila pucB5, pucA5, pucB6, pucB7, pucA7, pucB8, pucA8 and pucC genes and ORF151
2264	11449		0.97	1.3E-01	AW812104.1	EST_HUMAN	RC4-ST0173-191099-032-d12 ST0173 Homo sapiens cDNA
2347	11540		2.94	1.3E-01	AE001016.1	NT	Archaeoglobus fulgidus section 91 of 172 of the complete genome
2547	11735	20852	2.11	1.3E-01	M88918.1	NT	Carassius auratus keratin type I mRNA, complete cds
3034	12270	21397	0.59	1.3E-01	AL163207.2	NT	Homo sapiens chromosome 21 segment HS21C007
3332	12561	21699	0.63	1.3E-01	AF186779.1	NT	Homo sapiens transcription factor IGHM enhancer 3, JM11 protein, JM4 protein, JM5 protein, T54 protein, JM10 protein, A4 differentiation-dependent protein, triple LIM domain protein 6, and synaptophysin genes, complete cds; and L-type calcium channel a3
3428	12653	21783	1.07	1.3E-01	M21572.1	NT	Bovine branched chain alpha-keto acid dihydratoyl transacylase mRNA, complete cds
3702	12922	22040	0.81	1.3E-01	AP000001.1	NT	Pyrococcus horikoshii OT3 genomic DNA, 1-287000 nt. position (177)
3702	12922	22041	0.81	1.3E-01	AP000001.1	NT	Pyrococcus horikoshii OT3 genomic DNA, 1-287000 nt. position (177)

Table 4

## Single Exon Probes Expressed in HELA Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3709	12929	22047	0.63	1.3E-01	AB032159.1	NT	Homo sapiens DD4 gene for dihydroadipic dehydrogenase 4 [AKR 1C4], exon 2
3763	12922	22040	0.68	1.3E-01	AF000001.1	NT	Pyrococcus horikoshii OT3 genomic DNA, 1-287000 nt. position (177)
3763	12922	22041	0.66	1.3E-01	AF000001.1	NT	Pyrococcus horikoshii OT3 genomic DNA, 1-287000 nt. position (177)
3769	13007	22122	0.89	1.3E-01	6878840	NT	Rattus norvegicus Fibrinogen, gamma polypeptide (Fgg), mRNA
3968	13181		1.52	1.3E-01	AL161581.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 77
4028	9898	19013	0.9	1.3E-01	AJ277608.1	NT	Human calicivirus HUNLV/Girlington/93/UK RNA for capsid protein (ORF2), strain HUNLV/Girlington/93/UK
4028	9898	19014	0.9	1.3E-01	AJ277608.1	NT	Human calicivirus HUNLV/Girlington/93/UK RNA for capsid protein (ORF2), strain HUNLV/Girlington/93/UK
4120	13328		1.03	1.3E-01	AF020713.1	NT	Bacteriophage SPBc2 complete genome
4140	13346		3.88	1.3E-01	AW364341.1	EST_HUMAN	QV3-DT0018-081289-036-a03 DT0018 Homo sapiens cDNA
4148	13354	22456	2.2	1.3E-01	AF026805.1	NT	Schistosoma mansoni fructose biphosphate aldolase mRNA, complete cds
4167	13371	22470	21.57	1.3E-01	AW273741.1	EST_HUMAN	w23f10.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2813985 3'
4275	13478	22575	0.94	1.3E-01	AV752278.1	EST_HUMAN	AV752278 NP2 Homo sapiens cDNA clone NPDAZE02 5'
4275	13478	22576	0.94	1.3E-01	AV752278.1	EST_HUMAN	AV752278 NP2 Homo sapiens cDNA clone NPDAZE02 5'
4304	13505		1.33	1.3E-01	AL163280.2	NT	Homo sapiens chromosome 21 segment HS21C080
4475	13673	22763	0.68	1.3E-01	M21572.1	NT	Bovine branched chain alpha-keto acid dihydrolipoyl transacylase mRNA, complete cds
4531	13727	22824	2.2	1.3E-01	BE272339.1	EST_HUMAN	601126096F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:2890063 5'
5141	14320	23412	1.04	1.3E-01	AI432531.1	EST_HUMAN	h38c10.x1 NCI_CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2120562 3'
5281	14452		1.03	1.3E-01	D82918.1	NT	Gallus gallus domesticus mitochondrial DNA, D-loop region, strain: Ayam Kokok Belanggek
5375	14604	23713	1.84	1.3E-01	AW804417.1	EST_HUMAN	QVQ-UJM0093-100400-189-a06 UJM0093 Homo sapiens cDNA
5868	15084	24498	14.91	1.3E-01	AB031326.1	NT	Schizosaccharomyces pombe gene for Alp41, complete cds
5909	15126	24535	2.17	1.3E-01	X88891.1	NT	C.jacchus intron 4 of visual pigment gene (red allele)
6191	15373		1.64	1.3E-01	H48664.1	EST_HUMAN	yf33d02.r1 Soares fetal liver spleen TNF1S Homo sapiens cDNA clone IMAGE:207075 5'
6452	15849	25117	2.19	1.3E-01	11423294	NT	Homo sapiens PRO0611 protein (PRO0611), mRNA
6579	15775		4.64	1.3E-01	Z74102.1	NT	S. cerevisiae chromosome IV reading frame ORF YDL054c
6594	15790		3.41	1.3E-01	8923918	NT	Homo sapiens core histone macroH2A2.2 (MACROH2A2), mRNA
7227	16448		3.33	1.3E-01	BF330999.1	EST_HUMAN	MR4-BT0358-130700-010-H08 BT0358 Homo sapiens cDNA
7442	16650	26142	1.64	1.3E-01	H01883.1	EST_HUMAN	yf32d09.r1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:150449 5'
7681	16881	26363	1.67	1.3E-01	AF119117.1	NT	Homo sapiens dopamine transporter (SLC6A3) gene, complete cds
7803	16998		6.14	1.3E-01	6871745	NT	Mus musculus cofillin 2, muscle (C12), mRNA
8123	17257	26789	4.07	1.3E-01	BE279449.1	EST_HUMAN	601158052F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3504804 5'
8531	17557	23989	1.31	1.3E-01	BE018348.1	EST_HUMAN	601482741F1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3866003 5'
8678	17649		3.75	1.3E-01	AJ242780.1	NT	Gallus gallus scyc1 gene for lymphotactin, exons 1-3

Page 71 of 382  
Table 4  
Single Exon Probes Expressed in HELA Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9082	17891		2.08	1.3E-01	AB026828.1	NT	Ephratia fluvialis mRNA for sALK-6, complete cds
9090	17908		1.63	1.3E-01	AW001114.1	EST_HUMAN	wu24409.x1 Soares_Dieckgrafe_cdon_NHCD Homo sapiens cDNA clone IMAGE:2520977 3' similar to TR:O60287 O60287 KIAA0539 PROTEIN ;
388	9882	18819	10.48	1.2E-01	AI421744.1	EST_HUMAN	I93902.x1 NCI_CGAP_Brn23 Homo sapiens cDNA clone IMAGE:2088539 3' similar to gb:U05760_maf1
430	9296		1.32	1.2E-01	U66912.1	NT	ANNEXIN V (HUMAN);
554	9804		2.91	1.2E-01	AF039442.1	NT	Dictyostelium discoideum ORF DG1018 gene, partial cds
1383	10597	19763	2.4	1.2E-01	AU149146.1	EST_HUMAN	Homo sapiens colon cancer antigen NY-CO-45 mRNA, partial cds
1383	10597	19784	2.4	1.2E-01	AU149146.1	EST_HUMAN	AU149146 NT2RM4 Homo sapiens cDNA clone NT2RM4001691 3'
1380	10604		3.4	1.2E-01	AV735249.1	EST_HUMAN	AU149146 NT2RM4 Homo sapiens cDNA clone NT2RM4001691 3'
1608	10821	19897	5.44	1.2E-01	Q14934	SWISSPROT	AU735249 cda Homo sapiens cDNA clone cdaAAB11 5'
1628	10841	20018	2.84	1.2E-01	A1285402.1	EST_HUMAN	NUCLEAR FACTOR OF ACTIVATED T-CELLS, CYTOPLASMIC 4 (T CELL TRANSCRIPTION FACTOR NFAT3) (NF-ATC4) (NF-AT3)
1739	10951		20.58	1.2E-01	X89211.1	NT	q66908.x1 NCI_CGAP_Eso2 Homo sapiens cDNA clone IMAGE:1980553 3'
1886	11093		2.95	1.2E-01	AW449368.1	EST_HUMAN	H. sapiens DNA for endogenous retroviral like element
2148	11346	20563	2.6	1.2E-01	BF249490.1	EST_HUMAN	U1-H-B13-ak-e-10-Q-J1.s1 NCI_CGAP_Sub5 Homo sapiens cDNA clone IMAGE:2734554 3'
2551	11739	20850	1.17	1.2E-01	AW986558.1	EST_HUMAN	601821667F1 NIH_MGC_62 Homo sapiens cDNA clone IMAGE:4048224 5'
2795	12035	21159	1.4	1.2E-01	U18018.1	NT	QV3-BN0046-220300-12b-f10 BN0046 Homo sapiens cDNA
2854	12092	21222	2.39	1.2E-01	A1720470.1	EST_HUMAN	Human E1A enhancer binding protein (E1A-F) mRNA, partial cds
2885	12123	21256	3.54	1.2E-01	M16384.1	NT	as80c09.x1 Barstead cdon HPLRB7 Homo sapiens cDNA clone IMAGE:2335024 3' similar to gb:U05095
2884	12202	21337	0.81	1.2E-01	X56882.1	NT	60S RIBOSOMAL PROTEIN L30 (HUMAN);
3198	12431	21567	2.17	1.2E-01	AW370668.1	EST_HUMAN	Human creatine kinase-B mRNA, complete cds
3224	12458		1.01	1.2E-01	U67600.1	NT	Wheat mRNA for a group 3 late embryogenesis abundant protein (LEA)
3329	12558	21696	1.01	1.2E-01	AW503374.1	EST_HUMAN	QV1-BT0259-281099-021-d05 BT0259 Homo sapiens cDNA
3454	12678		0.71	1.2E-01	Z99118.1	NT	Methanococcus jannaschii section 142 of 150 of the complete genome
3494	12718	21854	0.8	1.2E-01	X56882.1	NT	U1-HF-BN0-akw-e-10-Q-J1.r1 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3078427 5'
3494	12718	21855	0.8	1.2E-01	X56882.1	NT	Bacillus subtilis complete genome (section 15 of 21): from 2785131 to 3013540
3584	12879		0.76	1.2E-01	Z99118.1	NT	Wheat mRNA for a group 3 late embryogenesis abundant protein (LEA)
4163	13367	22465	2.35	1.2E-01	Z54255.1	NT	Wheat mRNA for a group 3 late embryogenesis abundant protein (LEA)
4163	13367	22466	2.35	1.2E-01	Z54255.1	NT	Bacillus subtilis complete genome (section 15 of 21): from 2785131 to 3013540
4300	13501	22597	0.81	1.2E-01	M15861.1	NT	Wheat mRNA for a group 3 late embryogenesis abundant protein (LEA)
4943	14130	23225	15.91	1.2E-01	AF134904.1	NT	Bacillus subtilis complete genome (section 15 of 21): from 2785131 to 3013540
5078	14258	23342	2.21	1.2E-01	BE173168.1	EST_HUMAN	P. clarkei mRNA; repeat region (ID 2MR17)
							P. clarkei mRNA; repeat region (ID 2MR17)
							Chicken neural cell-adhesion molecule (N-CAM) gene, exon 19
							Schistosoma gregaria samphorin 2a mRNA, complete cds
							MR0-HT0559-240400-018-c09 HT0559 Homo sapiens cDNA

Page 72 of 382  
Table 4  
Single Exon Probes Expressed in HELA Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLASTE Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5078	14258	23343	2.21	1.2E-01	BE173186.1	EST_HUMAN	MRO-HT0559-240400-016-c09 HT0559 Homo sapiens cDNA
5284	14455	23524	0.73	1.2E-01	AW892592.1	EST_HUMAN	CM3-NN0004-100300-111-d08 NN0004 Homo sapiens cDNA
5337	14568	23842	2.63	1.2E-01	W33035.1	EST_HUMAN	zc08d02.r1 Soares parathyroid tumor NBHPA Homo sapiens cDNA clone IMAGE:321689 5'
5380	14609	23721	3.16	1.2E-01	Z88266.1	NT	Homo sapiens gene encoding plakophilin (exons 1-13)
5753	14972	24370	2.02	1.2E-01	BE620945.1	EST_HUMAN	601483518F1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3895613 5'
5788	15005	24409	2.3	1.2E-01	AW845275.1	EST_HUMAN	ILO-CT0031-Z21099-113-e04 CT0031 Homo sapiens cDNA
8446	15843	25110	4.78	1.2E-01	AI913753.1	EST_HUMAN	ws89g03.x1 NCI_CGAP_Co3 Homo sapiens cDNA clone IMAGE:2326804 3' similar to SW:GST2_HUMAN
6569	16795		4.99	1.2E-01	AW083852.1	EST_HUMAN	Q88735 MICROSOMAL GLUTATHIONE S-TRANSFERASE II; (HUMAN);
6606	15802		3.94	1.2E-01	AF053772.1	NT	Staphylococcus aureus plasmid pSK23 putative recombinase Sin (sin) gene, partial cds; and transcriptional regulator QacR (qacR) and multidrug efflux protein QacB (qacB) genes, complete cds
6877	15872		2.87	1.2E-01	U32714.1	NT	Haemophilus influenzae Rd section 29 of 163 of the complete genome
6948	16108	25573	4.01	1.2E-01	X77961.1	NT	S.cerevisiae HXT5 gene
7075	16252	25725	2.29	1.2E-01	AV710857.1	EST_HUMAN	AV710857 Cu Homo sapiens cDNA clone CUAKE08 5'
7463	16871		3.61	1.2E-01	D26184.1	NT	Yeast MPT5 gene for suppressor protein, complete cds
7633	16834		3.84	1.2E-01	BE962324.2	EST_HUMAN	601655578R1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3846283 3'
7707	16906		1.79	1.2E-01	BF314481.1	EST_HUMAN	601900763F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4130103 5'
8041	17177		1.98	1.2E-01	AF180463.1	NT	Homo sapiens dynein intermediate chain DNAI1 (DNAI1) gene, exon 17
8283	17405	26512	2.62	1.2E-01	AF180463.1	EST_HUMAN	Rabbit glycogen-associated protein phosphatase regulatory subunit (RG1) mRNA, complete cds
8659	17636		2.36	1.2E-01	AJ271736.1	NT	AV658033 GLC Homo sapiens cDNA clone GLCFIB12.3
8741	18317	23594	3.89	1.2E-01	QD4912	SWISSPROT	Homo sapiens Xq pseudautosomal region; segment 2/2 MACROPHAGE-STIMULATING PROTEIN RECEPTOR PRECURSOR (MSP RECEPTOR) (P185-RON) (CDW 139) (CD138 ANTIGEN)
8853	17758		1.79	1.2E-01	AF188892.1	NT	Drosophila melanogaster strain Oregon R potential RNA-binding protein gene, complete cds; and syntactin gene, partial cds
8855	9804		8.49	1.2E-01	AF039442.1	NT	Homo sapiens colon cancer antigen NY-CO-45 mRNA, partial cds
8969	17839		2.13	1.2E-01	X53981.1	NT	R.novglicus NF68 gene for 68kDa neurofilament
9043	18328	23601	1.55	1.2E-01	BE061418.1	EST_HUMAN	QV4-B10234-111199-031-g10 B10234 Homo sapiens cDNA
9086	17893	23900	8.08	1.2E-01	A1299903.1	EST_HUMAN	q120g05.x1 NCI_CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1898840 3'
9088	17907		2.44	1.2E-01	L10187.1	NT	Xenopus laevis integrin alpha 3 subunit mRNA, partial cds
9092	18249		5.45	1.2E-01	O96433	SWISSPROT	CYCLIN T
9120	17936	23878	1.47	1.2E-01	AE004428.1	NT	Vibrio cholerae chromosome II, section 85 of 93 of the complete chromosome

Page 73 of 382  
Table 4  
Single Exon Probes Expressed in HELA Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9274	18038		1.35	1.2E-01	BF314481.1	EST_HUMAN	601900763F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4130103 5'
571	9821	18942	1.05	1.1E-01	A1591003.1	EST_HUMAN	Int16d08.x1 NCI_CGAP_Bm25 Homo sapiens cDNA clone IMAGE:2167983 3'
621	9886	18987	2.28	1.1E-01	AA569008.1	EST_HUMAN	nm08g11.st NCI_CGAP_Co10 Homo sapiens cDNA clone IMAGE:1059620 3' similar to gb:X06985_rna1
1061	10287	18438	1.48	1.1E-01	BF697308.1	EST_HUMAN	HEME OXYGENASE 1 (HUMAN);
1083	10317		1.63	1.1E-01	AL161550.2	NT	602128847F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4286771 5'
1167	11687	19540	3.89	1.1E-01	AW972158.1	EST_HUMAN	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 60
1256	10472	18635	3.8	1.1E-01	D64004.1	NT	Synechocystis sp. PCC6803 complete genome, 23/27, 2868767-3002865
1508	10721	18863	2.15	1.1E-01	AU140363.1	EST_HUMAN	AU140363 PLACE2 Homo sapiens cDNA clone IMAGE:2000403 5'
2280	11475		2.2	1.1E-01	6755215	NT	Mus musculus pre T-cell antigen receptor alpha (Pitca), mRNA
2503	11953		1.9	1.1E-01	6978676	NT	Rattus norvegicus Procollagen II alpha 1 (Col2a1), mRNA
2807	12047	21168	1.04	1.1E-01	S82418.1	NT	Interleukin-12 p35 subunit [mouse, Genomic, 700 nt, segment 4 of 5]
2898	12235	21365	0.81	1.1E-01	F03265.1	EST_HUMAN	HSC1RF022 normalized infant brain cDNA Homo sapiens cDNA clone c-1rf02 3'
3315	12545		1.78	1.1E-01	6763231	NT	Mus musculus calcium channel, voltage-dependent, I type, alpha 1G subunit (Ca <sub>v</sub> 1a1g), mRNA
3398	12626	21757	2.28	1.1E-01	BE393186.1	EST_HUMAN	601308879F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3627066 5'
3428	12854	21784	1.56	1.1E-01	X62135.1	NT	C. reinhardtii nuclear gene on linkage group XIX
3486	12691	21828	0.7	1.1E-01	R96946.1	EST_HUMAN	Y662g08.s1 Soares fetal liver spleen 1NPLS Homo sapiens cDNA clone IMAGE:200414 3' similar to contains Alu repetitive element
3559	12782	21911	0.94	1.1E-01	Y07685.1	NT	A. Imnerus gene for transposase
3681	12802		0.78	1.1E-01	P97394	SWISSPROT	ANNEXIN XI (CALCYCLIN-ASSOCIATED ANNEXIN 50) (CAP-50)
3689	12910	22028	1.91	1.1E-01	X52708.1	NT	G.gallus gene encoding non-histone chromosomal protein HMG-14b, exons 4 and 5
4088	13297	22393	1.04	1.1E-01	AW818412.1	EST_HUMAN	MR3-ST0290-290100-025-g07 ST0290 Homo sapiens cDNA
4098	13297	22394	1.04	1.1E-01	AW818412.1	EST_HUMAN	MR3-ST0290-290100-025-g07 ST0290 Homo sapiens cDNA
4095	13303		0.68	1.1E-01	AF030001.1	NT	Mus musculus major histocompatibility locus class III region: butyrophilin-like protein gene, partial cds; Notch4, PBX2, RAGE, lysophosphatidic acid acyl transferase-alpha, palmitoyl-protein thioesterase 2 (PPT2), CREB-RP, and tenascin X (TNX) genes, complete
4240	13443		10.22	1.1E-01	AF157066.1	NT	Drosophila melanogaster klarsicht protein (klar) mRNA, complete cds
4272	13475	22572	0.63	1.1E-01	AW802056.1	EST_HUMAN	IL5-UM0070-020500-068-a08 UM0070 Homo sapiens cDNA
4641	13835	22824	1.09	1.1E-01	S44957.1	NT	Tape-1-integral membrane protein TAPA-1 [mouse, B cell lymphoma line 38C13, Genomic, 1973 nt, segment 1 of 7]
4848	14038	23131	1.24	1.1E-01	Y07695.1	NT	A. Imnerus gene for transposase
5045	13303		0.87	1.1E-01	AF030001.1	NT	Mus musculus major histocompatibility locus class III region: butyrophilin-like protein gene, partial cds; Notch4, PBX2, RAGE, lysophosphatidic acid acyl transferase-alpha, palmitoyl-protein thioesterase 2 (PPT2), CREB-RP, and tenascin X (TNX) genes, complete

Page 74 of 382  
Table 4  
Single Exon Probes Expressed in HELA Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5224	14398		0.62	1.1E-01	8923317	NT	Homo sapiens hypothetical protein FLJ20342 (FLJ20342), mRNA
5586	14810	24184	1.79	1.1E-01	X68851.1	NT	S.pombe ste8 gene encoding protein kinase
5601	14825	24201	4.71	1.1E-01	M86533.1	NT	Providencia rettgeri penicillin G amidase gene
5688	14908	24289	1.72	1.1E-01	BE769152.1	EST_HUMAN	PM3-FT0024-130600-004-f12 FT0024 Homo sapiens cDNA
5696	14816	24310	7.89	1.1E-01	AW653699.1	EST_HUMAN	RC3-CT0254-280999-011-a01 CT0254 Homo sapiens cDNA
5937	15153	24564	3.68	1.1E-01	O69635	SWISSPROT	ACETYL-COENZYME A SYNTHETASE (ACETATE-COA LIGASE) (ACYL-ACTIVATING ENZYME)
5966	15181		2.67	1.1E-01	AF032922.1	NT	Homo sapiens syntaxin 4 binding protein UNC-18c (UNC-18c) mRNA, complete cds
5985	15278	24708	2.49	1.1E-01	11432372	NT	Homo sapiens phosphatidylinositol glycan, class B (PIGB), mRNA
6305	15486	24930	7.65	1.1E-01	BF684628.1	EST_HUMAN	602140976F1 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4302019 5'
6305	15486	24931	7.65	1.1E-01	BF684628.1	EST_HUMAN	602140976F1 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4302019 5'
6361	15541	24996	1.77	1.1E-01	P41067	SWISSPROT	TRAB PROTEIN
6375	15555	25012	2.92	1.1E-01	AA788784.1	EST_HUMAN	eh31b06.s1 Soares parathyroid tumor NbHPA Homo sapiens cDNA clone 1240403 3' similar to gb:J03483
6581	15777	25237	3.04	1.1E-01	AL134349.1	EST_HUMAN	CHROMOGRANIN A PRECURSOR (HUMAN);
6780	15975	25432	3.04	1.1E-01	AA192153.1	EST_HUMAN	DKFZp547P194_r1 547 (synonym: hbr1) Homo sapiens cDNA clone DKFZp547P194 5'
6780	15975	25433	3.04	1.1E-01	AA192153.1	EST_HUMAN	z963b12.r1 Stratagene muscle 937209 Homo sapiens cDNA clone IMAGE:627743 5'
6821	16015	25480	4.16	1.1E-01	T72675.1	EST_HUMAN	z963b12.r1 Stratagene muscle 937209 Homo sapiens cDNA clone IMAGE:627743 5'
6910	16088		3.01	1.1E-01	BF085149.1	EST_HUMAN	y418h03.s1 Soares fetal liver spleen 1NPLS Homo sapiens cDNA clone IMAGE:108725 3' similar to gb:M81181 SODIUMPOTASSIUM-TRANSPORTING ATPASE BETA-2 (HUMAN);
7383	12235	21365	2.34	1.1E-01	F03265.1	EST_HUMAN	MR2-GN0027-040900-005-a08 GN0027 Homo sapiens cDNA
7496	16703		3.49	1.1E-01	AF169032.1	NT	HSC1RF022 normalized infant brain cDNA Homo sapiens cDNA clone c-1rf02 3'
7614	16817	26313	3.37	1.1E-01	R23708.1	EST_HUMAN	Caressius auratus activin beta A precursor, mRNA, complete cds
7620	16823	26319	1.98	1.1E-01	6981351	NT	yh36f12.r1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:131759 5' similar to contains Alu repetitive element; contains TAR1 repetitive element
7636	14788	24157	1.96	1.1E-01	AL110985.1	NT	Rattus norvegicus Phosphofructokinase, liver, B-type (PFK), mRNA
7736	16933	26441	1.93	1.1E-01	X70058.1	NT	Botrytis cinerea strain T4 cDNA library under conditions of nitrogen deprivation
7760	16956	26464	3.14	1.1E-01	Z11910.1	NT	M.musculus cytokine gene
7760	16956	26465	3.14	1.1E-01	Z11910.1	NT	Z.mobilis tgf and lig genes encoding RNA guanine transglycosylase and DNA ligase
7854	17044	26561	3.45	1.1E-01	P17437	SWISSPROT	Z.mobilis tgf and lig genes encoding RNA guanine transglycosylase and DNA ligase
8511	17547		2.88	1.1E-01	BE767023.1	EST_HUMAN	SKIN SECRETORY PROTEIN XP2 PRECURSOR (APEG PROTEIN)
8772	18117		2.2	1.1E-01	BE974556.1	EST_HUMAN	RC2-NT0112-120600-014-f03 NT0112 Homo sapiens cDNA
9212	17893	23865	5.88	1.1E-01	BF238753.1	EST_HUMAN	RC2-NT0112-120600-014-f03 NT0112 Homo sapiens cDNA
9283	18297		1.42	1.1E-01	Y081172.1	NT	601880551R2 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:3950604 3'
1208	10428		2.84	1.0E-01	O62855	SWISSPROT	601880550F1 NIH_MGC_54 Homo sapiens cDNA clone IMAGE:4134085 5'
							R.norvegicus mRNA for 2-arylpropionyl-CoA epimerase
							DEOXYRIBONUCLEASE II PRECURSOR (DNASE II) (ACID DNASE) (LYSOSOMAL DNASE II)

**Table 4**  
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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1279	10494	19653	1.97	1.0E-01	AI985499.1	EST_HUMAN	ws08d01.x1 NCI_GOAP_Kid11 Homo sapiens cDNA clone IMAGE:2496577 3' similar to contains MER7.13
1398	10610	19774	1.78	1.0E-01	AL161504.2	NT	MER7 repetitive element ;
3487	12711	21847	1.08	1.0E-01	BF033981.1	EST_HUMAN	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 16
3700	12820	22038	1.03	1.0E-01	BF239818.1	EST_HUMAN	601456301F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3859849 5'
3930	13148	22263	2.78	1.0E-01	BF365703.1	EST_HUMAN	601906489F1 NIH_MGC_54 Homo sapiens cDNA clone IMAGE:4134071 5'
4401	13601	22701	1.98	1.0E-01	AF002265.2	NT	QV2-NT0048-160800-316-e05 NT0048 Homo sapiens cDNA
4552	13747		0.99	1.0E-01	AI792349.1	EST_HUMAN	Chlamydia pneumoniae AR39, section 91 of 94 of the complete genome
4723	13914	23015	1.51	1.0E-01	U50450.1	NT	an32c04.y5 Gessler Wilms tumor Homo sapiens cDNA clone IMAGE:1700358 5'
4942	14129	23224	2.15	1.0E-01	AW952344.1	EST_HUMAN	Drosophila melanogaster tyrosine kinase p45 isoform (fer) mRNA, complete cds
5181	14357	23443	0.86	1.0E-01	BE389100.1	EST_HUMAN	EST384414 MAGE resequencs, MAGB Homo sapiens cDNA
5265	14438		0.93	1.0E-01	AV763960.1	EST_HUMAN	601286969F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3613552 5'
5345	14575		9.19	1.0E-01	W96490.1	EST_HUMAN	AV763960 MDS Homo sapiens cDNA clone MDSQB11 5'
5670	14891	24283	11.98	1.0E-01	AF274875.1	NT	zh62h04.s1 Soares fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:416895 3'
							Homo sapiens growth factor receptor-bound protein 7 (GRB7) gene, complete cds
							yh34h06.r1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:131675 5' similar to contains Alu
6095	15295		1.97	1.0E-01	R23821.1	EST_HUMAN	repetitive element;
6391	15571		2.51	1.0E-01	Y12488.1	NT	M.musculus wtn gene
6913	18101		2.59	1.0E-01	M76728.1	NT	Human pro-alpha-1 (V) collagen mRNA, complete cds
7050	16227	25702	12.87	1.0E-01	AB046799.1	NT	Homo sapiens mRNA for KIAA1579 protein, partial cds
7050	16227	25703	12.87	1.0E-01	AB046799.1	NT	Homo sapiens mRNA for KIAA1579 protein, partial cds
7261	16471		2.48	1.0E-01	AU159127.1	EST_HUMAN	AU159127 THYR01 Homo sapiens cDNA clone THYR01000895 3'
7600	16803	28287	3.47	1.0E-01	BF242946.1	EST_HUMAN	601877703F1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:4106089 5'
7600	16803	28298	3.47	1.0E-01	BF242946.1	EST_HUMAN	601877703F1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:4106089 5'
7638	17078	26606	4.68	1.0E-01	BE790543.1	EST_HUMAN	601582558F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3938734 5'
8497	17697		3.22	1.0E-01	BE537719.1	EST_HUMAN	601065554F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3451833 5'
8736	17682		2.74	1.0E-01	7662165	NT	Homo sapiens KIAA0514 gene product (KIAA0514), mRNA
8752	17695		1.76	1.0E-01	X00854.1	NT	Drosophila melanogaster ftz gene
9039	18308		2.64	1.0E-01	U52691.1	NT	Gonyaulax polyedra putative type-1 serine/threonine phosphatase (PP1) mRNA, complete cds
9070	17897		2.48	1.0E-01	BE537719.1	EST_HUMAN	601065554F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3451833 5'
9132	18280		12.74	1.0E-01	U68834.1	NT	Saccharomyces cerevisiae suppressor of ABF1 (SAB2) gene, complete cds
9194	17981		8.43	1.0E-01	AF001507.1	NT	Bacillus halodurans genomic DNA, section 1/14
							Drosophila melanogaster cAMP-dependent protein kinase type II regulatory subunit (pke-RII) mRNA, complete cds
2733	11912	21125	0.96	9.8E-02	AF274008.1	NT	
2740	14910	21433	1.16	9.8E-02	BE545554.1	EST_HUMAN	601070219F1 NIH_MGC_12 Homo sapiens cDNA clone IMAGE:3456365 5'



Table 4  
Single Exon Probes Expressed in HELA Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2740	11919	21134	1.16	9.9E-02	BE545554.1	EST_HUMAN	601070219F1 NIH_MGC_12 Homo sapiens cDNA clone IMAGE:3456385 5'
3233	12487	21588	1.43	9.9E-02	AF098810.1	NT	Homo sapiens neurodin II-alpha gene, partial cds
3928	13144	22261	0.79	9.8E-02	AIB21837.1	EST_HUMAN	zu45c03.x5 Soares ovary tumor NBH07 Homo sapiens cDNA clone IMAGE:740932 3'
6074	14520	23563	8.08	9.8E-02	D83710.1	NT	Aspergillus terreus BSD mRNA for blasticidin S deaminase, complete cds
6840	16045	25510	2.52	9.9E-02	6755111	NT	Mus musculus phospholipid transfer protein (Pltp), mRNA
570	9820		1.04	9.8E-02	X56338.1	NT	O sativa RAm3C gene for alpha-amylase
3110	12345	21472	3.7	9.8E-02	AF184274.1	NT	Daucus carota leucoanthocyanidin dioxygenase 2 (LDOX) mRNA, LDOX-2 allele, complete cds
4209	13412	22508	8.37	9.8E-02	AF257329.1	NT	Leptospira maculans beta-tubulin mRNA, complete cds
4208	13412	22507	8.37	9.8E-02	AF257328.1	NT	Leptospira maculans beta-tubulin mRNA, complete cds
7895	16430	25917	2.22	9.8E-02	BF037421.1	EST_HUMAN	601460793F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3884287 5'
8460	17516		1.34	9.8E-02	6393751	NT	Rattus norvegicus microtubule-associated protein tau (Mapt), mRNA
1358	10573	19739	1.29	9.7E-02	AB005808.1	NT	Aloe arborescens mRNA for NADP-malic enzyme, complete cds
1565	10778		3.75	9.7E-02	4503710	NT	Homo sapiens fibroblast growth factor receptor 3 (echondroplasia, thanatophoric dwarfism) (FGFR3) mRNA
2226	11422	20648	1.89	9.7E-02	BE168680.1	EST_HUMAN	QV1-HT0516-070300-095-a04 HT0516 Homo sapiens cDNA
3961	13176		4.12	9.7E-02	Q99795	SWISSPROT	CELL SURFACE A33 ANTIGEN PRECURSOR (GLYCOPROTEIN A33)
6206	15387	24830	2.95	9.7E-02	Z99119.1	NT	Bacillus subtilis complete genome (section 16 of 21): from 2897771 to 3213410
6732	15927	25398	2.42	9.7E-02	AIB53984.1	EST_HUMAN	wx78b06.x1 NCL CGAP_Ov38 Homo sapiens cDNA clone IMAGE:2549747 3' similar to gb:X52851_ma1
7751	16947		2.37	9.7E-02	U58337.1	NT	PEPTIDYL-PROLYL CIS-TRANS ISOMERASE A (HUMAN);
1983	11186	20395	3.52	9.6E-02	A080721.1	EST_HUMAN	Mus musculus ligandin (Lgb) mRNA, partial cds
1983	11186	20396	3.52	9.6E-02	A080721.1	EST_HUMAN	alpha47d11.x1 Soares NIHMPu_S1 Homo sapiens cDNA clone IMAGE:1678485 3'
4338	13539	22630	7.92	9.6E-02	Z32688.2	NT	alpha47d11.x1 Soares NIHMPu_S1 Homo sapiens cDNA clone IMAGE:1678485 3'
4695	13896	22687	0.98	9.6E-02	U37056.1	NT	Proteus mirabilis fibrinolytic operon, strain HI4320
5025	14211	23284	0.99	9.6E-02	AW968230.1	EST_HUMAN	Glostridium cellulovorans endo-1,4-beta-glucanase EngF (engF) gene, complete cds
5710	14928		3.07	9.6E-02	BE910039.1	EST_HUMAN	EST1378303 MAGE resequences, MAGI Homo sapiens cDNA
7153	16330	25813	4.32	9.6E-02	P08174	SWISSPROT	601480088F1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3900165 5'
7328	16544	26033	7.1	9.6E-02	Z79702.1	NT	COMPLEMENT DECAY-ACCELERATING FACTOR PRECURSOR (CD55)
8210	17341	26880	1.89	9.6E-02	AA625755.1	EST_HUMAN	Mycobacterium tuberculosis H37Rv complete genome, segment 102/162
9108	17928		1.56	9.6E-02	H14599.1	EST_HUMAN	zu91g01.x1 Soares testis_NHT Homo sapiens cDNA clone IMAGE:745392 3'
4079	13288	22388	2.65	9.5E-02	AW962395.1	EST_HUMAN	ym19n03.s1 Soares infant brain 1N1B Homo sapiens cDNA clone IMAGE:48653 3'
6208	15389	24833	4.86	9.5E-02	AB003473.1	NT	CM2-BN0023-050200-087-112 BN0023 Homo sapiens cDNA
6321	15503	24949	8.19	9.5E-02	AL161538.2	NT	Trimeresurus flavoviridis DNA for phospholipase A2 inhibitor, complete cds
6420	15617	25080	4.43	9.5E-02	BF035861.1	EST_HUMAN	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 38
							601453842F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3857243 5'

Table 4

## Single Exon Probes Expressed in HELA Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6420	15617	25081	4.43	9.5E-02	BF035861.1	EST_HUMAN	601453942F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3857243 5'
7271	16490	25980	4.04	9.6E-02	BF035861.1	EST_HUMAN	601453942F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3857243 5'
7271	16490	25981	4.04	9.5E-02	BF035861.1	EST_HUMAN	601453942F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3857243 5'
1801	11010	20202	3.64	9.4E-02	BF671063.1	EST_HUMAN	602150882F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4291917 5'
3861	13077	22193	5.59	9.4E-02	Z33059.1	NT	M. capricornus DNA for CONTIG MC073
5081	14261	23346	0.7	9.4E-02	6753517	NT	Mus musculus coding region determinant-binding protein (Ordbp), mRNA
6855	15850		2.23	9.4E-02	Z46883.1	NT	Acinetobacter sp. cysD, cobQ, sodM, lvsS, rubA, rubB, estB, oxyR, ppk, mtgA, ORF2 and ORF3 genes
7507	15511	24857	2.62	9.4E-02	L78833.1	NT	Human BRCA1, Rho7 and vail genes, complete cds, and ipf35 gene, partial cds
8345	18213		3.65	9.4E-02	U31815.1	NT	Rattus norvegicus calcium channel alpha-1C subunit (ROB2) mRNA, partial cds
2946	12184		2.07	9.3E-02	4808280	NT	Homo sapiens BAI1-associated protein 3 (BAIAP3) mRNA
2994	12231		8.36	9.3E-02	6912525	NT	Homo sapiens nasopharyngeal epithelium specific protein 1 (NESG1), mRNA
3223	12457	21591	1.95	9.3E-02	BF575511.1	EST_HUMAN	602133086F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4288269 5'
4134	13340	22439	4.02	9.3E-02	BE391943.1	EST_HUMAN	601286082F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3607653 5'
4134	13340	22440	4.02	9.3E-02	BE391943.1	EST_HUMAN	601286082F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3607653 5'
4746	13937		2.16	9.3E-02	AV732224.1	EST_HUMAN	AV732224 HTF Homo sapiens cDNA clone HTFAUA08 5'
5036	14221	23305	1	9.3E-02	AF115443.1	NT	HIV-1 isolate Br112 from Brazil gag protein (gag) gene, partial cds
5239	14413	23492	0.67	9.3E-02	D16583.1	NT	Human gene for L-histidine decarboxylase, complete cds
5239	14413	23493	0.67	9.3E-02	D16583.1	NT	Human gene for L-histidine decarboxylase, complete cds
7131	16308	25788	4.97	9.3E-02	Q15034	SWISSPROT	HYPOTHETICAL PROTEIN KIAA0032
7131	16308	25789	4.97	9.3E-02	Q15034	SWISSPROT	HYPOTHETICAL PROTEIN KIAA0032
7174	16351		4.06	9.3E-02	AW206117.1	EST_HUMAN	UI-H-B11-afk-t-05-0-UJ.s1 NCI_CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2723553 3'
8619	18137		2.93	9.3E-02	AJ248850.1	NT	Photobacterium damsela subsp. damsela partial gyrB gene for DNA gyrase B subunit
9003	18166		13.31	9.3E-02	AW488850.1	EST_HUMAN	hd28h12.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2910887 3'
9216	18212		1.48	9.3E-02	AF100956.1	NT	Mus musculus major histocompatibility locus class II region; Fas-binding protein Daxx (DAXX) gene, partial cds; Bing1 (BING1), tapasin (tapasin), RalGDS-like factor (RLF), KE2 (KE2), BING4 (BING4), beta1, 3-galactosyl transferase (beta1, 3-galactosyl tr>
234	9513	18639	8.2	9.2E-02	U60315.1	NT	Molluscum contagiosum virus subtype 1, complete genome
234	9513	18640	8.2	9.2E-02	U60315.1	NT	Molluscum contagiosum virus subtype 1, complete genome
234	9513	18641	8.2	9.2E-02	U60315.1	NT	Molluscum contagiosum virus subtype 1, complete genome
2194	11391		1.48	9.2E-02	R54156.1	EST_HUMAN	y98807.r1 Soares infant brain 1N1B Homo sapiens cDNA clone IMAGE:41618 5'
3144	12379	21510	3.99	9.2E-02	Q28631	SWISSPROT	MAJOR EPIDIDYMIS-SPECIFIC PROTEIN E4 (EPIDIDYMAL PROTEIN BE-20)
3276	12509	21639	0.68	9.2E-02	AA634354.1	EST_HUMAN	n179401.s1 NCI_CGAP_Co3 Homo sapiens cDNA clone IMAGE:928136 3'
3563	12786		1.46	9.2E-02	6755215	NT	Mus musculus pre T-cell antigen receptor alpha (Ptra), mRNA

Page 78 of 382  
Table 4

## Single Exon Probes Expressed in HELA Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4223	13426		1.12	9.2E-02	U92048.1	NT	Human herpesvirus 1 strain KOS-63, latency-associated transcript, promoter region
4285	13498		0.74	9.2E-02	BE286722.1	EST_HUMAN	600944385F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:2860178 5'
4840	13834	22823	1.21	9.2E-02	X98402.1	NT	G.gallus Mia-CK gene
6518	15714	25179	2.57	9.2E-02	X85256.1	NT	H. vulgare xylose isomerase gene
428	9284	18397	2.98	9.1E-02	X77685.1	NT	O. cuniculus k12 keratin gene
2378	11571	20791	1.02	9.1E-02	P78985	SWISSPROT	8-PHOSPHOFRUCTOKINASE (PHOSPHOFRUCTOKINASE) (PHOSPHOHEXOKINASE)
4481	13679	22769	1.85	9.1E-02	AL161554.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 54
6251	15432	24871	13.12	9.1E-02	AW160658.1	EST_HUMAN	zp38n12.s1 StrataGene muscle 837209 Homo sapiens cDNA clone IMAGE:611783 3' similar to au74a05.y1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2781988 5'
8528	18315		1.51	9.1E-02	AA178901.1	EST_HUMAN	SW:TRT3_HUMAN P45378 TROPONIN T, FAST SKELETAL MUSCLE, ISOFORM BETA ;
8907	17605		1.53	9.1E-02	AF052695.1	NT	Rattus norvegicus cell cycle protein p55CDC gene, complete cds
9081	18159		6.56	9.1E-02	AJ291390.1	NT	Homo sapiens partial MUC3B gene for MUC3B mucin, exons 1-11
752	9993	19137	3.57	9.0E-02	P15328	SWISSPROT	FOLATE RECEPTOR ALPHA PRECURSOR (FR-ALPHA) (FOLATE RECEPTOR 1) (FOLATE RECEPTOR, ADULT) (ADULT FOLATE-BINDING PROTEIN) (FBP) (OVARIAN TUMOR-ASSOCIATED ANTIGEN MOV18) (KB CELLS FBP)
1611	10824	18999	6.83	9.0E-02	BE220482.1	EST_HUMAN	hV39g10.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3175842 3' similar to contains Alu repetitive element;
2755	11634	21150	3.82	9.0E-02	AF138522.1	NT	HIV-1 p8c095-06 from USA envelope glycoprotein (env) gene, partial cds
2755	11634	21151	3.82	9.0E-02	AF138522.1	NT	HIV-1 p8c095-06 from USA envelope glycoprotein (env) gene, partial cds
3310	12540	21675	0.75	9.0E-02	AF279135.1	NT	Dictyostellium discoideum spore coat structural protein SP65 (cotE) gene, complete cds
4671	13865	22066	1.88	9.0E-02	X65740.2	NT	Plasmodium falciparum P-type ATPase 3 gene
5236	14410		0.98	9.0E-02	AJ132386.1	NT	Helicobacter pylori (strain P1) comB and pilA1gA (partial) genes, and partial ORF1 and ORF2
5652	14875	24262	12.37	9.0E-02	W56037.1	EST_HUMAN	zaf8a12.r1 Soares fetal lung_NbHL19W Homo sapiens cDNA clone IMAGE:287684 5' similar to PIR:S52171 S52171 small G protein - human ;
8928	17811		1.35	9.0E-02	AF022236.1	NT	Escherichia coli strain E2348/89 pathogenicity island, rOrf1 (rOrf1), rOrf2 (rOrf2), EscR (escR), EscS (escS), EscT (escT), EscU (escU), CsaD (cscD), EscC (escC), EscJ (escJ), SepZ (sepZ), EscV (escV), EscN (escN), SepQ (sepQ), Tir (tir), OrfU (orfU), >
1439	10653	19826	1.23	8.9E-02	BF071593.1	EST_HUMAN	602128030F2 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4285951 5'
1439	10653	19827	1.23	8.9E-02	BF071593.1	EST_HUMAN	602128030F2 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4285951 5'
4181	13385		1.76	8.9E-02	AF280655.1	NT	Atrichum angustatum AtranFla2 protein (AtranFla2) gene, partial cds
5234	14408		0.95	8.9E-02	AB025922.1	NT	Mus musculus GII1 mRNA, complete cds
5593	14817	24192	2.61	8.9E-02	AW452122.1	EST_HUMAN	UI-H-BI3-alo-408-0-UI.s1 NCI_CGAP_Sub5 Homo sapiens cDNA clone IMAGE:3068284 3'
5593	14817	24193	2.61	8.9E-02	AW452122.1	EST_HUMAN	UI-H-BI3-alo-408-0-UI.s1 NCI_CGAP_Sub5 Homo sapiens cDNA clone IMAGE:3068284 3'
5598	14822	24199	3.12	8.9E-02	11433478	NT	Homo sapiens similar to endoglycan (H. sapiens) (LOC883107), mRNA

Page 79 of 382  
Table 4  
Single Exon Probes Expressed in HELA Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6316	15496		2	8.8E-02	Z79021.1	NT	H. sapiens flow-sorted chromosome 6 HindIII fragment, SC6pA20F8
6854	15849	26308	7.54	8.9E-02	AA309319.1	EST_HUMAN	EST180187 Liver, hepatocellular carcinoma Homo sapiens cDNA 5' end
8344	18164		1.33	8.8E-02	P19524	SWISSPROT	MYOSIN-2 ISOFORM
8498	17540		4.1	8.8E-02	BF698918.1	EST_HUMAN	602128682F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:4286180 5'
1380	10584	19760	1.39	8.8E-02	Q27474	SWISSPROT	PROBABLE DNA LIGASE (POLYDEOXYRIBONUCLEOTIDE SYNTHASE [ATP])
4012	13224		4.05	8.8E-02	O00288	SWISSPROT	TRANSCRIPTION INITIATION FACTOR TF1D 135 KDA SUBUNIT (TAFII135) (TAFII130)
4224	13427		1.03	8.8E-02	4502804	NT	Homo sapiens chromogranin A (parathyroid secretory protein 1) (CHGA) mRNA
4288	13490		0.65	8.8E-02	4580423	NT	Homo sapiens paired box gene 6 (aniridia, keratitis) (PAX6), isoform b, mRNA
7678	16877	26382	3.02	8.8E-02	BE284455.1	EST_HUMAN	601191770F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3535648 5'
7678	16877	26383	3.02	8.8E-02	BE284455.1	EST_HUMAN	601191770F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3535648 5'
7813	17008	26519	11.51	8.8E-02	AL040129.1	EST_HUMAN	DKFZp434D1313_r1 434 (synonym: hies3) Homo sapiens cDNA clone DKFZp434D1313 5'
8577	17583	24001	1.56	8.8E-02	Z71561.1	NT	S. cerevisiae chromosome XIV, reading frame ORF YNL285w
1624	10837	20014	2.52	8.7E-02	A1167281.1	EST_HUMAN	aa65b01.s1 Soares_NHMPu_S1 Homo sapiens cDNA clone IMAGE:1681161 3'
3872	12893	22014	5.01	8.7E-02	U82895.2	NT	Homo sapiens zinc finger protein 92 (ZFP92), expressed-Xq28STS protein (XQ28ORF), and biglycan (BGN) genes, complete cds; and plasma membrane calcium ATPase isoform 3 (PMCA3) gene, partial cds
3872	12893	22015	5.01	8.7E-02	U82895.2	NT	Homo sapiens zinc finger protein 92 (ZFP92), expressed-Xq28STS protein (XQ28ORF), and biglycan (BGN) genes, complete cds; and plasma membrane calcium ATPase isoform 3 (PMCA3) gene, partial cds
4717	13908	23010	1.41	8.7E-02	AF178636.1	NT	Mus musculus JNK interacting protein-3a (Jip3) mRNA, complete cds
5341	14571	23646	5.63	8.7E-02	AA288875.1	EST_HUMAN	zs55g08.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:701438 3'
5341	14571	23647	5.63	8.7E-02	AA288875.1	EST_HUMAN	zs55g08.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:701438 3'
7300	16519		2.75	8.7E-02	L04758.1	NT	Oryctolagus cuniculus cytochrome P-450 (CYP4A4) gene, 5' end
7445	16853	28144	1.71	8.7E-02	A1823393.1	EST_HUMAN	wh53e07.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2384484 3'
7859	17049	26568	2.23	8.7E-02	AJ007763.1	NT	Gluconobacter oxydans tRNA-Ile and tRNA-Ala genes
8586	17586		1.74	8.7E-02	X17116.1	NT	Human DNA for immunoglobulin alpha heavy chain from a case of alpha heavy chain disease
8771	17705		1.7	8.7E-02	6678057	NT	Mus musculus nidogen 2 (Nid2), mRNA
1259	10474	19636	5.5	8.6E-02	AJ271736.1	NT	Homo sapiens Xq pseudautosomal region, segment 2/2
2208	11405	20629	2.12	8.6E-02	BE408687.1	EST_HUMAN	601304016F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3638843 5'
3151	12386	21518	2.46	8.6E-02	L05488.1	NT	Trichomonas vaginalis beta-tubulin (btub1) gene, complete cds
3623	12844		3.32	8.6E-02	AF153362.1	NT	Dictyostelium discoideum adenyl cyclase (aca) gene, complete cds
3762	12881		0.65	8.6E-02	U29187.1	NT	Mus musculus long incubation prion protein (Prnpb) and prion-like protein (Prnd) genes, complete cds

Table 4

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5269	14442		0.7	8.6E-02	BF570296.1	EST_HUMAN	602185716T1 NIH_MGC_45 Homo sapiens cDNA clone IMAGE:4310259 3'
5708	14925	24319	4.11	8.6E-02	Y10826.1	NT	Homo sapiens LCN1b gene
7519	16724	26214	1.93	8.6E-02	AF206551.1	NT	Lacerta media cytochrome c oxidase subunit 1 gene, partial cds; mitochondrial gene for mitochondrial product
7519	16724	26215	1.93	8.6E-02	AF206551.1	NT	Lacerta media cytochrome c oxidase subunit 1 gene, partial cds; mitochondrial gene for mitochondrial product
7801	16964	26507	3.98	8.6E-02	BF305606.1	EST_HUMAN	601893437F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4139216 5'
7801	16994	26508	3.98	8.6E-02	BF305606.1	EST_HUMAN	601893437F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4139216 5'
7978	16411	25897	6.33	8.6E-02	AE001073.1	NT	Archaeoglobus fulgidus section 34 of 172 of the complete genome
2361	11554	20776	2.26	8.5E-02	AE000652.1	NT	Halobacterium pylon 26895 section 130 of 134 of the complete genome
5540	14764		1.93	8.5E-02	P08089	SWISSPROT	M PROTEIN, SEROTYPE 6 PRECURSOR
5661	14884	24272	6.72	8.5E-02	AF233885.1	NT	Mus musculus phospholipase C-like protein mRNA, partial cds
6857	15852	25311	3.4	8.5E-02	6754779	NT	Mus musculus myosin XV (Myo15), mRNA
7022	16199	25676	4.07	8.5E-02	BE833054.1	EST_HUMAN	RC4-OT0037-200700-014-e05 OT0037 Homo sapiens cDNA
7022	16199	25677	4.07	8.5E-02	BE833054.1	EST_HUMAN	RC4-OT0037-200700-014-e05 OT0037 Homo sapiens cDNA
7716	16915		12.86	8.5E-02	AF15510.1	NT	Homo sapiens heparanase precursor, mRNA, complete cds
7730	16928	26436	4.49	8.5E-02	AB001562.1	NT	Streptococcus mutans gene for glucose-1-phosphate uridylyltransferase, complete cds
8978	18094		2.18	8.5E-02	AJ005588.1	NT	Antirrhinum majus mRNA for MYB-related transcription factor
9166	17957		2.25	8.5E-02	AA382834.1	EST_HUMAN	EST72738 Ovary II Homo sapiens cDNA 5' end
2627	12022	21027	2.95	8.4E-02	W69330.1	EST_HUMAN	z444e11.1 Soares_fetal_heart_NhhH19W Homo sapiens cDNA clone IMAGE:343532 5'
4347	13549	22641	1.01	8.4E-02	AF257213.1	NT	Cavia porcellus glycoprotein alpha-subunit mRNA, complete cds
4347	13549	22642	1.01	8.4E-02	AF257213.1	NT	Cavia porcellus glycoprotein alpha-subunit mRNA, complete cds
5218	14392	23477	1.41	8.4E-02	5463817	NT	Homo sapiens nucleobindin 1 (NUCB1), mRNA
5339	14588	23644	9.48	8.4E-02	BE267153.1	EST_HUMAN	601190436F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3534393 5'
5962	15177	24594	1.78	8.4E-02	AK024458.1	NT	Homo sapiens mRNA for FLJ00050 protein, partial cds
6474	15671	25142	2.87	8.4E-02	BE095074.1	EST_HUMAN	CM3-BT0790-260400-162-405 BT0790 Homo sapiens cDNA
8482	17531	24026	1.53	8.4E-02	R79408.1	EST_HUMAN	y83h12.1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:145895 5'
3570	12793	21920	6.45	8.3E-02	P75334	SWISSPROT	HYPOTHETICAL LIPOPROTEIN MG309 HOMOLOG PRECURSOR
3598	12819	21939	0.67	8.3E-02	A1436797.1	EST_HUMAN	th82g06.x1 Soares_NhhMPu_S1 Homo sapiens cDNA clone IMAGE:2125210 3'
3598	12819	21940	0.67	8.3E-02	A1436797.1	EST_HUMAN	th82g06.x1 Soares_NhhMPu_S1 Homo sapiens cDNA clone IMAGE:2125210 3'
4708	13899	22998	0.69	8.3E-02	AB038490.1	NT	Homo sapiens gene for fukutin, complete cds
5818	15035	24438	2.53	8.3E-02	AF052683.1	NT	Homo sapiens protocadherin 43 gene, exon 1
6456	15653	25122	3.77	8.3E-02	AF195787.1	NT	Rattus norvegicus dystrophin-related protein 2 A-form splice variant (Dp2) mRNA, complete cds
8582	18318		1.88	8.3E-02	BE958458.1	EST_HUMAN	601644770F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:3928983 5'

Table 4

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1388	10600		6.88	8.2E-02	Y08170.2	NT	Gallus gallus mRNA for OBCAM protein gamma isoform
1488	10699	19873	1.71	8.2E-02	AF167077.2	NT	Canis familiaris glutamate transporter (EAAT4) mRNA, complete cds
3038	12275		1.94	8.2E-02	AL163206.2	NT	Homo sapiens chromosome 21 segment HS21C006
3788	13006		1.65	8.2E-02	AL161498.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 10
3984	13198	22308	1.27	8.2E-02	AL163206.2	NT	Homo sapiens chromosome 21 segment HS21C006
4269	13472	22565	6.55	8.2E-02	P48960	SWISSPROT	LEUCOCYTE ANTIGEN CD97 PRECURSOR
4269	13472	22566	6.55	8.2E-02	P48960	SWISSPROT	LEUCOCYTE ANTIGEN CD97 PRECURSOR
4269	13472	22567	6.55	8.2E-02	P48960	SWISSPROT	LEUCOCYTE ANTIGEN CD97 PRECURSOR
5111	14291	23378	3.05	8.2E-02	U76009.1	NT	Mus musculus zinc transporter (ZnT-3) gene, complete cds
6088	15298	24728	3.38	8.2E-02	AF309555.1	NT	Bos taurus connective tissue growth factor precursor (CTGF) gene, complete cds
6981	16139	25609	8.44	8.2E-02	X04197.1	NT	Beet necrotic yellow vein virus RNA-2
8589	17588	24005	4.79	8.2E-02	AE002248.2	NT	Chlamydomonas reinhardtii AR329, section 73 of 84 of the complete genome
9007	18088		2.57	8.2E-02	AF275366.1	NT	Mus musculus epidermal growth factor receptor (Egfr) gene, exons 5 through 28, and complete cds, alternatively spliced
5	11957	18405	5.12	8.0E-02	AW054853.1	EST_HUMAN	EST368723 MAGE cDNAs, MAGC Homo sapiens cDNA
944	10171	18331	0.61	8.0E-02	U60315.1	NT	Molluscum contagiosum virus subtype 1, complete genome
1673	12000	20070	12.38	8.0E-02	D26535.1	NT	Human gene for dihydrolipoamide succinyltransferase, complete cds (exon 1-15)
1673	12000	20071	12.38	8.0E-02	D26535.1	NT	Human gene for dihydrolipoamide succinyltransferase, complete cds (exon 1-15)
1867	11074	20265	3.81	8.0E-02	BE067219.1	EST_HUMAN	PM3-BT0347-170200-001-b08 BT0347 Homo sapiens cDNA
2433	11624		2.31	8.0E-02	BF248744.1	EST_HUMAN	601855548F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4075819 5'
2772	10323	19474	2.25	8.0E-02	M23449.1	NT	Dictyosporium discoideum cyclic nucleotide phosphodiesterase gene, complete cds
2852	12090	21219	0.59	8.0E-02	AL445067.1	NT	Thermoplasma acidophilum complete genome, segment 5/5
3806	13024	22135	0.84	8.0E-02	AW098118.1	EST_HUMAN	EST378181 MAGE cDNAs, MAGI Homo sapiens cDNA
4826	14018		6.62	8.0E-02	X72794.1	NT	M. musculus gene for gelatinase B
5217	14391		1.38	8.0E-02	AL163213.2	NT	Homo sapiens chromosome 21 segment HS21C013
5277	10177	19331	0.75	8.0E-02	U60315.1	NT	Molluscum contagiosum virus subtype 1, complete genome
5610	14834	24209	3.45	8.0E-02	AF275948.1	NT	Homo sapiens ABCA1 (ABCA1) gene, complete cds
6156	14834	24209	1.69	8.0E-02	AF275948.1	NT	Homo sapiens ABCA1 (ABCA1) gene, complete cds
6502	15699	25165	3.26	8.0E-02	AL114993.1	NT	Babys chereza strain T4 cDNA library under conditions of nitrogen deprivation
7373	16589	26078	3.74	8.0E-02	AF21706.1	NT	Homo sapiens SCG10 like-protein, helixase-like protein NHL, M68, and ADP-ribosylation factor related protein 1 (ARFRP1) genes, complete cds
8620	17616	23870	3.35	8.0E-02	AJ005375.1	NT	Drosophila oreana hunchback region
9210	14495		1.7	8.0E-02	4503034	NT	Homo sapiens cAMP responsive element binding protein-like 2 (CREBL2) mRNA
2140	11338	20556	3.19	7.9E-02	BE250008.1	EST_HUMAN	600943191F1 NIH_MGC_15 Homo sapiens cDNA clone IMAGE:2858510 5'

Page 82 of 382  
Table 4  
Single Exon Probes Expressed in HELA Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2936	12174	21308	13.43	7.9E-02	AI582029.1	EST_HUMAN	ar98c08.x1 Bartshead colon HPLRB7 Homo sapiens cDNA clone IMAGE:2173846 3' similar to gb:Z26878
3834	13051	22161	3.02	7.9E-02	6881044	NT	90S RIBOSOMAL PROTEIN L38 (HUMAN);
3834	13051	22162	3.02	7.9E-02	6881044	NT	Mus musculus colony stimulating factor 1 receptor (Csf1r), mRNA
4828	14015		1.26	7.9E-02	AB008019.1	NT	Mus musculus colony stimulating factor 1 receptor (Csf1r), mRNA
4830	14118	23213	1.12	7.9E-02	L24757.1	NT	Arabidopsis thaliana RXW24L mRNA, partial cds
6475	15672	25143	4.71	7.9E-02	U27832.1	NT	Human bone sialoprotein (BSP) gene, exons 2, 3 and 4
							Saccharomyces cerevisiae suppressor of MIF2 Sm4p (SMI4) gene, complete cds
7083	16260	25736	7.66	7.9E-02	AI081844.1	EST_HUMAN	ou63b05.s1 NCI_CGAP_Br2 Homo sapiens cDNA clone IMAGE:1632465 3' similar to WP:C37A2.2
7083	16260	25737	7.66	7.9E-02	AI081844.1	EST_HUMAN	CE008811 ;
1218	10436	19591	1.27	7.8E-02	AI793275.1	EST_HUMAN	ou63b05.s1 NCI_CGAP_Br2 Homo sapiens cDNA clone IMAGE:1632465 3' similar to WP:C37A2.2
1218	10436	19592	1.27	7.8E-02	AI793275.1	EST_HUMAN	CE008811 ;
2360	11553	20774	1.02	7.8E-02	AF221942.1	NT	repetitive element ;
2360	11553	20775	1.02	7.8E-02	AF221942.1	NT	Sus scrofa telomerase RNA pseudogene
4806	13995	23103	0.59	7.8E-02	BE836331.1	EST_HUMAN	Sus scrofa telomerase RNA pseudogene
5118	12950		2.33	7.8E-02	BE250048.1	EST_HUMAN	PM3-FN0058-140700-005-09 FN0058 Homo sapiens cDNA
7257	16477	25988	2	7.8E-02	U32323.1	NT	800943055F1 NIH_MGC_15 Homo sapiens cDNA clone IMAGE:2856893 5'
9219	17998		3.82	7.8E-02	AF096349.1	NT	Human interleukin-11 receptor alpha chain gene, complete cds
1403	11694	19782	1.27	7.7E-02	AF181897.1	NT	HIV-1 strain 97USNG30 from USA, envelope glycoprotein (env) gene, partial cds
3564	12787		2.81	7.7E-02	AJ238093.1	NT	Homo sapiens WRN (WRN) gene, complete cds
5073	14200	23287	10.43	7.7E-02	AL161501.2	NT	Homo sapiens partial AF-4 gene, exons 2 to 7 and Alu repeat elements
6428	15625	25090	3.91	7.7E-02	AA402849.1	EST_HUMAN	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 13
7021	16198	25675	4.03	7.7E-02	P38080	SWISSPROT	zu53d11.11 Spares ovary tumor N6HOT Homo sapiens cDNA clone IMAGE:741717 5' similar to
7591	16786	26280	6.03	7.7E-02	11422757	NT	TR:G1173905 G1173905 SPICEOSOME ASSOCIATED PROTEIN ;
8823	18172		2.35	7.7E-02	11436859	NT	PROBABLE SERINE/THREONINE-PROTEIN KINASE YBR059C
3365	12593	21732	1.99	7.6E-02	BE514432.1	EST_HUMAN	Homo sapiens KIAA0628 gene product (KIAA0628), mRNA
3366	12613	21746	1.09	7.6E-02	AA296447.1	EST_HUMAN	Homo sapiens interferon regulatory factor 7 (IRF7), mRNA
3534	12757	21889	0.66	7.6E-02	AJ400877.1	NT	601318426F1 NIH_MGC_8 Homo sapiens cDNA clone IMAGE:3634903 5'
7036	16216		2.98	7.6E-02	AL139078.2	NT	EST112214 Cerebellum II Homo sapiens cDNA 5' end similar to similar to protocadherin 43
							Homo sapiens ASCL3 gene, CEGP1 gene, C11orf14 gene, C11orf15 gene, C11orf16 gene and C11orf17 gene
							Campylobacter jejuni NCTC11168 complete genome, segment 5/6

Table 4

## Single Exon Probes Expressed in HELA Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8177	17309	26852	2.52	7.6E-02	AW996645.1	EST_HUMAN	QV3-BN0046-150400-151-e04 BN0046 Homo sapiens cDNA
794	10034	19183	1.35	7.5E-02	5902093	NT	Homo sapiens solute carrier family 6 (neurotransmitter transporter, glycine), member 9 (SLC6A9), mRNA
794	10034	19184	1.35	7.5E-02	5902093	NT	Homo sapiens solute carrier family 6 (neurotransmitter transporter, glycine), member 9 (SLC6A9), mRNA
1887	11094	20284	1.13	7.5E-02	AL163278.2	NT	Homo sapiens chromosome 21 segment HS21C078
4509	13705	22799	0.73	7.5E-02	AB015891.1	NT	Homo sapiens IL-18 gene for interleukin-18, intron 1 and exon 2
484	9736	18869	1.55	7.4E-02	AW838547.1	EST_HUMAN	RC5-LT0054-260100-011-H09 LT0054 Homo sapiens cDNA
3572	12785	21821	0.77	7.4E-02	AI807885.1	EST_HUMAN	W43H01.X1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2358385 3'
4715	13008	23007	1.83	7.4E-02	L78810.1	NT	Homo sapiens ADP/ATP carrier protein (ANT-2) gene, complete cds
4805	13994	23102	2.72	7.4E-02	6978442	NT	Rattus norvegicus Actin receptor like kinase 1 (Acvrl), mRNA
4860	14147	23239	1.79	7.4E-02	6878492	NT	Mus musculus ubiquitin C-terminal hydrolase related polypeptide (Uchrlp), mRNA
5873	15091		1.94	7.4E-02	R17477.1	EST_HUMAN	Y914966.r1 Soares Infant brain 1N1B Homo sapiens cDNA clone IMAGE:32339 5'
8541	17568		1.41	7.4E-02	11525983	NT	Homo sapiens histone deacetylase 5 (NY-CO-9), mRNA
8815	18294		3.13	7.4E-02	AW379431.1	EST_HUMAN	CM4-HT0243-081189-037-d11 HT0243 Homo sapiens cDNA
8975	17844	23914	1.32	7.4E-02	BF035096.1	EST_HUMAN	801453813F1 NIH_MGC 66 Homo sapiens cDNA clone IMAGE:3857738 5'
9175	17968		1.77	7.4E-02	4826867	NT	Homo sapiens receptor tyrosine kinase-like orphan receptor 1 (ROR1), mRNA
475	9728	18859	1.45	7.3E-02	BE964981.2	EST_HUMAN	601658738R1 NIH_MGC 69 Homo sapiens cDNA clone IMAGE:3886209 3'
475	9728	18860	1.45	7.3E-02	BE964981.2	EST_HUMAN	601658738R1 NIH_MGC 69 Homo sapiens cDNA clone IMAGE:3886209 3'
691	9934	19084	5.5	7.3E-02	AE001789.1	NT	Thermoboga maritima section 101 of 136 of the complete genome
1474	11896	18864	2.54	7.3E-02	AW900281.1	EST_HUMAN	CMO-NM1004-130300-284-g08 NM1004 Homo sapiens cDNA
1812	12003		17.52	7.3E-02	AL163302.2	NT	Homo sapiens chromosome 21 segment HS21C102
5021	14208		1.28	7.3E-02	U12283.1	NT	Mus musculus transcription factor USF2 (USF2) gene, exons 8-10 and complete cds
6280	15460	24901	2.17	7.3E-02	P05143	SWISSPROT	PROLINE-RICH PROTEIN MP-3
6280	15460	24902	2.17	7.3E-02	P05143	SWISSPROT	PROLINE-RICH PROTEIN MP-3
7770	15087	24477	2.81	7.3E-02	AA776977.1	EST_HUMAN	z24a02.s1 Soares fetal liver spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:451178 3' similar to gb.L02428 26S PROTEASE SUBUNIT 4 (HUMAN);
120	9406	18538	1.42	7.2E-02	AE000882.1	NT	Methanobacterium thermoautotrophicum from bases 1029155 to 1039934 (section 88 of 148) of the complete genome
120	9406	18539	1.42	7.2E-02	AE000882.1	NT	Methanobacterium thermoautotrophicum from bases 1029155 to 1039934 (section 88 of 148) of the complete genome
1470	10683	19857	2.33	7.2E-02	AL163301.2	NT	Homo sapiens chromosome 21 segment HS21C101
1470	10683	19858	2.33	7.2E-02	AL163301.2	NT	Homo sapiens chromosome 21 segment HS21C101



Page 84 of 382  
Table 4  
Single Exon Probes Expressed in HELA Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2514	11703		2.79	7.2E-02	U14794.1	NT	Human immunodeficiency virus type 1 isolate 26 reverse transcriptase (pol) gene, internal fragment, partial cds
2932	12170	21303	1.39	7.2E-02	AF065133.1	NT	Drosophila melanogaster CLOCK (Clk) mRNA, complete cds
3864	13080	22188	0.89	7.2E-02	AW298322.1	EST_HUMAN	U1H-BW0-ajl-a-05-0-U1.s1 NCL_CGAP_Sub8 Homo sapiens cDNA clone IMAGE:2732049 3'
4339	13540	22631	4.22	7.2E-02	BF572307.1	EST_HUMAN	602077757F1 NIH_MGC_92 Homo sapiens cDNA clone IMAGE:4251850 5'
4703	13894	22963	0.59	7.2E-02	11466563	NT	Rhodomonas salina mitochondrion, complete genome
5317	14549	23619	3	7.2E-02	U67531.1	NT	Methanococcus jannaschii section 73 of 150 of the complete genome
5318	14550	23820	8.39	7.2E-02	P11120	SWISSPROT	CALMODULIN
6970	16148	25819	2.59	7.2E-02	AV712452.1	EST_HUMAN	AV712452 DCA Homo sapiens cDNA clone DCAAUG01 5'
7074	16251	25724	2.4	7.2E-02	AW873187.1	EST_HUMAN	hq24f11.x1 NCL_CGAP_Adr1 Homo sapiens cDNA clone IMAGE:3120333 3' similar to TR:Q9Z340 Q9Z340 ATYPICAL PKC SPECIFIC BINDING PROTEIN. ;
7181	16358	25837	2.63	7.2E-02	U82895.2	NT	Homo sapiens zinc finger protein 92 (ZFP92), expressed-Xq28STS protein (XQ28ORF), and biglycan (BGN) genes, complete cds, and plasma membrane calcium ATPase isoform 3 (PMCA3) gene, partial cds
7207	16384	25855	6.09	7.2E-02	BE565003.1	EST_HUMAN	601343928F1 NIH_MGC_53 Homo sapiens cDNA clone IMAGE:3685951 5'
7213	16390		3.32	7.2E-02	BE539214.1	EST_HUMAN	601065194F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3451559 5'
7487	16994	26178	4.78	7.2E-02	AF049874.1	NT	Rattus norvegicus bHLH transcription factor Mist1 (Mist1) gene, complete cds
8481	17530		2.86	7.2E-02	AJ230796.1	EST_HUMAN	AJ230798 Homo sapiens library (Seranski P) Homo sapiens cDNA clone PS13D5 3'
8543	17568		1.84	7.2E-02	AA584485.1	EST_HUMAN	nc05h08.s1 NCL_CGAP_Phe1 Homo sapiens cDNA clone IMAGE:1099839 3'
8608	17606		2.42	7.2E-02	U82828.1	NT	Homo sapiens ataxia telangiectasia (ATM) gene, complete cds
8822	18141		4.54	7.2E-02	AW900962.1	EST_HUMAN	CMA-NN1009-200300-116-c11 NN1009 Homo sapiens cDNA
9134	17943		1.42	7.2E-02	AA401779.1	EST_HUMAN	z67c12.r1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:726454 5'
1868	11075	20266	1.76	7.1E-02	L02280.1	NT	Human immunodeficiency virus type 1 (D9) proviral structural capsid protein (gag) gene, partial cds
2258	11451	20870	6.31	7.1E-02	BE208802.1	EST_HUMAN	601872281F1 NIH_MGC_53 Homo sapiens cDNA clone IMAGE:4092881 5'
8328	17427		6.31	7.1E-02	BE304784.1	EST_HUMAN	601143974F1 NIH_MGC_15 Homo sapiens cDNA clone IMAGE:3051234 5'
534	9785	18908	0.74	7.0E-02	Q07092	SWISSPROT	COLLAGEN ALPHA 1(XVI) CHAIN PRECURSOR
1491	10704		1.12	7.0E-02	X96877.1	NT	M. artifiella Mitcut-1 gene
1732	10944	20127	1.13	7.0E-02	AA056343.1	EST_HUMAN	z66f04.s1 Stralagene colon (#837204) Homo sapiens cDNA clone IMAGE:509589 3'
2995	12232	21363	2.07	7.0E-02	AW138152.1	EST_HUMAN	U1H-B1-acy-c-07-0-U1.s1 NCL_CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2716020 3'
3875	13091	22207	0.97	7.0E-02	AA815438.1	EST_HUMAN	ai65a12.s1 Soares_testis_NHT Homo sapiens cDNA clone 1375678 3' similar to gb:K03002 60S
4021	13233	22336	1.24	7.0E-02	BE070284.1	EST_HUMAN	RIBOSOMAL PROTEIN L32 (HUMAN);
4121	13327		1.01	7.0E-02	AW782962.1	EST_HUMAN	QV4-BT0407-280100-090-e10 BT0407 Homo sapiens cDNA
						EST_HUMAN	CM0-UM0001-060300-270-e12 UM0001 Homo sapiens cDNA

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4187	13401	22499	11.13	7.0E-02	AF077821.1	NT	Canis familiaris inducible nitric oxide synthase mRNA, complete cds
4950	14137	23231	8.23	7.0E-02	BF381087.1	EST_HUMAN	601816291F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4050071 5'
6959	16137	25608	2.22	7.0E-02	K02801.1	NT	Rat Ig germline epsilon H-chain gene C-region, 3' end
7912	17127	26857	2.69	7.0E-02	AA724295.1	EST_HUMAN	ah99a05.s1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1327184 3' similar to gb:U14837
520	9771	18894	16.86	6.8E-02	AL163210.2	NT	TIGHT JUNCTION PROTEIN ZO-1 (HUMAN);
520	9771	18895	16.86	6.9E-02	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C010
1341	10555		1.3	6.9E-02	4507888	NT	Homo sapiens chromosome 21 segment HS21C010
3775	12993	22108	1.48	6.9E-02	Q06384	SWISSPROT	Homo sapiens regulator of Gz-selective protein signaling (ZGAP1) mRNA, and translated products
3775	12993	22109	1.48	6.9E-02	Q06384	SWISSPROT	26S PROTEASOME REGULATORY SUBUNIT S3 (NUCLEAR ANTIGEN 21D7)
5182	14358		0.91	6.8E-02	AF079906.1	NT	26S PROTEASOME REGULATORY SUBUNIT S3 (NUCLEAR ANTIGEN 21D7)
8474	17527		3.36	6.9E-02	X74315.1	NT	Rabies virus isolate b615 glycoprotein gene, partial cds
8682	17639		1.32	6.9E-02	P44621	SWISSPROT	X laevis XFD2 mRNA for fork head protein
8887	17782		2.42	6.9E-02	AF105953.1	NT	PROTEIN TRANSPORT PROTEIN HOF6 HOMOLOG
1847	11055	20244	1.09	6.8E-02	AA498759.1	EST_HUMAN	Homo sapiens membrane-bound aminopeptidase P (XNPEP2) gene, complete cds
1847	11055	20245	1.09	6.8E-02	AA498759.1	EST_HUMAN	ae30f02.r1 Gessler Wilms tumor Homo sapiens cDNA clone IMAGE:897339 5' similar to gb:M22382
1871	11078	20268	3.81	6.8E-02	AF156673.1	EST_HUMAN	MITOCHONDRIAL MATRIX PROTEIN P1 PRECURSOR (HUMAN);
4550	13745		0.72	6.8E-02	BE141076.1	NT	ae30f02.r1 Gessler Wilms tumor Homo sapiens cDNA clone IMAGE:897339 5' similar to gb:M22382
6200	15381	24822	7.45	6.8E-02	AL163288.2	EST_HUMAN	MITOCHONDRIAL MATRIX PROTEIN P1 PRECURSOR (HUMAN);
6555	15751	25212	7.23	6.8E-02	AJ248287.1	NT	Homo sapiens putative hepatic transcription factor (WBSCR14) gene, complete cds
6555	15751	25213	7.23	6.8E-02	AJ248287.1	NT	MR0-HT00689-071 099-001-c05 HT00689 Homo sapiens cDNA
8273	18341		1.76	6.8E-02	T03214.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C068
8405	17481		2.35	6.8E-02	AA758014.1	EST_HUMAN	Pyrococcus abyssi complete genome; segment 5/6
9004	17852		2.51	6.8E-02	AW975839.1	EST_HUMAN	Pyrococcus abyssi complete genome; segment 5/6
9069	17898		2.42	6.8E-02	9910585	NT	FB4A8 Fetal brain, Stralagene Homo sapiens cDNA clone FB4A8 3' end similar to LINE-1
9270	18287	23685	1.75	6.8E-02	6978895	NT	ah67005.s1 Soares_testis_NHT Homo sapiens cDNA clone 1320705 3'
1514	10728		2.09	6.7E-02	AF115536.1	EST_HUMAN	EST1387848 MAGe resequences, MAGN Homo sapiens cDNA
1858	11065	20256	1.82	6.7E-02	AJ220285.1	EST_HUMAN	EST1387848 MAGe resequences, MAGN Homo sapiens cDNA
3698	12818	22035	5.07	6.7E-02	P17278	SWISSPROT	Mus musculus latent TGF beta binding protein (Tgfb), mRNA
1356	10571	19736	1.07	6.8E-02	AI735509.1	EST_HUMAN	Rattus norvegicus Growth factor independent-1 (Gfi1), mRNA
							Oncorhynchus mykiss TAP1 protein (OnmyTAP1) mRNA, OnmyTAP1-01 allele, complete cds
							qg79604.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1841406 3'
							HOMEOBOX PROTEIN HOXD4 (CHOX-A)
							af12a09.x1 Barstead acta HPLRB6 Homo sapiens cDNA clone IMAGE:2354920 3' similar to
							SW:LIN1_NYCCO P08548 LINE-1 REVERSE TRANSCRIPTASE HOMOLOG..

Table 4

## Single Exon Probes Expressed in HELA Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1377	10591	18757	1.01	6.6E-02	AF245118.1	NT	Drosophila melanogaster cactin mRNA, complete cds
2147	11345	20582	11.31	6.6E-02	AJ289241.1	NT	Mus musculus Capn12 gene for calpain 12, exons 1-21, three alternative transcripts
3440	12665	21799	10.35	6.6E-02	R64308.1	EST_HUMAN	y18b10.s1 Soares placenta N52-HP Homo sapiens cDNA clone IMAGE:139578 3'
3453	12678	21813	2.75	6.6E-02	7108357	NT	Homo sapiens mesothelin (MSLN), transcript variant 1, mRNA
3453	12678	21814	2.75	6.6E-02	7108357	NT	Homo sapiens mesothelin (MSLN), transcript variant 1, mRNA
4056	13266	22369	1.94	6.6E-02	AF260225.1	NT	Homo sapiens TESTIN 2 and TESTIN 3 genes, complete cds, alternatively spliced
4988	14185	23273	12.34	6.6E-02	Q61703	SWISSPROT	INTER-ALPHA-TRYPsin INHIBITOR HEAVY CHAIN H2 PRECURSOR (ITI HEAVY CHAIN H2)
4988	14185	23274	12.34	6.6E-02	Q61703	SWISSPROT	INTER-ALPHA-TRYPsin INHIBITOR HEAVY CHAIN H2 PRECURSOR (ITI HEAVY CHAIN H2)
5922	15139	24551	3.91	6.6E-02	X06411.1	NT	P. vulgaris mRNA for chalcone synthase
6441	15638	25105	2.34	6.6E-02	AF052572.1	NT	Homo sapiens chemokine receptor CXCR4 gene, promoter region and complete cds
7534	18739	26230	7.23	6.6E-02	BF374248.1	EST_HUMAN	MR1-SN0094-010600-008-a12 SN0064 Homo sapiens cDNA
8892	17777		2.4	6.6E-02	9937991	NT	Mus musculus DIPB gene (Dipb), mRNA
9201	17886		1.32	6.6E-02	AF167430.1	NT	Rattus norvegicus cytochrome P450 2E1 (CYP2E1) gene, 5' flanking region
589	8837	18956	1.66	6.5E-02	BF027639.1	EST_HUMAN	601671046F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3954178 5'
984	10228	19382	2.86	6.5E-02	7706068	NT	Homo sapiens E2F-like protein (LOC51270), mRNA
1395	10609	19773	3.06	6.5E-02	U47624.1	NT	Xenopus laevis alpha(E)-catenin mRNA, complete cds
1708	10920	20105	1.9	6.5E-02	AE000784.1	NT	Aquifex aeolicus section 98 of 109 of the complete genome
4887	14154	23246	3.91	6.5E-02	7661863	NT	Homo sapiens KIAA0019 gene product (KIAA0019), mRNA
5472	14688	24051	1.87	6.5E-02	AA443991.1	EST_HUMAN	zv48h12.s1 Soares ovary tumor NIH-HOT Homo sapiens cDNA clone IMAGE:756743 3' similar to gb:M26038
7233	16454	25943	6.3	6.5E-02	AA195648.1	EST_HUMAN	HLA CLASS II HISTOCOMPATIBILITY ANTIGEN, DR-5 BETA CHAIN (HUMAN);
8295	17406		3.32	6.5E-02	M21496.1	NT	z32g05.s1 Soares NIHMPU_S1 Homo sapiens cDNA clone IMAGE:965144 3'
8670	17845		4.71	6.5E-02	AF102893.1	NT	Rabbit microsomal epoxide hydrolase
582	9831	18949	2.37	6.4E-02	X94549.1	NT	Nectria haematococca kinesin related protein 2 (KRP2) gene, complete cds
5714	14932	24327	3.38	6.4E-02	AF052733.1	NT	A. carterae precursor of peridinin-chlorophyll-protein (PCP) gene
5714	14932	24328	3.38	6.4E-02	AF052733.1	NT	Heterodera glycines beta-1,4-endoglucanase-1 precursor (HG-eng-1) gene, complete cds
6005	15287	24718	4.78	6.4E-02	BE974448.1	EST_HUMAN	Heterodera glycines beta-1,4-endoglucanase-1 precursor (HG-eng-1) gene, complete cds
6576	15772		2.71	6.4E-02	6753323	NT	601680425R2 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:3950503 3'
6673	15988	25327	4.73	6.4E-02	AA083305.1	EST_HUMAN	Mus musculus chaperonin subunit 6a (zeta) (Cct6a), mRNA
6897	16175	25646	2.29	6.4E-02	AB011126.1	NT	k1419.seq.F Human fetal heart, Lambda ZAP Express Homo sapiens cDNA 5'
				6.4E-02	AB011126.1	NT	Homo sapiens mRNA for KIAA0554 protein, partial cds
8198	17331	26873	2.12	6.4E-02	U91328.1	NT	Human hereditary haemochromatosis region, histone 2A-like protein gene, hereditary haemochromatosis (HLA-H) gene, RoRet gene, and sodium phosphate transporter (NPT3) gene, complete cds

Table 4  
Single Exon Probes Expressed in HELA Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8189	17331	26874	2.12	6.4E-02	U91328.1	NT	Human hereditary haemochromatosis region, histone 2A-like protein gene, hereditary haemochromatosis (HLA-H) gene, RoRet gene, and sodium phosphate transporter (NPT3) gene, complete cds
8562	18248		3.94	6.4E-02	AF107890.1	NT	Homo sapiens mucin 5B (MUC5B) gene, partial cds
8613	17610	23865	2.47	6.4E-02	AJ277174.1	NT	Drosophila melanogaster mRNA for mod(mdg4)51.4 protein
1726	10638	20121	2.34	6.3E-02	AF109905.1	NT	Mus musculus major histocompatibility locus class III regions Hsc701 gene, partial cds; smRNP, G7A, NG23, MutS homolog, CLCP, NG24, NG25, and NG26 genes, complete cds; and unknown genes
3562	12804		2.89	6.3E-02	P37062	SWISSPROT	HEAT SHOCK PROTEIN 70 HOMOLOG
7077	16254	25727	5.25	6.3E-02	AB010162.1	NT	Hepatitis G virus RNA for polyprotein (NS5A region), partial cds, strain: GMR-152
7303	14946	24343	3.42	6.3E-02	BF210736.1	EST_HUMAN	601873318F1 NIH_MGC 54 Homo sapiens cDNA clone IMAGE:4067489 5'
8849	17632		1.45	6.3E-02	P15276	SWISSPROT	TRANSCRIPTIONAL REGULATORY PROTEIN ALGP (ALGINATE REGULATORY PROTEIN ALGR3)
4237	13440	22532	3.53	6.2E-02	AL161572.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 68
4331	13532		1.31	6.2E-02	AF271235.1	NT	Rattus norvegicus differentiation-associated Na-dependent inorganic phosphate cotransporter (DNPI) mRNA, complete cds
4561	13775		7.65	6.2E-02	Q82191	SWISSPROT	S2 KD RO PROTEIN (SJOGREN SYNDROME TYPE A ANTIGEN (SS-A)) (RO(SS-A)) (RO52)
7888	17104	26634	1.97	6.2E-02	AJ242735.1	NT	Metarhizium anisopliae mRNA for Chymotrypsin (chy1 gene)
8383	18372		6.97	6.2E-02	AE000750.1	NT	Aquifex aeolicus section 82 of 108 of the complete genome
8829	17741	23932	2.62	6.2E-02	BF112039.1	EST_HUMAN	737h08.x1 Soares_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:3523815 3' similar to TR-Q9Y4S6 Q9Y4S6 HYPOTHETICAL 30.3 KD PROTEIN. [1];
260	9536	18686	5.6	6.1E-02	D16471.1	NT	Human mRNA, Xq terminal portion
3969	13184		2.44	6.1E-02	U73325.1	NT	Arabidopsis thaliana K+ inward rectifying channel protein (AtKIC1) gene, complete cds
4657	13851	22846	0.95	6.1E-02	AF119413.1	NT	Lupinus albus 1-aminocyclopropane-1-carboxylate synthase 3 (ACS3) gene, complete cds
4657	13851	22847	0.95	6.1E-02	AF119413.1	NT	Lupinus albus 1-aminocyclopropane-1-carboxylate synthase 3 (ACS3) gene, complete cds
6549	15745	25205	4.27	6.1E-02	X99268.1	NT	H. sapiens mRNA for B-HLH DNA binding protein
7317	16535	26023	6.21	6.1E-02	BE179543.1	EST_HUMAN	IL3-HT0618-110500-136-C06 HT0618 Homo sapiens cDNA
8349	18289		7.82	6.1E-02	X70989.1	NT	S. japonicum mRNA for serine-enzyme
9089	17908		4.49	6.1E-02	AL163207.2	NT	Homo sapiens chromosome 21 segment HS21C007
1269	10484	18643	1.24	6.0E-02	AE001777.1	NT	Thermotoga maritima section 89 of 136 of the complete genome
2635	11818	21035	1.2	6.0E-02	AW968848.1	EST_HUMAN	EST1380924 IMAGE resequences, MAG1 Homo sapiens cDNA
2726	11907		1.34	6.0E-02	AB031289.1	NT	Mesocricetus corti mitochondrial DNA, NADH dehydrogenase subunit 4, tRNA-Gln, tRNA-Phe, tRNA-Met, ATPase subunit 6, and NADH dehydrogenase subunit 2
2867	8390	18519	0.97	6.0E-02	AA188730.1	EST_HUMAN	zp78c04.r1 Stragene HeLa cell s3 937216 Homo sapiens cDNA clone IMAGE:626310 5'
2887	8390	18520	0.97	6.0E-02	AA188730.1	EST_HUMAN	zp78c04.r1 Stragene HeLa cell s3 937216 Homo sapiens cDNA clone IMAGE:626310 5'

Table 4  
Single Exon Probes Expressed in HELA Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3195	12430	21565	1.53	6.0E-02	AA372376.1	EST_HUMAN	EST84268 Colon adenocarcinoma IV Homo sapiens cDNA 5' end similar to tissue-specific protein
3195	12430	21566	1.53	6.0E-02	AA372376.1	EST_HUMAN	EST84268 Colon adenocarcinoma IV Homo sapiens cDNA 5' end similar to tissue-specific protein
3613	12834		1.01	6.0E-02	BE984443.2	EST_HUMAN	601658150R1 NIH_MGC 68 Homo sapiens cDNA clone IMAGE:3876060 3'
6083	14529	23553	2.83	6.0E-02	5174688	NT	Homo sapiens stimulated trans-acting factor (50 kDa) (STAF50) mRNA
6083	14529	23554	2.83	6.0E-02	5174688	NT	Homo sapiens stimulated trans-acting factor (50 kDa) (STAF50) mRNA
6160	15343	24780	2.16	6.0E-02	BF382349.1	EST_HUMAN	601815274F2 NIH_MGC 50 Homo sapiens cDNA clone IMAGE:4049226 5'
6368	15548	25004	1.79	6.0E-02	A1204275.1	EST_HUMAN	qf58b08.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1754199 3'
6878	16069	25538	3.1	6.0E-02	AJ245385.1	NT	Acipenser baeri partial IGLV gene for Immunoglobulin light chain variable region, exons 1-2
6878	16069	25539	3.1	6.0E-02	AJ245385.1	NT	Acipenser baeri partial IGLV gene for Immunoglobulin light chain variable region, exons 1-2
7878	17066		2.05	6.0E-02	AA128386.1	EST_HUMAN	zn87c08.1 Stragelene lung carcinoma 937218 Homo sapiens cDNA clone IMAGE:565168 5' similar to
8612	17609	23964	1.52	6.0E-02	11431702	NT	gb:X69181 60S RIBOSOMAL PROTEIN L31 (HUMAN);
9016	17888		2.41	6.0E-02	A1808273.1	EST_HUMAN	Homo sapiens DNA-dependent protein kinase catalytic subunit-interacting protein 2 (KIP2), mRNA
235	9514	18842	5.1	5.9E-02	AW934719.1	EST_HUMAN	wf69h03.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2360885 3' similar to TR:O60298
2940	12178	21313	2.36	5.9E-02	AF190269.1	NT	RC1-DT0001-290100-012-e10 DT0001 Homo sapiens cDNA
5249	14422	23498	0.67	5.9E-02	AW028748.1	EST_HUMAN	Mus musculus p53 tumor suppressor gene, exon 10 and 11, partial cds; alternatively spliced
5249	14422	23498	0.67	5.9E-02	AW028748.1	EST_HUMAN	w34402.x1 NCI_CGAP_Ov18 Homo sapiens cDNA clone IMAGE:2531450 3' similar to TR:O65386
6660	15855	25314	2.7	5.9E-02	9055249	NT	O65386 F12F1.20 PROTEIN ;
7366	16582	26286	3.4	5.9E-02	6879870	NT	O65386 F12F1.20 PROTEIN ;
7590	16794	26286	2.73	5.9E-02	11433356	NT	Mus musculus iroquois related homeobox 5 (Drosophila) (Irx5), mRNA
8075	17210		1.66	5.9E-02	BF572539.1	EST_HUMAN	Mus musculus follistatin-like (Fst), mRNA
8089	17224		1.97	5.9E-02	AJ240733.1	EST_HUMAN	Homo sapiens ninein (LOC51189), mRNA
941	10174		6.49	5.8E-02	D90110.1	NT	602078548F1 NIH_MGC 62 Homo sapiens cDNA clone IMAGE:4243834 5'
3844	12865	21983	13.82	5.8E-02	AE001775.1	NT	Gallus gallus HKC9 telomere junction
4348	13550	22643	5.33	5.8E-02	AW051927.1	EST_HUMAN	Thiococcus ferrooxidans merC, merA genes and URF-1
4348	13550	22644	5.33	5.8E-02	AW051927.1	EST_HUMAN	Thermoboga maritima section 87 of 138 of the complete genome
4544	13739	22838	5.2	5.8E-02	A1247505.1	EST_HUMAN	wx24c02.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2544578 3'
4544	13739	22839	5.2	5.8E-02	A1247505.1	EST_HUMAN	wx24c02.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2544578 3'
4571	13765		2.44	5.8E-02	AF086264.1	NT	qf56601.x1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:1848697 3' similar to
							gb:M13142 COAGULATION FACTOR XI PRECURSOR (HUMAN);
							Gallus gallus tyrosine kinase JAK1 (JAK1) mRNA, complete cds

Page 89 of 382  
Table 4  
Single Exon Probes Expressed in HELA Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5151	14330	23421	0.6	5.8E-02	AF275388.1	NT	Mus musculus epidermal growth factor receptor (Egfr) gene, exons 5 through 28, and complete cds, alternatively spliced
5151	14330	23422	0.6	5.8E-02	AF275388.1	NT	Mus musculus epidermal growth factor receptor (Egfr) gene, exons 5 through 28, and complete cds, alternatively spliced
5233	14407	25002	0.94	5.8E-02	L76979.1	NT	Schizosaccharomyces pombe HMG-CoA reductase (hmg1+) gene, complete cds
6367	15547	25002	2.53	5.8E-02	M99150.1	NT	Human polymorphic microsatellite DNA
6367	15547	25003	2.53	5.8E-02	M99150.1	NT	Human polymorphic microsatellite DNA
8498	17539		2.41	5.8E-02	AF220177.1	NT	Drosophila melanogaster male fruitless type-A (fru) mRNA, complete cds
8805	18359		6.22	5.8E-02	AA604289.1	EST_HUMAN	no75611.s1 NCL_CGAP_AA1 Homo sapiens cDNA clone IMAGE:1112684 3'
3022	12258	21386	1.34	5.7E-02	AI081944.1	EST_HUMAN	cu63b05.s1 NCL_CGAP_Br2 Homo sapiens cDNA clone IMAGE:1632465 3' similar to WP.C37A2.2 CE08811
3036	12272	21400	1.43	5.7E-02	AF119117.1	NT	Homo sapiens dopamine transporter (SLC6A3) gene, complete cds
3687	12908		0.93	5.7E-02	AF001282.1	NT	Chironomus thummi thummi globin VIIA.1 (ctt-7A.1), globin 9.1 (ctt-9.1), globin II-beta (ctt-2beta), non-functional globin XIII (ctt-13RT), globin XII (ctt-12) and globin XI (ctt-11) genes, complete cds
3786	13004	22119	2.32	5.7E-02	AW968791.1	EST_HUMAN	EST1378865 MAGE resequences, MAGI Homo sapiens cDNA
4591	13882		1.01	5.7E-02	M95098.1	NT	Bos taurus lysozyme gene (cow 3), complete cds
7743	16939	26448	4.13	5.7E-02	AI752885.1	EST_HUMAN	cn18b09.y1 Normal Human Trabecular Bone Cells Homo sapiens cDNA clone NHTBC_cn18b09 random
7743	16939	26449	4.13	5.7E-02	AI752885.1	EST_HUMAN	cn18b09.y1 Normal Human Trabecular Bone Cells Homo sapiens cDNA clone NHTBC_cn18b09 random
8718	18169		7	5.7E-02	D50320.1	NT	Pig DNA for SPAL-2, complete cds
8959	18244		2.48	5.7E-02	AF217490.1	NT	Homo sapiens fragile 16D oddo reductase (FOR) gene, exons 8, 9, and partial cds
9105	18349		4.1	5.7E-02	AF261280.1	NT	Pan troglodytes apolipoprotein-E gene, complete cds
4842	13836	22925	1.34	5.6E-02	AB013100.1	NT	Lycopodium esculentum LE-ACS8 mRNA for 1-aminocyclopropane-1-carboxylate synthase, complete cds
4706	13897	22998	1.32	5.6E-02	AA280598.1	EST_HUMAN	zs43501.s1 NCL_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:700416 3'
5956	15172	24587	4.45	5.6E-02	AW172708.1	EST_HUMAN	402c10.x1 NCL_CGAP_U12 Homo sapiens cDNA clone IMAGE:2656050 3' similar to TR:084979 084979 KIAA0905 PROTEIN
6140	15324	24769	3.23	5.6E-02	BE008001.1	EST_HUMAN	QVO-BN0147-280400-214-007 BN0147 Homo sapiens cDNA
6717	15912	25370	3.92	5.6E-02	BE542663.1	EST_HUMAN	601067158F-1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3453278 5'
6717	15912	25371	3.92	5.6E-02	BE542663.1	EST_HUMAN	601067158F-1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3453278 5'
8099	17233		2.72	5.6E-02	AF260225.1	NT	Homo sapiens TESTIN 2 and TESTIN 3 genes, complete cds, alternatively spliced
2616	11800	21016	5.48	5.5E-02	X97989.1	NT	H. sapiens gene encoding Le autoantigen
3181	12416	21551	3.98	5.5E-02	6755501	NT	Mus musculus SH3 domain protein 1B (Sh3d1B), mRNA

Table 4

## Single Exon Probes Expressed in HELA Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4199	13403	22500	1.12	5.5E-02	L41581.1	NT	Gallid herpesvirus mRNA fragment
5158	14337		1.07	5.5E-02	U87518.1	NT	Methanococcus jannaschii section 60 of 150 of the complete genome
5516	14741	24107	3.4	5.5E-02	Q01174	SWISSPROT	TROPOMYOSIN ALPHA CHAIN, NON MUSCLE
5671	14741	24107	4.13	5.5E-02	Q01174	SWISSPROT	TROPOMYOSIN ALPHA CHAIN, NON MUSCLE
7589	16793	26285	14.31	5.5E-02	U09771.1	NT	Citrobacter freundii DSM 30040 cyclopropane fatty acid synthase (cfa) gene, partial cds, dihydroxyacetone kinase (dhaK), glycerol dehydrogenase (dhaD), transcriptional activator (dhaR), 1,3-propanediol dehydrogenase (dhaT), glycerol dehydratase (dhaB), >
1286	10511		0.8	5.4E-02	AF157623.1	NT	Homo sapiens HTRA serine protease (PRSS11) gene, complete cds
2884	12221		1.01	5.4E-02	AJ277488.1	NT	Oryza sativa rbb3-1 gene for putative Bowman Birk trypsin inhibitor
3400	14477		7.28	5.4E-02	BE073488.1	EST_HUMAN	RC5-BT0559-140200-012-Q03 BT0559 Homo sapiens cDNA
3889	13105	22223	0.72	5.4E-02	U85806.1	NT	Hirudo medicinalis SNAP-25 homolog mRNA, complete cds
7289	16508	25899	2.68	5.4E-02	U20790.1	NT	Neurospora crassa ubiquinol-cytochrome c oxidoreductase subunit VIII (QCR8) mRNA, complete cds
8598	18163		1.71	5.4E-02	U44894.1	NT	Rana catesbeiana heat shock protein 30 (HSP30) mRNA, complete cds
1080	10288	19436	1.14	5.3E-02	AW391248.1	EST_HUMAN	QV0-ST0213-021289-082-e09 ST0213 Homo sapiens cDNA
1090	10288	19437	1.14	5.3E-02	AW391248.1	EST_HUMAN	QV0-ST0213-021289-082-e09 ST0213 Homo sapiens cDNA
1496	10709	19882	11.81	5.3E-02	T94759.1	EST_HUMAN	ye37712.1 Stratagene lung (#837210) Homo sapiens cDNA clone IMAGE:118951 5' similar to gb:K01508 HLA CLASS II HISTOCOMPATIBILITY ANTIGEN, DP(1) ALPHA CHAIN (HUMAN);
2490	11651	20872	2.39	5.3E-02	AJ276408.1	NT	Pseudomonas putida tgsS gene
2893	12131	21266	0.92	5.3E-02	M58417.1	NT	Drosophila melanogaster laminin B2 gene, complete cds
2893	12131	21267	0.92	5.3E-02	M58417.1	NT	Drosophila melanogaster laminin B2 gene, complete cds
3115	12350	21478	3.95	5.3E-02	AJ276408.1	NT	Pseudomonas putida tgsS gene
5120	14299	23387	8.22	5.3E-02	M80463.1	NT	Mus musculus caudal type homeobox-1 (Cdx-1) gene, complete cds
5343	14573	23649	1.95	5.3E-02	AE000527.1	NT	Helicobacter pylori 26695 section 5 of 134 of the complete genome
5343	14573	23650	1.95	5.3E-02	AE000527.1	NT	Helicobacter pylori 26695 section 5 of 134 of the complete genome
6034	15242	24663	4.21	5.3E-02	8695413	NT	Lymphocystis disease virus 1, complete genome
6236	15417		2.31	5.3E-02	S78221.1	NT	nuclear protein TIF1 isoform [mice, mRNA, 4053 nt]
9242	18013	23850	1.36	5.3E-02	AF276815.1	NT	Branchiostoma floridae homeodomain-containing protein Hox13 (Hox13) gene, exon 2 and partial cds
2249	11444		91.98	5.2E-02	5031808	NT	Homo sapiens mespin A, alpha (PABA peptide hydrolase) (MEP1A) mRNA
3078	12314	21435	2.27	5.2E-02	AJ277661.1	NT	Homo sapiens partial LMO1 gene for LIM domain only 1 protein, exon 1
3078	12314	21436	2.27	5.2E-02	AJ277661.1	NT	Homo sapiens partial LMO1 gene for LIM domain only 1 protein, exon 1
3913	13129	22246	0.7	5.2E-02	AF236101.1	NT	Arabidopsis thaliana putative dicarboxylate diion protein (Crd1) mRNA, complete cds
4263	13466	22557	2.68	5.2E-02	U07132.1	NT	Human steroid hormone receptor Nr-1 mRNA, complete cds

Page 91 of 382  
Table 4  
Single Exon Probes Expressed in HELA Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5199	14375	23462	0.72	5.2E-02	AB035201.1	NT	Rattus norvegicus mRNA for thyroglobulin, complete cds
2332	11525		1.1	5.1E-02	AL134071.1	EST_HUMAN	DKFZp547D073_r1 547 (synonym: hibr1) Homo sapiens cDNA clone DKFZp547D073 5'
4186	13390	22489	0.81	5.1E-02	AE001301.1	NT	Chlamydia trachomatis section 28 of 87 of the complete genome
5080	14260	23345	1.07	5.1E-02	BE957423.2	EST_HUMAN	601653569R2 NIH_MGC 55 Homo sapiens cDNA clone IMAGE:3838361 3'
5235	14409	23490	0.71	5.1E-02	P01785	SWISSPROT	IG HEAVY CHAIN V REGION MOO
8021	14511	23569	1.77	5.1E-02	BF378825.1	EST_HUMAN	QV0-UM0051-250800-350-808 UM0051 Homo sapiens cDNA
7016	16192	25666	6.18	5.1E-02	AF012898.1	NT	Candida albicans protein phosphatase Sac1 homolog (SSD1) gene, complete cds
7408	16818	26108	2.98	5.1E-02	AF083930.1	NT	Homo sapiens ES18 mRNA, partial cds
7408	16818	26108	2.88	5.1E-02	AF083930.1	NT	Homo sapiens ES18 mRNA, partial cds
8856	17759		1.7	5.1E-02	AF082487.1	NT	Homo sapiens ES18 mRNA, partial cds
489	9742	18872	1	5.0E-02	AF098004.1	NT	Cucumis melo polygalacturonase precursor (MPC3) mRNA, complete cds
1212	10430	19588	10.56	5.0E-02	Z69104.1	NT	Mus musculus fatty acid amide hydrolase gene, exon 10
1959	11163	20366	6.31	5.0E-02	P02810	SWISSPROT	Bacillus subtilis complete genome (section 1 of 21): from 1 to 213080
2770	10225	19381	1.08	5.0E-02	U72742.1	NT	SALVARY ACIDIC PROLINE-RICH PHOSPHOPROTEIN 1/2 PRECURSOR (PRP-1/PRP-3) (PRP-2/PRP-4) (PIF-FPIF-S) (PROTEIN A/PROTEIN C) [CONTAINS: PEPTIDE P-C]
3311	12541		1.45	5.0E-02	U32782.1	NT	Oryctolagus cuniculus UDP-glucuronosyltransferase (UGT2B13) mRNA, complete cds
3573	12796		0.94	5.0E-02	U32782.1	NT	Mus musculus Ure-51 like kinase 2 (C. elegans) (Ulk2), mRNA
3684	12885	22008	4.54	5.0E-02	U12769.2	NT	Haemophilus influenzae Rd section 97 of 163 of the complete genome
4837	14026		0.98	5.0E-02	P40232	SWISSPROT	Anthrax toxin period clock protein homolog mRNA, complete cds
6307	15488	24933	11.19	5.0E-02	P35616	SWISSPROT	CASEIN KINASE II BETA CHAIN (CK II)
8025	17162	26689	2.78	5.0E-02	U67600.1	NT	NEUROFILAMENT TRIPLET L PROTEIN (NEUROFILAMENT LIGHT POLYPEPTIDE) (NF-L)
8360	18205		4.81	5.0E-02	Q04047	SWISSPROT	Methanococcus jannaschii section 142 of 150 of the complete genome
229	9507		34.14	4.9E-02	M14230.1	NT	NO-ON-TRANSIENT A PROTEIN
374	9640	18774	2.22	4.9E-02	AF275948.1	NT	Chicken 28-kDa vitamin D-dependent calcium-binding protein (CaBP-28) mRNA, complete cds
374	9640	18775	2.22	4.9E-02	AF275948.1	NT	Homo sapiens ABCA1 (ABCA1) gene, complete cds
2826	12065	21188	0.77	4.9E-02	U32836.1	NT	Homo sapiens ABCA1 (ABCA1) gene, complete cds
3257	12490	21621	1.72	4.9E-02	P54258	SWISSPROT	Zea mays phytoene synthase (Y1) gene, complete cds
3545	12788		0.76	4.9E-02	AA188940.1	EST_HUMAN	ATROPHIN-1 (DENTATORUBRAL-PALLIDOLYSIAN ATROPHY PROTEIN)
3569	12792	21918	1.13	4.9E-02	AA400914.1	EST_HUMAN	zq48a12.s1 Stragene NNT neuron (#837233) Homo sapiens cDNA clone IMAGE:632926 3' similar to contains Alu repetitive element; contains element MSR1 repetitive element;
3569	12792	21919	1.13	4.9E-02	AA400914.1	EST_HUMAN	z178a03.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:728428 3'
4858	14046	23140	1.62	4.9E-02	AW167821.1	EST_HUMAN	z178a03.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:728428 3'
4858	14046	23141	1.62	4.9E-02	AW167821.1	EST_HUMAN	xg56g10.x1 NCI_CGAP_U14 Homo sapiens cDNA clone IMAGE:2632386 3'
5382	14611	23723	1.8	4.9E-02	L00122.1	NT	xg56g10.x1 NCI_CGAP_U14 Homo sapiens cDNA clone IMAGE:2632386 3'
							Rat elastase II gene, exon 6



Table 4

## Single Exon Probes Expressed in HELA Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5382	14811	23724	1.8	4.8E-02	U0122.1	NT	Rat elastase II gene, exon 8
7940	17080	26508	3.81	4.9E-02	AF008030.1	NT	Homo sapiens prepro placental TGF-beta gene, complete cds
8777	17707		1.6	4.9E-02	8923880	NT	Homo sapiens CS box-containing WD protein (LOC55884), mRNA
8058	17888		4.4	4.8E-02	M19364.1	NT	Human gamma-B-crystallin (gamma 1-2) and gamma-C-crystallin (gamma 2-1) genes, complete cds
9119	18277		1.28	4.8E-02	Z59118.1	NT	Bacillus subtilis complete genome (section 13 of 21): from 2395281 to 2613730
335	9804	18733	1.4	4.8E-02	D16471.1	NT	Human mRNA, Xq terminal portion
338	9804	18733	3	4.8E-02	D16471.1	NT	Human mRNA, Xq terminal portion
495	9748	18877	7.4	4.8E-02	AF003100.1	NT	Arabidopsis thaliana AP2 domain containing protein RAP2.7 mRNA, partial cds
2238	11433	20657	1.55	4.8E-02	W51983.1	EST_HUMAN	z49b02.s1 Soares_senescent_fibroblasts_NbHSF Homo sapiens cDNA clone IMAGE:325611 3' similar to gb:M30938 LUPUS KU AUTOANTIGEN PROTEIN P86 (HUMAN);
3175	12410	21548	2.47	4.8E-02	X17144.1	NT	Tetrahymena rostrata histone H3II and histone H4II intergenic DNA
4874	13868		1.11	4.8E-02	Z54280.1	NT	S. scrofa gene for skeletal muscle ryanodine receptor
5160	14339	23428	0.63	4.8E-02	U91914.1	NT	Streptococcus constellatus D-alanine:D-alanine ligase gene, partial cds
8847	17830		1.35	4.8E-02	9632893	NT	Streptococcus thermophilus bacteriophage Sfi19, complete genome
6010	15280	24694	3.54	4.7E-02	W01153.1	EST_HUMAN	yc37109.r1 Soares melanocyte 2NBHM Homo sapiens cDNA clone IMAGE:291017 5' similar to contains Alu repetitive element;
6050	15218	24638	2.13	4.7E-02	M62752.1	NT	Rat statin-related protein (s1) gene, complete CDS
6543	15739	25200	13.84	4.7E-02	X15543.1	NT	B. taurus mRNA for RF-36-DNA-binding protein
6836	16030	25495	12.53	4.7E-02	X15543.1	NT	B. taurus mRNA for RF-36-DNA-binding protein
7338	16555	26043	1.93	4.7E-02	6754565	NT	Mus musculus ligand of numb-protein X (Lnx), mRNA
8090	17225	26760	2.02	4.7E-02	U73621.1	NT	Bos taurus paired box protein (pax-6) gene, partial cds
8090	17225	26761	2.02	4.7E-02	U73621.1	NT	Bos taurus paired box protein (pax-6) gene, partial cds
8580	18360		1.79	4.7E-02	AV648521.1	EST_HUMAN	AV648521 GLC Homo sapiens cDNA clone GLOBK002 3'
8947	18363		1.48	4.7E-02	P82951	SWISSPROT	HOMEBOX PROTEIN GBX-2 (GASTRULATION AND BRAIN-SPECIFIC HOMEBOX PROTEIN 2)
9198	17985		1.24	4.7E-02	AJ277692.1	NT	Homo sapiens partial TUB gene for tubby (mouse) homolog and LMO1 gene for LIM domain only 1 protein
275	9550	18681	1.16	4.6E-02	BE153583.1	EST_HUMAN	PMO-HT0339-251199-003-q05 HT0339 Homo sapiens cDNA
747	9888	19131	3.98	4.6E-02	AE000445.1	NT	Escherichia coli K-12 MG1655 section 335 of 400 of the complete genome
1299	10514		1.09	4.6E-02	A1014255.1	EST_HUMAN	pm50d02.s1 Johnston frontal cortex Homo sapiens cDNA clone HTCBW/C01 5'
1367	10581	19748	2.77	4.6E-02	AV727059.1	EST_HUMAN	P90533 LIMA :contains element LTR1 repetitive element ;
2452	11643	20863	1.64	4.6E-02	AW236023.1	EST_HUMAN	AV727059 HTC Homo sapiens cDNA clone HTCBW/C01 5'
							m24f03.x1 NCI_OGAP_Kid11 Homo sapiens cDNA clone IMAGE:2694653 3' similar to SW:GRF1_HUMAN
							Q12849 G-RICH SEQUENCE FACTOR-1 ;

Page 93 of 382  
Table 4  
Single Exon Probes Expressed in HELA Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2760	9550	18681	1.53	4.6E-02	BE153583.1	EST_HUMAN	PMO-HT0339-251199-003-g05 HT0339 Homo sapiens cDNA
2969	12207	21343	0.62	4.6E-02	BE153583.1	EST_HUMAN	PMO-HT0339-251199-003-g05 HT0339 Homo sapiens cDNA
3304	12207	21343	0.6	4.6E-02	BE153583.1	EST_HUMAN	PMO-HT0339-251199-003-g05 HT0339 Homo sapiens cDNA
3471	12207	21343	0.67	4.6E-02	BE153583.1	EST_HUMAN	PMO-HT0339-251199-003-g05 HT0339 Homo sapiens cDNA
4103	13310		1.27	4.6E-02	AF220385.1	NT	Mus musculus nuclear RNA helicase II(Gu (dxb21) gene, complete cds
5765	14984	24383	3.35	4.6E-02	X61624.1	NT	C.reinhardtii atp2 (atpB) mRNA
5765	14984	24384	3.35	4.6E-02	X61624.1	NT	C.reinhardtii atp2 (atpB) mRNA
6870	15865	25325	4.77	4.6E-02	BE154005.1	EST_HUMAN	PMO-HT0339-060400-008-G12 HT0339 Homo sapiens cDNA
7941	17081	26609	4.08	4.6E-02	AA913328.1	EST_HUMAN	ci27h09.s1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1524737 3'
8928	18358		1.28	4.6E-02	L11692.1	NT	Oryctolagus cuniculus macrophage scavenger receptor type II mRNA, complete cds
9163	17962		4.09	4.6E-02	X57808.1	NT	Human germline immunoglobulin lambda light chain gene
453	9706	18844	2.45	4.5E-02	P22448	SWISSPROT	RETINOIC ACID RECEPTOR BETA (RAR-BETA)
1226	10444	19589	0.95	4.5E-02	AF005730.1	NT	Marburg virus strain M/S.Africa/Johannesburg/1975/Ozolin VP35 gene, complete cds
1226	10444	19600	0.95	4.5E-02	AF005730.1	NT	Marburg virus strain M/S.Africa/Johannesburg/1975/Ozolin VP35 gene, complete cds
1773	10983	20174	5.37	4.5E-02	P32182	SWISSPROT	HEPATOCYTE NUCLEAR FACTOR 3-BETA (HNF-3B)
2080	11280	20498	1.63	4.5E-02	AE003984.1	NT	Xyella fastidiosa, section 110 of 229 of the complete genome
3703	12923	22042	4.72	4.5E-02	AL163278.2	NT	Homo sapiens chromosome 21 segment HS21C078
5766	14985	24385	1.65	4.5E-02	AJ400877.1	NT	Homo sapiens ASCL3 gene, CEGP1 gene, C11orf14 gene, C11orf15 gene, C11orf16 gene and C11orf17 gene
6597	15793	25251	2.49	4.5E-02	AF036884.1	NT	Arabidopsis thaliana CCAAT-box binding factor HAP3 homolog gene, complete cds
7054	16231	25706	5.35	4.5E-02	AA325216.1	EST_HUMAN	EST28167 Cerebellum II Homo sapiens cDNA 5' end similar to neuro-D4 protein
8578	17592	24000	2.59	4.5E-02	11418013	NT	Homo sapiens ret finger protein-like 3 (RPLP3), mRNA
8989	18250	23709	5.94	4.5E-02	AA191097.1	EST_HUMAN	zq43f11.r1 Stralagene hNT neuron (#937233) Homo sapiens cDNA clone IMAGE:632493 5'
224	9503		4.97	4.4E-02	BE872733.1	EST_HUMAN	901952154F1 NIH_MGC 82 Homo sapiens cDNA clone IMAGE:3935388 5'
1032	10258	19409	0.88	4.4E-02	L19295.1	NT	Drosophila melanogaster extracellular (EXD) mRNA, complete cds
2066	11267		4.76	4.4E-02	P31568	SWISSPROT	HYPOTHETICAL PROTEIN (ORF 2280)
2453	11644	20864	1.05	4.4E-02	AW875475.1	EST_HUMAN	QV2-PT0012-010300-070-g02 PT0012 Homo sapiens cDNA
3348	12574	21714	0.93	4.4E-02	X06212.1	NT	Chironomus tentans ecdysone-controlled gene I-18c
3619	12840	21959	1.8	4.4E-02	AF159160.1	NT	Myxococcus xanthus serine/threonine kinase Pkn10 (pkn10) gene, complete cds
4629	13823	22611	1.22	4.4E-02	AF109807.1	NT	Homo sapiens S164 gene, partial cds; PS1 and hypothetical protein genes, complete cds; and S171 gene, partial cds
4629	13823	22912	1.22	4.4E-02	AF109807.1	NT	Homo sapiens S164 gene, partial cds; PS1 and hypothetical protein genes, complete cds; and S171 gene, partial cds
4754	13945		2.85	4.4E-02	AJ222696.1	NT	Ovis aries CCAAT-enhancer binding protein epsilon gene

Page 94 of 382  
Table 4  
Single Exon Probes Expressed in HELA Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptbr
6702	15897	25358	3.19	4.4E-02	AA736868.1	EST_HUMAN	hw13h03.s1 NCI_CGAP_SS1 Homo sapiens cDNA clone IMAGE:1239221 3'
7639	16839	26336	5.01	4.4E-02	AF060669.1	NT	Hepatitis E virus strain HEV-US2 polyprotein (ORF1), (ORF3), and capsid protein (ORF2) genes, complete cds
7753	16949	26457	3.27	4.4E-02	AA496739.1	EST_HUMAN	ae33904.r1 Gessler Wilms tumor Homo sapiens cDNA clone IMAGE:897631 5'
8280	17403		1.83	4.4E-02	AB040928.1	NT	Homo sapiens mRNA for KIAA1493 protein, partial cds
8477	18373		1.48	4.4E-02	BF241245.1	EST_HUMAN	601878746F1 NIH_MGC 59 Homo sapiens cDNA clone IMAGE:4107418 5'
780	10030	19179	7.71	4.3E-02	AF003249.1	NT	Marone scapitis myosin heavy chain FM3A (FM3A) mRNA, complete cds
2533	11721	20838	2.39	4.3E-02	AV704878.1	EST_HUMAN	AV704878 ADB Homo sapiens cDNA clone ADBAOH08 5'
3408	12634	21765	8.87	4.3E-02	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C010
3639	12860		1.05	4.3E-02	AF060568.1	NT	Homo sapiens promyelocytic leukemia zinc finger protein (PLZF) gene, complete cds
5256	14428	23505	1.34	4.3E-02	D10006.1	NT	yeast RHO3 gene, complete cds
5874	15082	24504	4.79	4.3E-02	P30427	SWISSPROT	PLECTIN
5874	15082	24505	4.79	4.3E-02	P30427	SWISSPROT	PLECTIN
8544	17568		1.41	4.3E-02	AL139077.2	NT	Campylobacter jejuni NCTC11168 complete genome, segment 4/8
832	10070	19225	2.2	4.2E-02	AU123327.1	EST_HUMAN	AU123327 NT2RM2 Homo sapiens cDNA clone NT2RM2000020 5'
876	10112		2.66	4.2E-02	AU123327.1	EST_HUMAN	AU123327 NT2RM2 Homo sapiens cDNA clone NT2RM2000020 5'
906	10141	18303	0.71	4.2E-02	AW003645.1	EST_HUMAN	wx34g01.x1 NCI_CGAP_Pit1 Homo sapiens cDNA clone IMAGE:2545584 3' similar to TR:Q63291 Q63291 L1 RETROPOSON, ORF2 MRNA ; contains L1.3 L1 L1 repetitive element ;
1695	10907		1.55	4.2E-02	AL445086.1	NT	Thermoplasma acidophilum complete genome, segment 4/5
1748	10960	20142	1.25	4.2E-02	P23091	SWISSPROT	TRANSFORMING PROTEIN MAF
3845	12866	21884	1.56	4.2E-02	P23091	SWISSPROT	TRANSFORMING PROTEIN MAF
4088	13306	22406	1.01	4.2E-02	BE262605.1	EST_HUMAN	601150833F1 NIH_MGC 19 Homo sapiens cDNA clone IMAGE:3503505 5'
4756	13947	23048	0.67	4.2E-02	BF342895.1	EST_HUMAN	602017105F1 NCI_CGAP_Bm64 Homo sapiens cDNA clone IMAGE:4152672 5'
6302	15483	24927	4.36	4.2E-02	AF276752.1	NT	Legionella pneumophila catalase-peroxidase (katA) gene, complete cds
6721	15916	26375	5.82	4.2E-02	P05095	SWISSPROT	ALPHA-ACTININ 3, NON MUSCULAR (F-ACTIN CROSS LINKING PROTEIN)
7855	17045	26582	2.53	4.2E-02	BE815822.1	EST_HUMAN	PM3-BN0174-250500-009-d10 BN0174 Homo sapiens cDNA
7855	17045	26583	2.53	4.2E-02	BE815822.1	EST_HUMAN	PM3-BN0174-250500-009-d10 BN0174 Homo sapiens cDNA
8038	17174	26714	1.97	4.2E-02	AF176458.1	NT	PRRS isolate PRRSV36 envelope glycoprotein gene, complete cds
8851	18301		2.53	4.2E-02	A1883494.1	EST_HUMAN	w449g10.x1 NCI_CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2510850 3'
4488	13686		9.32	4.1E-02	AW893484.1	EST_HUMAN	QV1-NN0012-180400-184-08 NN0012 Homo sapiens cDNA
5152	14331		0.59	4.1E-02	X85880.1	NT	L monocytogenes type 3 partial lap gene (strain 443)
6295	15476	24918	1.84	4.1E-02	7682347	NT	Homo sapiens KIAA0887 protein (KIAA0887), mRNA

Table 4

## Single Exon Probes Expressed in HELA Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6401	15582	25039	2.71	4.1E-02	AF028198.1	NT	Fugu rubripes neural cell adhesion molecule L1 homolog (L1-CAM) gene, complete cds; putative protein 1 (PUT1) gene, partial cds; mitosis-specific chromosome segregation protein SMC1 homolog (SMC1) gene, complete cds; and calcium channel alpha-1 subunit>
9189	18302	23689	23.13	4.1E-02	AJ271908.1	NT	Brassica napus gln gene for plastid glutamine synthetase, exons 1-12
9275	18039	23845	1.3	4.1E-02	AF254822.1	NT	Homo sapiens SMARCA4 isoform (SMARCA4) gene, complete cds, alternatively spliced
3210	12444	21578	3.38	4.0E-02	AB040804.1	NT	Homo sapiens mRNA for KIAA1471 protein, partial cds
3782	13000	22115	0.97	4.0E-02	L11910.1	NT	Human retinoblastoma susceptibility gene exons 1-27, complete cds
5153	14332	23423	0.9	4.0E-02	AB042297.1	NT	Homo sapiens PTS gene for 8-pyruvyltetrahydropterin synthase, complete cds
5385	14814	23727	5.43	4.0E-02	AF280107.1	NT	Homo sapiens cytochrome P450 polypeptide 43 (CYP3A43) gene, partial cds; cytochrome P450 polypeptide 4 (CYP3A4) and cytochrome P450 polypeptide 7 (CYP3A7) genes, complete cds; and cytochrome P450 polypeptide 5 (CYP3A5) gene, partial cds
6372	15552	25009	5.78	4.0E-02	L23838.1	NT	Strongylocentrotus purpuratus homolog of human bone morphogenetic protein 1 (submp) mRNA, complete cds
6687	15882	25341	3.68	4.0E-02	P08640	SWISSPROT	GLUCOAMYLASE SU/S2 PRECURSOR (GLUCAN 1,4-ALPHA-GLUCOSIDASE) (1,4-ALPHA-D-GLUCAN GLUCOHYDROLASE)
8243	17372	23809	1.71	4.0E-02	AJ001018.1	NT	Kluyveromyces fragilis gene for Ca++ ATPase
8461	18114	23809	7.93	4.0E-02	AJ001056.1	NT	Ovis aries mRNA for acetyl-coA carboxylase
1128	10352	19504	4.68	3.9E-02	BF518149.1	EST_HUMAN	UI-HBW1-arg-h-08-0-UI.st1 NC1_CGAP_Sub7 Homo sapiens cDNA clone IMAGE:3084134 3'
1352	10567	19731	1.9	3.9E-02	P41047	SWISSPROT	FAS ANTIGEN LIGAND
1931	11135	20330	2.37	3.9E-02	AJ403366.1	NT	M.musculus DNA for desmin-binding fragment DesD7
2665	11846		1.53	3.9E-02	4506862	NT	Homo sapiens succinate dehydrogenase complex, subunit C, integral membrane protein, 15kD (SDHC) mRNA
5077	14257	23340	1.42	3.9E-02	U61380.1	NT	Bacillus megaterium germination protein (gerAA, gerAC, gerAB) genes, complete cds
5077	14257	23341	1.42	3.9E-02	U61380.1	NT	Bacillus megaterium germination protein (gerAA, gerAC, gerAB) genes, complete cds
5117	14297	23385	0.8	3.9E-02	U92882.1	NT	Mus musculus slow skeletal muscle troponin T (Tnni1) gene, complete cds
5169	14348	23436	1.01	3.9E-02	AW392417.1	EST_HUMAN	RC8-ST0258-171199-021-C09 ST0258 Homo sapiens cDNA
5192	14388	23454	1	3.9E-02	8924019	NT	Homo sapiens hypothetical protein PRO1163 (PRO1163), mRNA
5192	14388	23455	1	3.9E-02	8924019	NT	Homo sapiens hypothetical protein PRO1163 (PRO1163), mRNA
7948	15593	25055	1.69	3.9E-02	P48778	SWISSPROT	ANTIGEN GOR
8317	18258		10.48	3.9E-02	AB042553.1	NT	Felis catus G-CSF gene for granulocyte colony-stimulating factor, complete cds
8998	17857		2.16	3.9E-02	U66061.1	NT	Human germ-line T-cell receptor beta chain TCRBV17S1A1T, TCRBV2S1, TCRBV10S1P, TCRBV28S1P, TCRBV18S1P, TCRBV15S1, TCRBV11S1A1T, HVB relic, TCRBV28S1P, TCRBV34S1, TCRBV14S1, TCRBV3S1, TCRBV4S1A1T, TRY4, TRY5, TRY6, TRY7, TRY8, TCRBD1, TCRBJ1S1, TCRBJ1S2,>

Table 4

## Single Exon Probes Expressed in HELA Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9123	18180		7.38	3.9E-02	AL049888.2	NT	Mus musculus chromosome X contigB; X-linked lymphocyte regulated 5 gene, Zinc finger protein 275, Zinc finger protein 92, mmxq28orf
4896	14084	23177	4.3	3.8E-02	AF000580.1	NT	Dictyostellium discoideum plasmod Ddp5, complete genome
7246	18466	25957	2.32	3.8E-02	AF143952.2	NT	Homo sapiens PELOTA (PELOTA) gene, complete cds
999	10230	19385	6.13	3.7E-02	P19137	SWISSPROT	LAMININ ALPHA-1 CHAIN PRECURSOR (LAMININ A CHAIN)
2203	11400	20825	4.9	3.7E-02	A1984806.1	EST_HUMAN	wf85e08.x1 NCI_CGAP_K1d11 Homo sapiens cDNA clone IMAGE:2494502 3'
3015	12251	21381	1.02	3.7E-02	P78944	SWISSPROT	EMESODERMIN
3017	12253	21382	5.68	3.7E-02	BF312063.1	EST_HUMAN	601896233F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4125584 5'
8358	17450	26941	4.56	3.7E-02	BF124974.1	EST_HUMAN	601782117F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:4024973 5'
9080	18150	23753	12.69	3.7E-02	11418392	NT	Homo sapiens solute carrier family 22 (organic cation transporter), member 1 (SLC22A1), mRNA
3634	12855	21974	0.78	3.6E-02	X73221.1	NT	H. vulgare Ss1 gene for sucrose synthase
3642	12863	21981	0.84	3.6E-02	AL096906.1	NT	Homo sapiens genomic region containing hypervariable minisatellites chromosome 10[10q26.3] of Homo sapiens
5967	15182	24597	4.29	3.6E-02	AW945916.1	EST_HUMAN	CM2-EN0013-110500-192-b-10 EN0013 Homo sapiens cDNA
5967	15182	24598	4.29	3.6E-02	AW945916.1	EST_HUMAN	CM2-EN0013-110500-192-b-10 EN0013 Homo sapiens cDNA
6119	15303	24735	1.68	3.6E-02	AF025952.1	NT	Chromatium vinosum sulfur globule protein Cyt2 precursor (sgp2) gene, complete cds
6209	15390	24834	2.73	3.6E-02	AA714521.1	EST_HUMAN	hw20e05.s1 NCI_CGAP_GCB0 Homo sapiens cDNA clone IMAGE:1241024 3' similar to gb:J00314_mae2
6873	16084	25530	3.35	3.6E-02	U20608.1	NT	TUBULIN BETA-1 CHAIN (HUMAN); Dictyostellium discoideum unknown spore germination-specific protein-like protein, orf1, orf2 and orf3 genes, complete cds
6873	16084	25531	3.35	3.6E-02	U20608.1	NT	Dictyostellium discoideum unknown spore germination-specific protein-like protein, orf1, orf2 and orf3 genes, complete cds
805	10140	19302	1.14	3.5E-02	U09506.1	NT	Drosophila melanogaster tigrin mRNA, complete cds
1016	10245	19397	1.05	3.5E-02	AF253417.1	NT	Homo sapiens microsomal epoxide hydrolase (EPHX1) gene, complete cds
1546	10760	19933	0.91	3.5E-02	BF678085.1	EST_HUMAN	602085136F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4249377 5'
1546	10760	19934	0.91	3.5E-02	BF678085.1	EST_HUMAN	602085136F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4249377 5'
4196	13400	22498	1.84	3.5E-02	AE001773.1	NT	Thermoplasma maritima section 85 of 138 of the complete genome
4306	13507	22603	1.35	3.5E-02	P53780	SWISSPROT	CYSTATHIONINE BETA-LYASE PRECURSOR (CBL) (BETA-CYSTATHIONASE) (CYSTEINE LYASE)
5761	14980	24378	1.69	3.5E-02	J01238.1	NT	Maize actin 1 gene (MAct1), complete cds
6682	15857	25316	3.7	3.5E-02	BE958970.1	EST_HUMAN	601844701R2 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:3829737 3'
8028	17165	26702	1.89	3.5E-02	AW861641.1	EST_HUMAN	PM1-CT0326-291299-002-h03 CT0326 Homo sapiens cDNA
8028	17165	26703	1.89	3.5E-02	AW861641.1	EST_HUMAN	PM1-CT0326-291299-002-h03 CT0326 Homo sapiens cDNA
9054	18193		4.1	3.5E-02	BE276948.1	EST_HUMAN	601178765F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3543833 5'

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
585	8834	18952	1.36	3.4E-02	AK024424.1	NT	Homo sapiens mRNA for FLJ00013 protein, partial cds
585	8834	18953	1.36	3.4E-02	AK024424.1	NT	Homo sapiens mRNA for FLJ00013 protein, partial cds
586	8834	18952	3.54	3.4E-02	AK024424.1	NT	Homo sapiens mRNA for FLJ00013 protein, partial cds
586	8834	18953	3.54	3.4E-02	AK024424.1	NT	Homo sapiens mRNA for FLJ00013 protein, partial cds
1058	10284	19434	4.44	3.4E-02	AW274020.1	EST_HUMAN	x28d07.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2814253 3' similar to SW:C211_HUMAN P53801 PUTATIVE SURFACE GLYCOPROTEIN C21ORF1 PRECURSOR ;
1214	10432		8.37	3.4E-02	11345458	NT	Homo sapiens hypothetical protein FLJ13220 (FLJ13220), mRNA
2355	11548	20769	1.57	3.4E-02	T57160.1	EST_HUMAN	yc20a06.r1 Stratiogene lung (#837210) Homo sapiens cDNA clone IMAGE:81250 5' similar to contains MER29 repetitive element
3409	12635	21768	1.11	3.4E-02	AL163208.2	NT	Homo sapiens chromosome 21 segment HS21C008
3757	12976	22091	0.78	3.4E-02	BE839514.1	EST_HUMAN	RC3-FN0155-080700-011-d10 FN0155 Homo sapiens cDNA
3897	13113	22231	3.91	3.4E-02	AW784952.1	EST_HUMAN	RC6-UM0015-210200-021-A10 UM0015 Homo sapiens cDNA
4588	13792	22883	3.59	3.4E-02	X59799.1	NT	M.musculus S-antigen gene promoter region
5092	14272		2.41	3.4E-02	Q26457	SWISSPROT	LA PROTEIN HOMOLOG (LA RIBONUCLEOPROTEIN) (LA AUTOANTIGEN HOMOLOG)
5108	14288	23373	1.24	3.4E-02	AJ012469.1	NT	Caenorhabditis elegans mRNA for DYS-1 protein, partial
6019	14509	23567	4.27	3.4E-02	U24393.1	NT	Human lysyl oxidase-like protein gene, exon 3
6548	15744		4.73	3.4E-02	A1888629.1	EST_HUMAN	w199d04.x1 NCI_CGAP_Bm25 Homo sapiens cDNA clone IMAGE:2433031 3'
6751	15946						zq04f11.s1 Stratiogene muscle 637209 Homo sapiens cDNA clone IMAGE:628749 3' similar to TR:G1017425 G1017425
377	9843		6.27	3.4E-02	AA194308.1	EST_HUMAN	IPISGKPLPKVTLSDGVPLKATMRFNTEITAEINTLNKESVTADAGRYEITAANSSTTKAFINIWLDPRG ... ;
1175	10396	19548	13.74	3.3E-02	AA398735.1	EST_HUMAN	z175d08.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:728188 3'
1616	10829	20004	15.21	3.3E-02	AB035887.1	NT	Cricetulus griseus CYP2A17 mRNA for cytochrome P450 2A17, complete cds
1712	10924		1.02	3.3E-02	AF110763.1	NT	Homo sapiens skeletal muscle LIM-protein 1 (FHL1) gene, complete cds
2053	11254		1.2	3.3E-02	AE000700.1	NT	Aquifex aeolicus section 32 of 109 of the complete genome
3337	12566	21704	2.44	3.3E-02	R08112.1	EST_HUMAN	y125c09.r1 Soares_fetal_liver_spleen_TNFSL Homo sapiens cDNA clone IMAGE:127888 5'
4158	10829	20004	0.61	3.3E-02	H02389.1	EST_HUMAN	y35h02.r1 Soares_placenta_Nb2HP Homo sapiens cDNA clone IMAGE:150771 5'
4463	13691	22755	1.9	3.3E-02	AF110763.1	NT	Homo sapiens skeletal muscle LIM-protein 1 (FHL1) gene, complete cds
4825	14014	23114	2.12	3.3E-02	6755862	NT	Mus musculus tumor rejection antigen gp98 (Trat), mRNA
5095	14265	23352	0.65	3.3E-02	AW275698.1	EST_HUMAN	xp40004.x1 NCI_CGAP_HN11 Homo sapiens cDNA clone IMAGE:2742789 3'
5843	15060	24469	1	3.3E-02	AW500191.1	EST_HUMAN	U1HF-BNO-alc-q-10-q-U1.r1 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3076785 5'
5843	15060	24469	15.35	3.3E-02	BF245995.1	EST_HUMAN	601853910F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4073787 5'
7681	16880	26387	15.35	3.3E-02	BF245995.1	EST_HUMAN	601853910F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4073787 5'
			4.07	3.3E-02	BF691107.1	EST_HUMAN	602247171F1 NIH_MGC_62 Homo sapiens cDNA clone IMAGE:4332497 5'

Page 98 of 382  
Table 4  
Single Exon Probes Expressed in HELA Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8563	17583		1.52	3.3E-02	T66545.1	EST_HUMAN	ye48f11.1 Soares fetal liver spleen 1NfLS Homo sapiens cDNA clone IMAGE:121101 5'
8691	17659		1.26	3.3E-02	AF289695.1	NT	Mus musculus EIF4H gene, partial cds; LIMK1 gene, complete cds; and ELN gene, partial cds
8722	17675		1.73	3.3E-02	M81890.1	NT	Human interleukin 11 (IL11) gene, complete mRNA
129	9412	18547	2.2	3.2E-02	AJ002005.1	NT	Oryctolagus cuniculus gene encoding ileal sodium-dependent bile acid transporter
1134	10357	19508	26.12	3.2E-02	AF096275.1	NT	Drosophila melanogaster heat shock protein 68 (hsp68) gene, hsp68d allele, complete cds
1134	10357	19509	26.12	3.2E-02	AF096276.1	NT	Drosophila melanogaster heat shock protein 88 (hsp88) gene, hsp88d allele, complete cds
2089	11288		0.9	3.2E-02	P28695	SWISSPROT	LARGE TEGUMENT PROTEIN
3069	12335	21462	13.54	3.2E-02	BE867353.1	EST_HUMAN	601442431F1 NIH_MGC 65 Homo sapiens cDNA clone IMAGE:3846727 5'
3695	12815	22034	1.75	3.2E-02	AL163203.2	NT	Homo sapiens chromosome 21 segment HS21C003
3937	13153	22269	0.66	3.2E-02	Z74103.1	NT	S. cerevisiae chromosome IV reading frame ORF YDL055c
3937	13153	22270	0.66	3.2E-02	Z74103.1	NT	S. cerevisiae chromosome IV reading frame ORF YDL055c
4202	13405		18.44	3.2E-02	X94768.1	NT	H. sapiens RP3 gene (XLRP gene 3)
4778	13967	23069	3.67	3.2E-02	AF114182.1	NT	Saxifraga nidifica maturase (matK) gene, chloroplast gene encoding chloroplast protein, partial cds
4844	14033	23125	4.95	3.2E-02	AF067083.1	NT	Vitreoscilla sp. outer membrane protein homolog gene, complete cds; Trp repressor binding protein gene, partial cds; and unknown genes
5460	14686	24036	1.85	3.2E-02	X68709.1	NT	S. griseocaneum whiG-Stv gene
5460	14686	24037	1.85	3.2E-02	X68709.1	NT	S. griseocaneum whiG-Stv gene
5888	15105	24516	2.33	3.2E-02	M32437.1	NT	Rat/polyomavirus left junction in cell line W98.14
5889	15106		30.79	3.2E-02	T89367.1	EST_HUMAN	y433h12.s1 Soares fetal liver spleen 1NfLS Homo sapiens cDNA clone IMAGE:110087 3' similar to contains
5936	15154	24565	3.94	3.2E-02	AF173845.1	NT	Alu repetitive element/contains LTR1 repetitive element;
6560	15756	25219	4.07	3.2E-02	6680565	NT	Seguinus oedipus tissue kallikrein gene, complete cds
7092	16299		2.68	3.2E-02	AA719795.1	EST_HUMAN	Mus musculus kinase family member 3c (KIF3c), mRNA
1267	10482		1.86	3.1E-02	4503416	NT	gbL08441 CYTOCHROME C OXIDASE POLYPEPTIDE III (HUMAN);
1312	10528	19689	2.11	3.1E-02	P18845	SWISSPROT	Homo sapiens dual specificity phosphatase 4 (DUSP4) mRNA
1867	11084	20255	0.94	3.1E-02	6671564	NT	NEURONAL ACETYLCHOLINE RECEPTOR PROTEIN ALPHA-3 CHAIN PRECURSOR (GF-ALPHA-3)
5373	14602		2.56	3.1E-02	AA278478.1	EST_HUMAN	Mus musculus adaptor-related protein complex AP-3, delta subunit (Ap3d), mRNA
1600	10814		1.73	3.0E-02	AF187125.1	NT	zs81406.r1 NCL CGAP_GCB1 Homo sapiens cDNA clone IMAGE:703853 5'
3541	12764	21895	1.22	3.0E-02	M94176.1	NT	Pitykites minutus cytochrome oxidase I gene, partial cds; mitochondrial gene for mitochondrial product
3633	12854	21973	2.79	3.0E-02	AF247644.1	NT	Seccharomyces cerevisiae stem-loop mutation suppressor SSL2 gene, complete cds
3726	12945		0.62	3.0E-02	AW820223.1	EST_HUMAN	Pseudomonas fluorescens family II aminotransferase gene, complete cds
							QV2-ST0298-150200-040-609 ST0298 Homo sapiens cDNA

Page 99 of 382  
Table 4  
Single Exon Probes Expressed in HELA Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3924	13140		0.89	3.0E-02	AA364003.1	EST_HUMAN	EST74530 Pitneal gland II Homo sapiens cDNA 5' end
4701	13892		38.75	3.0E-02	AI240487.1	EST_HUMAN	qh10g06.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1844314 3'
5083	14283	23348	7.54	3.0E-02	AF281074.1	NT	Homo sapiens neuropilin 2 (NRP2) gene, complete cds, alternatively spliced
5083	14283	23349	7.54	3.0E-02	AF281074.1	NT	Homo sapiens neuropilin 2 (NRP2) gene, complete cds, alternatively spliced
5393	14922		3.03	3.0E-02	AB046783.1	NT	Homo sapiens mRNA for KIAA1573 protein, partial cds
5993	15278	24706	3.37	3.0E-02	AJ242906.1	NT	Cyprinus carpio mRNA for inducible nitric oxide synthase (iNOS) gene
6044	15212	24631	3.32	3.0E-02	BE888948.1	EST_HUMAN	601512206F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3913848 5'
6044	15212	24632	3.32	3.0E-02	BE888948.1	EST_HUMAN	601512206F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3913848 5'
6114	15208	24627	1.95	3.0E-02	AF213884.1	NT	Homo sapiens nuclear factor of kappa light polypeptide gene enhancer in B-cells 1 (NFKB1) gene, complete cds
6114	15208	24628	1.95	3.0E-02	AF213884.1	NT	Homo sapiens nuclear factor of kappa light polypeptide gene enhancer in B-cells 1 (NFKB1) gene, complete cds
7203	16380	25861	2.8	3.0E-02	AE001797.1	NT	Thermotoga maritima section 109 of 136 of the complete genome
7784	16978	26492	3.51	3.0E-02	M81357.1	NT	Human coagulation factor VII (F7) gene exon 1 and factor X (F10) gene, exon 1
8187	17319	26862	9.3	3.0E-02	AA48216.1	EST_HUMAN	ne87804.s1 NC1_CGAP_Kid1 Homo sapiens cDNA clone IMAGE:911263
8873	18351	23607	1.99	3.0E-02	R32019.1	EST_HUMAN	YH63d04.s1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:134407 3'
9044	17885		7.15	3.0E-02	AW895565.1	EST_HUMAN	QV4-NN0038-270400-187-H05 NN0038 Homo sapiens cDNA
9085	18345		3.1	3.0E-02	AF048887.1	NT	Rattus norvegicus UDP-Galglucosylceramide beta-1,4-galactosyltransferase mRNA, complete cds
2949	12187	21320	0.92	2.9E-02	BE565844.1	EST_HUMAN	601338428F1 NIH_MGC_53 Homo sapiens cDNA clone IMAGE:3680695 5'
2949	12187	21321	0.92	2.9E-02	BE565844.1	EST_HUMAN	601338428F1 NIH_MGC_53 Homo sapiens cDNA clone IMAGE:3680695 5'
3903	13119	22237	0.79	2.9E-02	HY2805.1	EST_HUMAN	y007e10.r1 Soares fetal liver spleen 1NFSL Homo sapiens cDNA clone IMAGE:233130 5'
6782	15000	24403	6.95	2.9E-02	BF032233.1	EST_HUMAN	601452661F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3856598 5'
6184	15386	24806	10.62	2.9E-02	BE271437.1	EST_HUMAN	601140728F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3049830 5'
572	9822		0.7	2.8E-02	AW970153.1	EST_HUMAN	EST382234 IMAGE resequences, MAGK Homo sapiens cDNA
3345	12573	21712	1.21	2.8E-02	AF066063.1	NT	Homo sapiens retinal fascic (FSCN2) gene, exon 2
3345	12573	21713	1.21	2.8E-02	AF066063.1	NT	Homo sapiens retinal fascic (FSCN2) gene, exon 2
5435	14682	23815	11.9	2.8E-02	BE741083.1	EST_HUMAN	601594078F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3949087 5'
8977	17846		1.33	2.8E-02	X06322.1	NT	Yeast CN31C chromosome III RAHS DNA (right arm transcription hot-spot)
3410	12836	21767	2.05	2.7E-02	AL161494.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 6
4184	13388	22486	1.81	2.7E-02	N47258.1	EST_HUMAN	y86h12.r1 Soares multiple sclerosis_2NBHMSHP Homo sapiens cDNA clone IMAGE:280487 5'
4184	13388	22487	1.81	2.7E-02	N47258.1	EST_HUMAN	y86h12.r1 Soares multiple sclerosis_2NBHMSHP Homo sapiens cDNA clone IMAGE:280487 5'
6112	15206	24625	1.94	2.7E-02	AA993571.1	EST_HUMAN	cd89h03.s1 Soares_total_fetus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:1624861 3'
578	9827	18948	0.91	2.6E-02	AL163282.2	NT	Homo sapiens chromosome 21 segment HS21C082



Table 4

## Single Exon Probes Expressed in HELA Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2334	11527	20748	2.34	2.6E-02	AA490021.1	EST_HUMAN	ab02b02.s1 Strategene fetal retina 937202 Homo sapiens cDNA clone IMAGE:839595 3'
2338	11529	20750	2.19	2.6E-02	6754241	NT	Mus musculus histidine rich calcium binding protein (Hrc), mRNA
2339	11529	20751	2.19	2.6E-02	6754241	NT	Mus musculus histidine rich calcium binding protein (Hrc), mRNA
2868	12104		1.22	2.6E-02	AF109006.1	NT	Mus musculus MHC class III region RD gene, partial cds; Bf, C2, G9A, NG22, G9, HSP70, HSP70, HSC70, and snRNP genes, complete cds; G7A gene, partial cds; and unknown genes
3917	13133		10.04	2.6E-02	AA071307.1	EST_HUMAN	zmn73109.s1 Strategene neuroepithelium (#937231) Homo sapiens cDNA clone IMAGE:531305 3'
4278	13481		1.53	2.6E-02	Y07848.1	NT	Homo sapiens EWS, gar22, rrp22 and bant22 genes
4828	14114	23209	3.97	2.6E-02	L12032.1	NT	Chicken dorsalin-1 mRNA, complete cds
5098	14278	23362	1.62	2.6E-02	AE002014.1	NT	Deinococcus radiodurans R1 section 151 of 229 of the complete chromosome 1
5124	14303	23392	1.87	2.6E-02	AW241154.1	EST_HUMAN	xa52b04.x1 NCL CGAP_Sar4 Homo sapiens cDNA clone IMAGE:2570383 3' similar to SW:Y069_HUMAN Q15041 HYPOTHETICAL PROTEIN KIAA0069 ;
5278	14449	23522	0.83	2.6E-02	AE000825.1	NT	Methanobacterium thermoautotrophicum from bases 340940 to 352162 (section 31 of 148) of the complete genome
5759	14978		6.88	2.6E-02	AI206030.1	EST_HUMAN	qg27f11.x1 NCL CGAP_Kid3 Homo sapiens cDNA clone IMAGE:1762317 3'
5839	15056	24463	2.12	2.6E-02	BE621748.1	EST_HUMAN	6014934731 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3895578 3'
6047	15215	24635	6.57	2.6E-02	6981271	NT	Rattus norvegicus Nerve growth factor receptor, fast (Ngfr), mRNA
7928	17139		2.09	2.6E-02	AA279351.1	EST_HUMAN	zs84c02.r1 NCL CGAP_GCB1 Homo sapiens cDNA clone IMAGE:704162 5'
8097	17231	26770	1.78	2.6E-02	AW500547.1	EST_HUMAN	U1-HF-BNO-ek-e-10-0-U1.r1 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3077466 5'
8595	18338	23604	1.41	2.6E-02	BF343827.1	EST_HUMAN	602015501F1 NCL CGAP_Bm84 Homo sapiens cDNA clone IMAGE:1557827 5'
538	9789	18912	1.61	2.5E-02	AI793130.1	EST_HUMAN	on26f06.y5 NCL CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1557827 5'
538	9789	18913	1.61	2.5E-02	AI793130.1	EST_HUMAN	on26f06.y5 NCL CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1557827 5'
819	10057	19210	20.77	2.5E-02	BE974314.1	EST_HUMAN	601680305R2 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:3950685 3'
879	10115	19277	6.14	2.5E-02	BE974314.1	EST_HUMAN	601680305R2 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:3950685 3'
2718	11897		2.76	2.5E-02	U12571.1	NT	Rattus norvegicus rabphilin-3A mRNA, complete cds
2808	12147	21281	3.33	2.5E-02	X96897.1	NT	H. carterae mRNA for fucoxanthin chlorophyll a/c binding protein, Fcp1
2808	12147	21282	3.33	2.5E-02	X96897.1	NT	H. carterae mRNA for fucoxanthin chlorophyll a/c binding protein, Fcp1
4022	14468	22337	0.86	2.5E-02	BE701165.1	EST_HUMAN	PM2-NN0128-080700-001-e12 NN0128 Homo sapiens cDNA
4022	14468	22338	0.86	2.5E-02	BE701165.1	EST_HUMAN	PM2-NN0128-080700-001-e12 NN0128 Homo sapiens cDNA
4188	13392	22490	5.68	2.5E-02	AW592114.1	EST_HUMAN	h330f08.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2834015 3'
							7e30e09.x1 NCL CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3284008 3' similar to contains L1.11 L1 repetitive element ;
5751	14970		4.59	2.5E-02	BE670126.1	EST_HUMAN	601578393F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3928054 5'
5756	14975		4.28	2.5E-02	BE748888.1	EST_HUMAN	601578393F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3928054 5'
7387	16601	26089	2.37	2.5E-02	Q10335	SWISSPROT	HYPOTHETICAL 48.7 KD PROTEIN C19G10.05 IN CHROMOSOME 1
7387	16601	26090	2.37	2.5E-02	Q10335	SWISSPROT	HYPOTHETICAL 48.7 KD PROTEIN C19G10.05 IN CHROMOSOME 1

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7458	16668		4.1	2.5E-02	AF050157.1	NT	Mus musculus major histocompatibility locus class II region: major histocompatibility protein class II alpha chain (IiAlpha) and major histocompatibility protein class II beta chain (IiBeta) genes, complete cds; butyrophilin-like (NG9), butyrophilin-Ii>
8238	17367		2.11	2.5E-02	AB007546.1	NT	Homo sapiens gene for LECT2, complete cds
8552	18271		1.92	2.5E-02	11420078	NT	Homo sapiens similar to ALEX3 protein (H. sapiens) (LOC363634), mRNA
8747	18138		2.01	2.5E-02	11433220	NT	Homo sapiens mitogen-activated protein kinase kinase MkcA (mkcA) gene, complete cds
8842	17751		1.29	2.5E-02	U00169.1	NT	Dicotyledonum discoidium putative protein kinase MkcA (mkcA) gene, complete cds
8869	17768	23939	1.38	2.5E-02	BE973327.1	EST_HUMAN	801852365R2 NIH_MGC 82 Homo sapiens cDNA clone IMAGE:3935513 3'
177	9457	18590	0.62	2.4E-02	A1378582.1	EST_HUMAN	ic72c07.x1 Soares NIHMPu_S1 Homo sapiens cDNA clone IMAGE:2070156 3'
1578	10791	19987	1.76	2.4E-02	H65884.1	EST_HUMAN	y75f11.r1 Soares fetal liver spleen 1NfLS Homo sapiens cDNA clone IMAGE:211149 5'
2011	12008	20423	1.44	2.4E-02	P01901	SWISSPROT	H-2 CLASS I HISTOCOMPATIBILITY ANTIGEN, K-B ALPHA CHAIN PRECURSOR (H-2K(B))
2011	12008	20424	1.44	2.4E-02	P01901	SWISSPROT	H-2 CLASS I HISTOCOMPATIBILITY ANTIGEN, K-B ALPHA CHAIN PRECURSOR (H-2K(B))
4362	13564	22659	1.72	2.4E-02	J05110.1	NT	T. thermophila calcium-binding 25 kDa (TCBP 25) protein mRNA, complete cds
4521	13717	22811	1.22	2.4E-02	P01901	SWISSPROT	H-2 CLASS I HISTOCOMPATIBILITY ANTIGEN, K-B ALPHA CHAIN PRECURSOR (H-2K(B))
4521	13717	22812	1.22	2.4E-02	P01901	SWISSPROT	H-2 CLASS I HISTOCOMPATIBILITY ANTIGEN, K-B ALPHA CHAIN PRECURSOR (H-2K(B))
5204	14378		1.01	2.4E-02	AL161595.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 91
5286	14457		0.63	2.4E-02	U18466.1	NT	African swine fever virus, complete genome
6630	15826	25288	17.19	2.4E-02	N69442.1	EST_HUMAN	z35g11.s1 Soares fetal liver spleen 1NfLS Homo sapiens cDNA clone IMAGE:284596 3' similar to gb K02809 RATSR7K Rat (RNA); contains A3R.b1 A3R repetitive element ;
7014	16191	25685	3.55	2.4E-02	AV592954.1	EST_HUMAN	AV682854 GK6 Homo sapiens cDNA clone GKCDSC03 5'
7067	16244	25718	4.02	2.4E-02	AA493894.1	EST_HUMAN	rh07b12.s1 NCI_CGAP_Thy1 Homo sapiens cDNA clone IMAGE:843583 similar to contains Alu repetitive element; contains element PTR5 repetitive element ;
8106	17240	28778	2.22	2.4E-02	AF109905.1	NT	Mus musculus major histocompatibility locus class III regions Hsc70i gene, partial cds; smRNP, G7A, NG23, MuS homolog, CLCP, NG24, NG25, and NG28 genes, complete cds; and unknown genes
8106	17240	28779	2.22	2.4E-02	AF109905.1	NT	Mus musculus major histocompatibility locus class III regions Hsc70i gene, partial cds; smRNP, G7A, NG23, MuS homolog, CLCP, NG24, NG25, and NG28 genes, complete cds; and unknown genes
8341	17438		1.8	2.4E-02	9627808	NT	Bacteriophage b1.67, complete genome
8465	17538	24028	2.66	2.4E-02	6753635	NT	Mus musculus DinB homolog 1 (E. coli) (DinB1), mRNA
8554	17576	23965	1.58	2.4E-02	BE928869.1	EST_HUMAN	MR0-FT0175-310800-202-a08 FT0175 Homo sapiens cDNA
8611	17608	23963	1.27	2.4E-02	U78187.1	NT	Rattus norvegicus cAMP-regulated guanine nucleotide exchange factor 1 (cAMP-GEF1) mRNA, complete cds

Page 102 of 382  
Table 4  
Single Exon Probes Expressed in HELA Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8811	17608	24007	1.27	2.4E-02	U78167.1	NT	Rattus norvegicus cAMP-regulated guanine nucleotide exchange factor 1 (cAMP-GEFI) mRNA, complete cds
8793	17720		6.39	2.4E-02	AB008589.1	NT	Caenorhabditis elegans mRNA for iron-sulfur subunit of mitochondrial succinate dehydrogenase, complete cds
8820	17737		1.23	2.4E-02	N42880.1	EST_HUMAN	908a08.r1 Soares melanocyte 2NbHM Homo sapiens cDNA clone IMAGE:270610 5'
8826	17740		1.35	2.4E-02	BF679477.1	EST_HUMAN	602153281F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4284173 5'
9282	18378		1.22	2.4E-02	S58644.1	NT	Integrin beta 5 subunit [rats, NPK cells, mRNA Partial, 603 nt]
1838	11046		6.31	2.3E-02	W05340.1	EST_HUMAN	2a84g08.r1 Soares_fetal_lung_NbHL19W Homo sapiens cDNA clone IMAGE:288294 5'
1852	11059		6.86	2.3E-02	U94165.1	NT	4 Homo sapiens mammary tumor-associated protein INT6 (INT6) gene, exon 4
1977	11180	20388	1.04	2.3E-02	AW787355.1	EST_HUMAN	CM2-UM0038-280400-172-b11 UM0038 Homo sapiens cDNA
2319	11512	20733	2.33	2.3E-02	Z14293.1	NT	S.cerevisiae chromosome IV reading frame ORF YDL245c
3662	12883	22004	7.23	2.3E-02	Z20377.1	EST_HUMAN	HSAAACADH P, Human fetal Brain Whole tissue Homo sapiens cDNA
3698	12616		0.84	2.3E-02	L23429.1	NT	Canis beta-galactosides-binding lectin (LGALS3) mRNA, 3'end
4131	13337	22436	0.87	2.3E-02	L24789.1	NT	Gallus gallus connexin 45.6 (Cx45.6) gene, complete cds
4131	13337	22437	0.87	2.3E-02	L24789.1	NT	Gallus gallus connexin 45.6 (Cx45.6) gene, complete cds
4412	13612	22708	1.19	2.3E-02	AW699107.1	EST_HUMAN	CM4-NN0080-280400-160-b04 NN0080 Homo sapiens cDNA
4443	13643	22735	1.17	2.3E-02	BE935225.1	EST_HUMAN	CM3-MT0118-010800-318-g07 MT0118 Homo sapiens cDNA
4443	13643	22736	1.17	2.3E-02	BE935225.1	EST_HUMAN	CM3-MT0118-010800-318-g07 MT0118 Homo sapiens cDNA
4444	14470	22737	1.01	2.3E-02	AW693693.1	EST_HUMAN	xs25d08.x1 NCI_CGAP_U02 Homo sapiens cDNA clone IMAGE:2770871 3'
4444	14470	22738	1.01	2.3E-02	AW693693.1	EST_HUMAN	xs25d08.x1 NCI_CGAP_U02 Homo sapiens cDNA clone IMAGE:2770871 3'
4594	13788	22880	2.54	2.3E-02	BF026487.1	EST_HUMAN	8016727279F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3955388 5'
4594	13788	22881	2.54	2.3E-02	BF026487.1	EST_HUMAN	8016727279F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3955388 5'
5043	14227		1.06	2.3E-02	7682173	NT	Homo sapiens KIAA0547 gene product (KIAA0547), mRNA
5183	14359	23444	0.65	2.3E-02	AF257110.1	NT	Rattus norvegicus guanine nucleotide binding protein gamma subunit 11 mRNA, complete cds
5183	14359	23445	0.65	2.3E-02	AF257110.1	NT	Rattus norvegicus guanine nucleotide binding protein gamma subunit 11 mRNA, complete cds
5193	14369	23456	0.82	2.3E-02	AE000775.1	NT	Aquifex aeolicus section 107 of 108 of the complete genome
5383	14612	23725	3.87	2.3E-02	U86303.1	NT	Caulobacter crescentus topoisomerase IV ParE subunit (parE) gene, complete cds, and propionyl-CoA
5942	15158	24570	4.97	2.3E-02	AL161505.2	NT	carboxylase beta chain (pccB) homolog gene, partial cds
6419	15616	25079	6.05	2.3E-02	U83610.1	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 17
7085	16262	25739	2.2	2.3E-02	AE000198.1	NT	Human plectin (PLEC1) gene, exons 3-32, and complete cds
7085	16262	25740	2.2	2.3E-02	AE000198.1	NT	Escherichia coli K-12 MG1655 section 89 of 400 of the complete genome
7085	16262	25740	2.2	2.3E-02	AE000198.1	NT	Escherichia coli K-12 MG1655 section 89 of 400 of the complete genome
7363	16579	26070	2.17	2.3E-02	P08640	SWISSPROT	GLUCOAMYLASE S1/S2 PRECURSOR (GLUCAN 1,4-ALPHA-GLUCOSIDASE) (1,4-ALPHA-D-GLUCAN GLUCOHYDROLASE)

Table 4

## Single Exon Probes Expressed in HELA Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8468	18123		5.76	2.3E-02	BE278331.1	EST_HUMAN	601179859F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3546567 5'
9014	17868	23890	2.12	2.3E-02	U39394.1	NT	Streptomyces sp. alpha-1,3/4-fucosidase precursor gene, complete cds
9072	18378		1.87	2.3E-02	U11077.1	NT	Dictyostelium discoideum extracellular signal-regulated protein kinase (ERK1) mRNA, complete cds
745	8986	19129	3.5	2.2E-02	AF018287.1	NT	Columba livia nucleoside diphosphate kinase (NDPK) gene, nuclear gene encoding mitochondrial protein, complete cds
1719	10831		1.51	2.2E-02	4557448	NT	Homo sapiens chromodomain helicase DNA binding protein 2 (CHD2) mRNA
1882	11185	20394	1.57	2.2E-02	Z82001.1	NT	S. pneumoniae pcpA gene and open reading frames
2885	12024	21079	1.84	2.2E-02	AF109633.1	NT	Mus musculus ets variant protein ERB1 gene, exons 1 through 4
3413	12839		1.8	2.2E-02	AA577785.1	EST_HUMAN	nm24e04.s1 NCI_CGAP_Gas1 Homo sapiens cDNA clone IMAGE:1084782 3'
3825	12848		3.43	2.2E-02	AF083094.1	NT	Infectious bursal disease virus segment B strain IL4 VP1 gene, complete cds
3896	13112	22230	0.63	2.2E-02	Z74283.1	NT	S. cerevisiae chromosome IV reading frame ORF YDL245c
5099	14279	23363	1.65	2.2E-02	Z73597.1	NT	S. cerevisiae chromosome XVI reading frame ORF YPL241c
6183	15365	24805	3.57	2.2E-02	AV698721.1	EST_HUMAN	AV698721 GKB Homo sapiens cDNA clone GKBAND03 3'
7758	18954	26462	1.7	2.2E-02	BE797601.1	EST_HUMAN	601584309F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3938571 5'
8750	17683		2.64	2.2E-02	AA503553.1	EST_HUMAN	ne47h07.s1 NCI_CGAP_Co3 Homo sapiens cDNA clone IMAGE:900541 3' similar to contains Alu repetitive element
425	9678		5.24	2.1E-02	AV761502.1	EST_HUMAN	AV761502 MDS Homo sapiens cDNA clone MDSADG01 5'
455	9708		8.19	2.1E-02	AF029726.1	NT	Dictyostelium discoideum histidine kinase C (dhkC) mRNA, complete cds
1270	10485	19644	6.21	2.1E-02	U72073.1	NT	Bacillus subtilis cotKLM cluster, CotK (cotK), CotL (cotL), and spore coat protein CotM (cotM) genes, complete cds
1752	10994	20147	0.89	2.1E-02	P02438	SWISSPROT	KERATIN, HIGH-SULFUR MATRIX PROTEIN, B2A
1752	10864	20148	0.89	2.1E-02	P02438	SWISSPROT	KERATIN, HIGH-SULFUR MATRIX PROTEIN, B2A
1752	10964	20149	0.89	2.1E-02	P02438	SWISSPROT	KERATIN, HIGH-SULFUR MATRIX PROTEIN, B2A
2768	10028	19177	3.47	2.1E-02	N29268.1	EST_HUMAN	y43h07.t1 Soares melanocyte 2N6HM Homo sapiens cDNA clone IMAGE:264541 5'
3560	12783	21912	1.05	2.1E-02	AA461271.1	EST_HUMAN	z63b09.r1 Soares_t0tal_fetus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:796121 5'
4113	13320	22420	0.64	2.1E-02	Z74283.1	NT	S. cerevisiae chromosome IV reading frame ORF YDL245c
4297	13498	22594	0.77	2.1E-02	BF343655.1	EST_HUMAN	602015306F1 NCI_CGAP_Bm64 Homo sapiens cDNA clone IMAGE:4151161 5'
4437	13637	22730	1.76	2.1E-02	U44914.1	NT	Borrelia burgdorferi plasmid cp32-2, erpC and erpD genes, complete cds, and unknown genes
4448	13648	22744	1.73	2.1E-02	A198127.1	EST_HUMAN	wg81d11.x1 Soares_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:2371509 3'
4497	13695		0.63	2.1E-02	Y19213.1	NT	Homo sapiens putative psihHbA pseudogene for hair keratin, exons 2 to 7
4681	13696		1.31	2.1E-02	Y19213.1	NT	Homo sapiens putative psihHbA pseudogene for hair keratin, exons 2 to 7
4720	13911	23013	5.72	2.1E-02	Y08501.1	NT	A.thaliana mitochondrial genome, part A
4741	13932	23036	0.63	2.1E-02	AA685737.1	EST_HUMAN	ag55g12.s1 Gessler Wilms tumor Homo sapiens cDNA clone IMAGE:1126918 3'

Table 4

## Single Exon Probes Expressed in HELA Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4834	14023	23117	0.62	2.1E-02	AB23432.1	EST_HUMAN	wh54e05.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2384528 3'
8731	13695		8.84	2.1E-02	Y19213.1	NT	Homo sapiens putative psilHbA pseudogene for hair keratin, exons 2 to 7
9173	17966	23856	3.85	2.1E-02	AF183913.1	NT	Azospirillum brasilense major outer membrane protein OmsA precursor (omsA) gene, complete cds
9288	18044		2.59	2.1E-02	BF093512.1	EST_HUMAN	CM1-TN0141-140900-407-H08 TN0141 Homo sapiens cDNA
18	9314	18416	0.85	2.0E-02	BF002932.1	EST_HUMAN	7g51c08.x1 NCI_CGAP_P128 Homo sapiens cDNA clone IMAGE:3308998 3' similar to contains MER1.13
19	9315	18417	0.16	2.0E-02	AW895565.1	EST_HUMAN	MER1 repetitive element;
263	8539	18668	2.99	2.0E-02	6753635	NT	QV4-NN0038-270400-187-H05 NN0038 Homo sapiens cDNA
300	8573	18706	2.59	2.0E-02	AA456538.1	EST_HUMAN	Mus musculus DnB homolog 1 (E. coli) (DnB1), mRNA
808	10047	19198	2.09	2.0E-02	6753635	NT	aa15b10.r1 Soares NIHMPu_S1 Homo sapiens cDNA clone IMAGE:813307 5'
1095	10319	19471	0.88	2.0E-02	AL068805.1	NT	Mus musculus DnB homolog 1 (E. coli) (DnB1), mRNA
1207	10426	19582	1.71	2.0E-02	8922391	NT	Homo sapiens genomic region containing hypervariable minisatellites chromosome 1 [1p36.33] of Homo sapiens
1207	10428	19583	1.71	2.0E-02	8922391	NT	Homo sapiens hypothetical protein FLJ10379 (FLJ10379), mRNA
1839	11047	20236	1.93	2.0E-02	8922453	NT	Homo sapiens hypothetical protein FLJ10379 (FLJ10379), mRNA
1839	11047	20237	1.93	2.0E-02	8922453	NT	Homo sapiens hypothetical protein FLJ10486 (FLJ10486), mRNA
2751	11630		1.84	2.0E-02	AL161532.2	NT	Homo sapiens hypothetical protein FLJ10486 (FLJ10486), mRNA
3044	9314	18416	1.58	2.0E-02	BF002932.1	EST_HUMAN	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 32
3109	12344		2.29	2.0E-02	7305474	NT	7g51c08.x1 NCI_CGAP_P128 Homo sapiens cDNA clone IMAGE:3308998 3' similar to contains MER1.13
3183	12428		1.67	2.0E-02	AF095588.1	NT	MER1 repetitive element;
3683	13197	22305	1.53	2.0E-02	MA18095.1	NT	Mus musculus sema domain, transmembrane domain (TM), and cytoplasmic domain, (semaphorin) 68
7031	16208		2.37	2.0E-02	U70408.1	NT	(Sem6b), mRNA
7236	16437	25945	2.06	2.0E-02	Z73966.1	NT	Arabidopsis thaliana C2H2 zinc finger protein FZF mRNA, complete cds
7911	17126	26656	3.17	2.0E-02	D88184.1	NT	P. vulgaris hydroxyproline-rich glycoprotein (HRGP) mRNA, 3' end
8281	14502	23587	1.4	2.0E-02	AA456538.1	EST_HUMAN	Japanese encephalitis virus envelope protein mRNA, partial cds
8769	11930		1.55	2.0E-02	AL161532.2	NT	Mycobacterium tuberculosis H37Rv complete genome; segment 93/182
9247	18146		1.53	2.0E-02	BE786595.1	EST_HUMAN	Equus caballus DNA for 17alpha-hydroxylase/17,20-lyase, complete cds
9254	18022		5.01	2.0E-02	T80037.1	EST_HUMAN	aa15b10.r1 Soares NIHMPu_S1 Homo sapiens cDNA clone IMAGE:813307 5'
700	9942	18076	2.49	1.9E-02	AA572764.1	EST_HUMAN	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 32
2008	11209	20418	2.75	1.9E-02	AL163303.2	NT	601478819F1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3881477 5'
							y04c09.r1 Soares Infant brain 1N1B Homo sapiens cDNA clone IMAGE:24675 5'
							nf18a07.s1 NCI_CGAP_P11 Homo sapiens cDNA clone IMAGE:914186 similar to contains L1.11 L1
							repetitive element;
							Homo sapiens chromosome 21 segment HS21C103

Table 4  
Single Exon Probes Expressed in HELA Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2006	11209	20419	2.75	1.8E-02	AL163303.2	NT	Homo sapiens chromosome 21 segment HS21C103
2471	11662	20882	1.22	1.8E-02	AL161550.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 50
2857	12095	21224	8.45	1.8E-02	AA713856.1	EST_HUMAN	nm004f05.s1 NCI CGAP_SS1 Homo sapiens cDNA clone IMAGE:1238337 3'
2905	12143	21278	1.71	1.8E-02	AV648689.1	EST_HUMAN	AV648689 GLC Homo sapiens cDNA clone GLCBLH07 3'
3228	12460		0.63	1.8E-02	AB033611.1	NT	Utricularia latipalpis mitochondrial gene for cytochrome b, complete cds
3589	12810		1.06	1.8E-02	NS2250.1	EST_HUMAN	y228b02.s1 Soares multiple_sclerosis_2NbrMSP Homo sapiens cDNA clone IMAGE:284331 3'
3683	12804		8.88	1.8E-02	BE738088.1	EST_HUMAN	601672882F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:3839564 5'
4024	13235	22340	1.34	1.8E-02	AF141940.1	NT	Mycoplasma imitans VihA1 precursor (VihA1) and VihA2 precursor (VihA2) genes, partial cds
4175	13378	22479	1.56	1.8E-02	P08081	SWISSPROT	HOMEOTIC BICOID PROTEIN (PRD-4)
4175	13379	22480	1.56	1.8E-02	P08081	SWISSPROT	HOMEOTIC BICOID PROTEIN (PRD-4)
4538	13733	22831	3.05	1.8E-02	AI452999.1	EST_HUMAN	ly46d04.x1 Soares NSF_F8_gw_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:2144551 3' similar to contains Alu repetitive element;
5037	11662	20882	5.49	1.8E-02	AL161550.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 50
8505	18128	23813	3.08	1.8E-02	AF101085.1	NT	Hirudo medicinalis intermediate filament glicrin mRNA, complete cds
9203	17688	23882	1.48	1.8E-02	X68271.1	NT	H. sapiens MUC18 gene exon 18
351	8619	18746	1.42	1.8E-02	AW771104.1	EST_HUMAN	hm52c06.x1 NCI CGAP_Co17 Homo sapiens cDNA clone IMAGE:3027274 3' similar to contains element
692	8635	19065	0.65	1.8E-02	BF308122.1	EST_HUMAN	MER28 repetitive element;
1188	10369	19541	1.27	1.8E-02	X17664.1	NT	601894329F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4139983 5'
2638	11821	21037	1	1.8E-02	AE004544.1	NT	H. francisci mRNA for myelin basic protein (MBP)
3177	12412		0.78	1.8E-02	AB05828.1	EST_HUMAN	Pseudomonas aeruginosa PA01, section 105 of 529 of the complete genome
3866	13082	22198	1.11	1.8E-02	AW878122.1	EST_HUMAN	le52a09.x1 Soares NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2090286 3'
3866	13082	22199	1.11	1.8E-02	AW878122.1	EST_HUMAN	MR1-OT0011-280300-009-g04 OT0011 Homo sapiens cDNA
4062	13273		1.4	1.8E-02	AA861446.1	EST_HUMAN	MR1-OT0011-280300-009-g04 OT0011 Homo sapiens cDNA
4422	13622	22717	1.36	1.8E-02	AW636363.1	EST_HUMAN	ak24h04.s1 Soares testis_NHT Homo sapiens cDNA clone IMAGE:1406835 3'
4975	14162	23253	1.18	1.8E-02	O60810	SWISSPROT	QV4-DT0021-301289-071-b11 DT0021 Homo sapiens cDNA
6001	15283	24716	4.21	1.8E-02	P14310	SWISSPROT	HYPOTHETICAL PROTEIN DJ845024.2
7074	16409	25894	1.87	1.8E-02	AB002337.2	NT	HYPOTHETICAL 7.9 KD PROTEIN IN FIXW 5'REGION
7974	16409	25895	1.87	1.8E-02	AB002337.2	NT	Homo sapiens mRNA for KIAA0339 protein, partial cds
8136	17269	26814	1.92	1.8E-02	AF000006.1	NT	Homo sapiens mRNA for KIAA0339 protein, partial cds
8145	17277	26821	3.39	1.8E-02	U62749.1	NT	Pyrococcus horikoshii OT3 genomic DNA, 1166001-1485000 nt. position (8/7)
9230	18102		1.25	1.8E-02	AF047475.1	NT	Zea mays acidic ribosomal protein P2a-3 (pp2a-3) mRNA, partial cds
916	10151	19311	1.51	1.7E-02	BE394869.1	EST_HUMAN	Drosophila melanogaster projectin (projectin) gene, partial cds
							601310626F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3632160 5'

Table 4

## Single Exon Probes Expressed in HELA Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1760	10971	20157	2.19	1.7E-02	AW573183.1	EST_HUMAN	hf34e03.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2833740 3' similar to contains L1.11 L1 repetitive element ;
1760	10971	20158	2.19	1.7E-02	AW573183.1	EST_HUMAN	hf34e03.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2833740 3' similar to contains L1.11 L1 repetitive element ;
1837	11045		3.2	1.7E-02	AL163204.2	NT	Homo sapiens chromosome 21 segment HS21C004
2083	11283		12.09	1.7E-02	AB004816.1	NT	Oryctolagus cuniculus mRNA for mitsugumin29, complete cds
2604	11788		1.15	1.7E-02	7657495	NT	Homo sapiens putative Rab5 GDP/GTP exchange factor homologue (RABEX5), mRNA
2955	12193	21328	1	1.7E-02	AI147815.1	EST_HUMAN	qb22a08.x1 Soares_pregnant_uterus_NHPU Homo sapiens cDNA clone IMAGE:1696982 3'
3486	12710		4.88	1.7E-02	AW827368.1	EST_HUMAN	hm45a04.x1 NCI CGAP_RDF1 Homo sapiens cDNA clone IMAGE:3015534 3' similar to contains L1.11 L1 repetitive element ;
3603	12824		0.6	1.7E-02	P04929	SWISSPROT	HISTIDINE-RICH GLYCOPROTEIN PRECURSOR
4151	13357		1.17	1.7E-02	AA689618.1	EST_HUMAN	ac19f04.s1 Stratiogene ovary (H937217) Homo sapiens cDNA clone IMAGE:856827 3' similar to contains Alu repetitive element; contains element MER24 repetitive element ;
4182	13366		2.03	1.7E-02	R02506.1	EST_HUMAN	ye8f08.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:124847 5'
4448	13847	22743	0.65	1.7E-02	AJ05279.1	EST_HUMAN	qm08g07.x1 NCI CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1881276 3' similar to gb.X52359 ZINC FINGER PROTEIN 30 (HUMAN);
4725	13916	23017	1.88	1.7E-02	V00841.1	NT	Messenger RNA for anglerfish (Lophius americanus) somatostatin II
4828	14017		6.58	1.7E-02	AJ015078.1	EST_HUMAN	ov51e02.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1640858 3'
5100	14280	23384	0.67	1.7E-02	6981288	NT	Rattus norvegicus N-arginine diisocyanate 1 (Nrd1), mRNA
5721	14939	24335	1.65	1.7E-02	AJ768247.1	EST_HUMAN	wg35f09.x1 Soares_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:2367113 3' similar to contains Alu repetitive element
5917	15134	24543	1.76	1.7E-02	AJ038280.1	EST_HUMAN	oy65h03.x1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:1672661 3'
6168	15350	24788	2.17	1.7E-02	8400716	NT	Homo sapiens nebulin (NEB), mRNA
6394	15574		1.83	1.7E-02	AJ010770.1	NT	Homo sapiens hyperion gene, exons 1-50
9087	18303	23690	2.29	1.7E-02	AW903482.1	EST_HUMAN	CM4-NN1030-040400-130-008 NN1030 Homo sapiens cDNA
9177	17870		1.46	1.7E-02	Q03211	SWISSPROT	PISTIL-SPECIFIC EXTENSIN-LIKE PROTEIN PRECURSOR (PELP)
517	9788		1.96	1.8E-02	AL021929.1	NT	Mycobacterium tuberculosis H37Rv complete genome, segment 137162
2213	11410	20633	1.08	1.8E-02	Q84176	SWISSPROT	LIVER CARBOXYL ESTERASE 22 PRECURSOR (EGASYN) (ESTERASE-22)
2213	11410	20634	1.09	1.8E-02	Q84176	SWISSPROT	LIVER CARBOXYL ESTERASE 22 PRECURSOR (EGASYN) (ESTERASE-22)
2531	11719	20836	1	1.8E-02	AJ006345.1	NT	Homo sapiens KVLQT1 gene
2608	11790	21010	0.99	1.8E-02	AA484872.1	EST_HUMAN	ne81d06.s1 NCI CGAP_Ew1 Homo sapiens cDNA clone IMAGE:910687
2654	11837		0.93	1.8E-02	AB014534.1	NT	Homo sapiens mRNA for KIAA0634 protein, partial cds
2881	12218	21353	0.83	1.6E-02	AF112282.1	NT	Lasaea sp. isolate 1Bd cytochrome oxidase III gene, partial cds; mitochondrial gene for mitochondrial product

Table 4

## Single Exon Probes Expressed in HELA Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3499	12723	21859	5.65	1.6E-02	AW850652.1	EST_HUMAN	IL3-CT0219-180200-063-007 CT0219 Homo sapiens cDNA
3832	13049	22159	1.23	1.6E-02	AL163301.2	NT	Homo sapiens chromosome 21 segment HS21C101
4158	13362		1.49	1.6E-02	AF110520.1	NT	Mus musculus major histocompatibility complex region NG27, NG28, RPS28, NADH oxidoreductase, NG28, KFC1, Fas-binding protein, BING1, tapasin, RalGDS-like, KE2, BING4, beta 1,3-galactosyl transferase, and RPS18 genes, complete cds; Sacm21 gene, partial>
5157	14336		0.68	1.6E-02	NB0156.1	EST_HUMAN	z665607.s1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:297444 3'
5952	15168	24581	2.2	1.6E-02	AB015281.1	NT	Candida albicans CaGCR3 gene, complete cds
6520	15716		2.8	1.6E-02	X05151.1	NT	Human apoC-II gene for preproapolipoprotein C-II
7087	16264		3.13	1.6E-02	AF079784.1	NT	Drosophila melanogaster enhancer of polycomb (E(Pc)) mRNA, complete cds
7483	18078	26173	2.46	1.6E-02	Z94828.1	NT	G gallus microsatellite DNA (LEI0260 (=T18III11))
7765	16961	26472	2.87	1.6E-02	AL161508.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 20
8044	17180	26719	2.23	1.6E-02	A1373558.1	EST_HUMAN	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 20
8478	11410	20633	1.65	1.6E-02	Q84176	SWISSPROT	q28610.x1 Soares pregnant uterus NBHPU Homo sapiens cDNA clone IMAGE:2042442 3'
8478	11410	20634	1.65	1.6E-02	Q84176	SWISSPROT	LIVER CARBOXYLESTERASE 22 PRECURSOR (EGASYN) (ESTERASE-22)
8865	17766		1.54	1.6E-02	X82751.1	NT	LIVER CARBOXYLESTERASE 22 PRECURSOR (EGASYN) (ESTERASE-22)
759	10000		78.83	1.5E-02	8923734	NT	R. norvegicus gene for choline acetyltransferase, exon 1 (non coding)
2110	11309	20522	3.85	1.5E-02	N39521.1	EST_HUMAN	Homo sapiens transcription factor (HSA130894), mRNA
2141	11339	20557	1.25	1.5E-02	AL161594.2	NT	W27b07.s1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:243925 3'
3705	12925	22044	1.13	1.5E-02	BF092942.1	EST_HUMAN	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 90
4123	13328	22427	0.6	1.5E-02	AA160987.1	EST_HUMAN	MR4-TN0115-080800-201-b12 TN0115 Homo sapiens cDNA
6217	15398		1.63	1.5E-02	11467282	NT	Zq40g10.r1 Stratagene hNT neuron (#937233) Homo sapiens cDNA clone IMAGE:632228 5'
6421	15618	25082	5.18	1.5E-02	11417739	NT	Cyanophora paradoxa cyanella, complete genome
7727	16925	26435	2.59	1.5E-02	L40609.1	NT	Homo sapiens vely-RNA synthetase 2 (VARS2), mRNA
8710	18170		1.65	1.5E-02	AW750834.1	EST_HUMAN	Plasmodium falciparum (strain FCR3) variant-specific surface protein (var-2, var-3) genes, complete cds's
423	9876		1.46	1.4E-02	AE002230.2	NT	RC4-CN0049-140100-011-c11 CN0049 Homo sapiens cDNA
1126	10350	19501	3.57	1.4E-02	7705880	NT	Chlamydomonas reinhardtii AR39, section 58 of 84 of the complete genome
1263	10478		0.9	1.4E-02	U32800.1	NT	Homo sapiens NESH protein (LOC51225), mRNA
1305	10521		3.25	1.4E-02	U87779.1	NT	Haemophilus influenzae Rd section 115 of 163 of the complete genome
						NT	Xeropus laevis neurogenin related 1b (X-NGNR-1b) mRNA, complete cds
3176	12414	21548	1.78	1.4E-02	AF160969.2	NT	Bifidobacterium longum Na+/H+ antiporter (nhaB), cytosine deaminase, and alpha-galactosidase (eglL) genes, complete cds; and N-acetylglucosaminylxylose repressor protein (nagCxyR) gene, partial cds
3376	12604	21739	0.96	1.4E-02	AW074212.1	EST_HUMAN	xb09409.x1 NC1_CGAP_GU1 Homo sapiens cDNA clone IMAGE:2575783 3'



Table 4

## Single Exon Probes Expressed in HELA Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3459	12884	21818	6.64	1.4E-02	AL181588.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 82
3459	12884	21819	6.64	1.4E-02	AL181588.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 82
3493	12717	21853	0.59	1.4E-02	4503628	NT	Homo sapiens coagulation factor XII (Hageman factor) (F12), mRNA
3636	12857	21976	7.91	1.4E-02	6886918	NT	Mus musculus histocompatibility 2, complement component factor B (H2-B), mRNA
4488	13684	22774	8.97	1.4E-02	AW962688.1	EST_HUMAN	EST374761 MAGE resequencing, MAGG Homo sapiens cDNA
4488	13684	22775	8.97	1.4E-02	AW962688.1	EST_HUMAN	EST374761 MAGE resequencing, MAGG Homo sapiens cDNA
4665	13859	22958	0.96	1.4E-02	8922391	NT	Homo sapiens hypothetical protein FLJ10379 (FLJ10379), mRNA
4665	13859	22959	0.96	1.4E-02	8922391	NT	Homo sapiens hypothetical protein FLJ10379 (FLJ10379), mRNA
4893	14081	23174	7.33	1.4E-02	BE733142.1	EST_HUMAN	601567403F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3842280 5'
4893	14081	23175	7.33	1.4E-02	BE733142.1	EST_HUMAN	601567403F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3842280 5'
5834	15051	24457	4.63	1.4E-02	AA559030.1	EST_HUMAN	nl11c04.s1 NCJ_CGAP_Br2 Homo sapiens cDNA clone IMAGE:1028990 3' similar to contains Alu repetitive element
5834	15051	24458	4.63	1.4E-02	AA559030.1	EST_HUMAN	nl11c04.s1 NCJ_CGAP_Br2 Homo sapiens cDNA clone IMAGE:1028990 3' similar to contains Alu repetitive element
6877	16088	25537	2.98	1.4E-02	BE544581.1	EST_HUMAN	601078239F1 NIH_MGC_12 Homo sapiens cDNA clone IMAGE:3464241 5'
8388	17469	28591	4.44	1.4E-02	X60459.1	NT	Human IFNAR gene for interferon alpha/beta receptor
8764	17702		1.95	1.4E-02	AF324985.1	NT	Arabidopsis thaliana F21J9.2 mRNA, complete cds
9058	17889		2.17	1.4E-02	11426968	NT	Homo sapiens sperm associated antigen 7 (SPAG7), mRNA
1825	11128	20323	2.04	1.3E-02	AL163201.2	NT	Homo sapiens chromosome 21 segment HS21C001
3180	12415	21549	2.04	1.3E-02	BF697081.1	EST_HUMAN	602129475F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:4286203 5'
3180	12415	21550	2.04	1.3E-02	BF697081.1	EST_HUMAN	602129475F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:4286203 5'
3946	13182		1.42	1.3E-02	AF169288.1	NT	Mus musculus beta-sarcoglycan gene, complete cds
6326	15507	24653	4.82	1.3E-02	A031593.1	EST_HUMAN	ow08g05.x1 Soares_parathyroid_tumor_NbHPA Homo sapiens cDNA clone IMAGE:1646072 3' similar to contains Alu repetitive element
6621	15917	25276	2.43	1.3E-02	AF156861.1	NT	Homo sapiens human endogenous retrovirus W gagC3.37 G gag (gag) gene, complete cds
7136	16313	25764	2.67	1.3E-02	M63707.1	NT	Mouse kidney androgen-regulated protein (KAP) gene, complete cds
7564	16769	26259	4.34	1.3E-02	AW268563.1	EST_HUMAN	xv34e03.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2815036 3'
7564	16769	26260	4.34	1.3E-02	AW268563.1	EST_HUMAN	xv34e03.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2815036 3'
8366	18326		2.66	1.3E-02	X51780.1	NT	Yeast ABP1 gene for actin binding protein
8874	17771		1.98	1.3E-02	96330089	NT	Human herpesvirus 6B, complete genome
9063	18093		12.49	1.3E-02	AF152238.1	NT	Homo sapiens V1b vasopressin receptor (VPR3) gene, complete cds
9268	18364	23609	1.4	1.3E-02	AF009179.1	NT	Oryza sativa replication protein A1 (Os-RPA1) mRNA, complete cds
360	9627	18757	4.87	1.2E-02	AA059289.1	EST_HUMAN	z65g01.r1 Soares retina N2b4HR Homo sapiens cDNA clone IMAGE:381840 5' similar to contains element L1 repetitive element

Table 4

## Single Exon Probes Expressed in HELA Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
459	9712	18947	2.56	1.2E-02	P38898	SWISSPROT	HYPOTHETICAL 17.1 KD PROTEIN IN PUR6 3'REGION
746	8987	19130	10.01	1.2E-02	A1183522.1	EST_HUMAN	q668a12.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1734670 3' similar to contains L1.t1 L1 repetitive element;
2143	11341	20559	1.46	1.2E-02	AL163213.2	NT	Homo sapiens chromosome 21 segment HS21C013
2406	11598	20819	1.16	1.2E-02	AW172350.1	EST_HUMAN	x37609.x1 Soares_NFL_T_QBC_S1 Homo sapiens cDNA clone IMAGE:2659432 3'
2446	11637	20858	1.3	1.2E-02	AL163218.2	NT	Homo sapiens chromosome 21 segment HS21C018
2900	11598	20819	25.94	1.2E-02	AW172350.1	EST_HUMAN	x37609.x1 Soares_NFL_T_QBC_S1 Homo sapiens cDNA clone IMAGE:2659432 3'
3066	12302		6.86	1.2E-02	AA075418.1	EST_HUMAN	zn88a03.r1 Stratagene ovarian cancer (#837219) Homo sapiens cDNA clone IMAGE:546020 5'
3256	12489	21620	2.15	1.2E-02	R62805.1	EST_HUMAN	y11b08.s1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:138803 3'
3258	12491	21622	0.84	1.2E-02	A1668094.1	EST_HUMAN	zb66a07.x5 Soares_fetal_lung_NbHL19W Homo sapiens cDNA clone IMAGE:308532 3' similar to contains element MER22 repetitive element;
4835	14122	23217	2.88	1.2E-02	U91328.1	NT	Human hereditary haemochromatosis region, histone 2A-like protein gene, hereditary haemochromatosis (HLA-H) gene, RoRet gene, and sodium phosphate transporter (NPT3) gene, complete cds
5067	14247		1.27	1.2E-02	AB019786.1	NT	Cynops pyrrhogaster Cplbq1 mRNA, partial cds
5114	14284	23382	1.49	1.2E-02	AV731704.1	EST_HUMAN	AV731704 HTF Homo sapiens cDNA clone HTFBHG11 5'
5551	14775	24142	1.95	1.2E-02	D78589.1	NT	Rana rugosa mRNA for calreticulin, complete cds
6089	15290	24723	5.53	1.2E-02	AF175412.1	NT	Mus musculus DNA methyltransferase (Dnmt1) gene, exons 2, 3, 4, and 5
6212	15393	24837	8.59	1.2E-02	AV732093.1	EST_HUMAN	AV732093 HTF Homo sapiens cDNA clone HTFBJC09 5'
6483	15660	25132	3.83	1.2E-02	Q11205	SWISSPROT	CMP-N-ACETYLNEURAMINATE-BETA-GALACTOSAMIDE-ALPHA-2,3-SIALYLTRANSFERASE (BETA-GALACTOSIDE ALPHA-2,3-SIALYLTRANSFERASE) (ALPHA 2,3-ST) (GAL-NAc6S) (GAL-BETA-1,3-GALNAc-ALPHA-2,3-SIALYLTRANSFERASE) (ST3GALA.2) (SIAT4-B)
6977	16155	25628	3.56	1.2E-02	AB031013.1	NT	Norwalk-like virus genogroup 2 gene for capsid protein, complete cds
8442	17505	24015	1.26	1.2E-02	O15534	SWISSPROT	PERIOD CIRCADIAN PROTEIN 1 (CIRCADIAN PACEMAKER PROTEIN RIGUJ) (HPER)
8877	18187		1.27	1.2E-02	P17139	SWISSPROT	COLLAGEN ALPHA 1(IV) CHAIN PRECURSOR
9071	17898		4.48	1.2E-02	G18119.1	EST_HUMAN	C18119 Human placenta cDNA (TFujimura) Homo sapiens cDNA clone GEN-557G06 5'
1276	10491	19650	1.91	1.1E-02	AA070384.1	EST_HUMAN	zn69a11.s1 Stratagene neuroepithelium (#837231) Homo sapiens cDNA clone IMAGE:530924 3'
1681	10853	20080	1.32	1.1E-02	X75491.1	NT	H. sapiens LIPA gene, exon 4
1681	10853	20081	1.32	1.1E-02	X75491.1	NT	H. sapiens LIPA gene, exon 4
2005	11208	20417	4.75	1.1E-02	BF345263.1	EST_HUMAN	602018037F1 NCL_CGAP_Bm67 Homo sapiens cDNA clone IMAGE:4153808 5'
2831	12070		4.23	1.1E-02	N99523.1	EST_HUMAN	zn40e05.r1 Soares fetal liver spleen TNF1S Homo sapiens cDNA clone IMAGE:295040 5'
3496	12720	21857	3.07	1.1E-02	A1653508.1	EST_HUMAN	iq95b10.x1 NCL_CGAP_Ov23 Homo sapiens cDNA clone IMAGE:2216539 3' similar to SW:XP_F_HUMAN Q92889 DNA-REPAIR PROTEIN COMPLEMENTING XP-F CELL;
3998	13211		63.05	1.1E-02	BE144637.1	EST_HUMAN	PM3-HT0175-300989-001-H08 HT0175 Homo sapiens cDNA

Table 4  
Single Exon Probes Expressed in HELA Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4085	13284		0.85	1.1E-02	AW813786.1	EST_HUMAN	RC3-ST0197-120200-015-g11 ST0197 Homo sapiens cDNA
4847	14036	23129	2.48	1.1E-02	AL048383.2	EST_HUMAN	DKFZp586E0924_s1 586 (synonym: hula1) Homo sapiens cDNA clone DKFZp586E0924
6331	15512	24958	2.06	1.1E-02	BE149611.1	EST_HUMAN	RC1-HT0258-100300-016-h07 HT0258 Homo sapiens cDNA
6744	15939	25400	7.88	1.1E-02	Q81982	SWISSPROT	NEUROGENIC LOCUS NOTCH 3 PROTEIN
7047	16224	25699	2.79	1.1E-02	AA082578.1	EST_HUMAN	zn24a01.1 Stratagene neuroepithelium NT2RAM1 937234 Homo sapiens cDNA clone IMAGE:548328 5'
7107	16284	25765	5.97	1.1E-02	AA314665.1	EST_HUMAN	EST188484 Colon carcinoma (HCC) cell line II Homo sapiens cDNA 5' end
7552	18757	26251	3.86	1.1E-02	11435505	NT	Homo sapiens T-box 5 (TBX5), mRNA
8327	17428		3	1.1E-02	AA688239.1	EST_HUMAN	ab77611.s1 Stratagene fetal retina 937202 Homo sapiens cDNA clone IMAGE:853005 3' similar to contains Alu repetitive element
6	8302	18406	8.12	1.0E-02	AW846120.1	EST_HUMAN	MR3-CT0176-111089-003-e10 CT0176 Homo sapiens cDNA
2536	11724		0.94	1.0E-02	AA806389.1	EST_HUMAN	cc22h08.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1350495 3'
3055	12291	21417	3.03	1.0E-02	BE835556.1	EST_HUMAN	RCO-FN0025-250500-021-d02 FN0025 Homo sapiens cDNA
3229	12463	21595	1.34	1.0E-02	BE688999.1	EST_HUMAN	601849667R1 NIH_MGC_74 Homo sapiens cDNA clone IMAGE:3893689 3'
3874	13080	22208	0.8	1.0E-02	AL163302.2	NT	Homo sapiens chromosome 21 segment HS21C102
4786	13975	23078	4.78	1.0E-02	6753521	NT	Mus musculus corticotropin releasing hormone receptor 2 (Cnr2), mRNA
4881	14048	23143	5.39	1.0E-02	R86567.1	EST_HUMAN	y454h01.1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:199633 5'
5208	14383		1.84	1.0E-02	BE064970.1	EST_HUMAN	RC1-BT0313-130400-016-e09 BT0313 Homo sapiens cDNA
5745	14984	24363	2.8	1.0E-02	AW577113.1	EST_HUMAN	MR4-BT0356-070100-201-h01 BT0356 Homo sapiens cDNA
5745	14984	24364	2.8	1.0E-02	AW577113.1	EST_HUMAN	MR4-BT0356-070100-201-h01 BT0356 Homo sapiens cDNA
6874	16065	25532	7.87	1.0E-02	BF036331.1	EST_HUMAN	601459570F1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3863177 5'
6874	16065	25533	7.87	1.0E-02	BF036331.1	EST_HUMAN	601459570F1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3863177 5'
7814	17007		2.34	1.0E-02	AF157559.1	NT	Citridia fasciculata 27 kDa guide RNA-binding protein mRNA, complete cds; mitochondrial gene for mitochondrial product
7807	17122	26653	2.08	1.0E-02	AV760016.1	EST_HUMAN	AV760016 MDS Homo sapiens cDNA clone MDSBDC10 5'
8407	18384		1.45	1.0E-02	Q62203	SWISSPROT	SPICEOSOME ASSOCIATED PROTEIN 92 (SAP 92) (SPLICING FACTOR 3A SUBUNIT 2) (SF3A66)
8467	18145	23751	4.31	1.0E-02	AW935521.1	EST_HUMAN	RC2-DT0007-120200-016-h02 DT0007 Homo sapiens cDNA
8487	18202		5.37	1.0E-02	S70330.1	NT	Homo sapiens renal dipeptidase (RDP) gene, complete cds
8049	18259		3.4	1.0E-02	X62654.1	NT	H sapiens gene for Me491/CD63 antigen
9271	18034	23842	1.34	1.0E-02	AB039887.1	NT	Homo sapiens WDR4 gene for WD repeat protein, complete cds
9290	18105		20.92	1.0E-02	D17522.1	NT	Z. mobilis zIE and zIS genes for expression and secretion activator protein, complete cds
903	10138	19300	1.76	9.0E-03	A1796128.1	EST_HUMAN	wh4209.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2383433 3' similar to contains element
1271	10486		1.88	9.0E-03	BE781889.1	EST_HUMAN	MER22 MER22 repetitive element ;
							601470242F1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3873346 5'

Table 4  
Single Exon Probes Expressed in HELA Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2359	11552	20773	2.28	9.0E-03	AL161559.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 59
2368	11561	20783	1.95	9.0E-03	AF099934.1	NT	Mus musculus MHC class III protein RP1 (Rp1) mRNA, partial cds
2858	12098	21225	0.68	9.0E-03	A1251744.1	EST_HUMAN	qh90f08.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1854281 3'
2858	12098	21226	0.68	9.0E-03	A1251744.1	EST_HUMAN	qh90f08.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1854281 3'
3849	12870	21987	1.08	9.0E-03	J05184.1	NT	S acidocaldarius thermopsis gene, complete cds
5008	14195	23284	1.11	8.0E-03	BE047849.1	EST_HUMAN	h244e10.y1 NCL_CGAP_Bim52 Homo sapiens cDNA clone IMAGE:2281468 5'
5948	15164		4.8	9.0E-03	BE745888.1	EST_HUMAN	601573438F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3834762 5'
7558	16763		1.7	9.0E-03	Y18000.1	NT	Homo sapiens NF2 gene
7583	16788	26283	1.77	9.0E-03	BE395380.1	EST_HUMAN	601310881F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3632181 5'
8628	18385		1.56	9.0E-03	BF351141.1	EST_HUMAN	PM1-HT0452-281299-001-e09 HT0452 Homo sapiens cDNA
8848	18370		15.49	9.0E-03	BE348385.1	EST_HUMAN	hw17609.x1 NCL_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3183161 3'
8180	17959		14.22	9.0E-03	BF351141.1	EST_HUMAN	PM1-HT0452-281299-001-e09 HT0452 Homo sapiens cDNA
9215	17895		1.23	9.0E-03	P16241	SWISSPROT	POU-DOMAIN PROTEIN CF1A (CHORION FACTOR 1A) (CF1-A) (VENTRAL VEINS LACKING PROTEIN) (DRIFTER PROTEIN)
508	9780		5.44	8.0E-03	AA723007.1	EST_HUMAN	zh30603.s1 Soares_pineal_gland_N3HPG Homo sapiens cDNA clone IMAGE:413598 3' similar to contains Alu repetitive element
996	10228	19383	61.85	8.0E-03	AF108656.1	NT	Homo sapiens adenylosuccinate lyase gene, complete cds
2125	11324	20542	1.11	8.0E-03	AL163283.2	NT	Homo sapiens chromosome 21 segment HS21C083
2517	11708	20919	1.37	8.0E-03	P10286	SWISSPROT	RETROVIRUS-RELATED POL POLYPROTEIN [CONTAINS: REVERSE TRANSCRIPTASE ; ENDONUCLEASE]
3281	12512	21643	1.07	8.0E-03	BE171225.1	EST_HUMAN	RC1-HT0545-120200-011-b09 HT0545 Homo sapiens cDNA
3334	12563	21701	0.88	8.0E-03	AJ131016.1	NT	Homo sapiens SCL gene locus
3856	12877	21896	1.46	8.0E-03	P32844	SWISSPROT	HYPOTHETICAL 127.0 KD PROTEIN IN RAD24-BMH1 INTERGENIC REGION
3856	12877	21897	1.46	8.0E-03	P32844	SWISSPROT	HYPOTHETICAL 127.0 KD PROTEIN IN RAD24-BMH1 INTERGENIC REGION
4244	13447	22538	1.19	8.0E-03	BE840049.1	EST_HUMAN	QV0-FN0181-140700-304-q10 FN0181 Homo sapiens cDNA
4377	13579	22878	6.14	8.0E-03	BF363327.1	EST_HUMAN	CM4-NN0119-300600-223-b05 NN0119 Homo sapiens cDNA
4728	13918	23021	0.65	8.0E-03	P03181	SWISSPROT	HYPOTHETICAL BHLF1 PROTEIN
4728	13919	23022	0.65	8.0E-03	P03181	SWISSPROT	HYPOTHETICAL BHLF1 PROTEIN
5452	14678	23838	2.83	8.0E-03	AF110520.1	NT	Mus musculus major histocompatibility complex region NG27, NG28, RPS28, NADH oxidoreductase, NG29, KIFC1, Fas-binding protein, BING1, tapasin, RalGDS-like, KE2, BING4, beta 1,3-galactosyl transferase, and RPS18 genes, complete cds; Sacm21 gene, partial>
5980	15194	24610	4.28	8.0E-03	P55577	SWISSPROT	PROBABLE PEPTIDASE Y4NA
6309	15490		1.8	8.0E-03	AB038287.1	NT	Tursiops truncatus mRNA for p40-phox, complete cds
6748	15943	25403	4	8.0E-03	AW808692.1	EST_HUMAN	MR1-ST0111-111198-011-h06 ST0111 Homo sapiens cDNA

Page 112 of 382  
Table 4  
Single Exon Probes Expressed in HELA Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7053	16230		8.75	8.0E-03	BE086509.1	EST_HUMAN	QV1-BT0677-040400-131-g03 BT0677 Homo sapiens cDNA
7557	16762		2.97	8.0E-03	Z49652.1	NT	S. cerevisiae chromosome X reading frame ORF YJR152w
7920	17135	26665	1.9	8.0E-03	AA828817.1	EST_HUMAN	cd80g09.s1 NCI_CGAP_Ov2 Homo sapiens cDNA clone IMAGE:1374232
7920	17135	26668	1.9	8.0E-03	AA828817.1	EST_HUMAN	cd80g09.s1 NCI_CGAP_Ov2 Homo sapiens cDNA clone IMAGE:1374232
8208	17337	26877	5.58	8.0E-03	AF064589.1	NT	Homo sapiens melanoma-associated antigen (MAGE-G1) gene, complete cds
8336	17434		1.97	8.0E-03	M69035.1	NT	Oryctolagus cuniculus eIF-2a kinase mRNA, complete cds
8383	17466		2.41	8.0E-03	AB038161.1	NT	Homo sapiens ABCG1 gene for ABC transporter (ATP-binding cassette, sub-family G (WHITE), member 1), complete cds
701	8943	19077	15.31	7.0E-03	AF097183.1	NT	Cryptosporidium parvum HC-10 gene, complete cds
701	8943	19078	15.31	7.0E-03	AF097183.1	NT	Cryptosporidium parvum HC-10 gene, complete cds
984	10215	19371	9.6	7.0E-03	AF243376.1	NT	Glycine max glutathione S-transferase GST 21 mRNA, partial cds
1124	10348	19489	3.32	7.0E-03	AV731712.1	EST_HUMAN	AV731712 HTF Homo sapiens cDNA clone HTFAZF10.5'
1372	10586		1	7.0E-03	O81060	SWISSPROT	FORKHEAD BOX PROTEIN D3 (HNF3/FH TRANSCRIPTION FACTOR GENESIS) (HEPATOCYTE NUCLEAR FACTOR 3 FORKHEAD HOMOLOG 2) (HFH-2)
1399	10613	19777	3.43	7.0E-03	AA688288.1	EST_HUMAN	ab79b09.s1 Stratiotes fetal retina 937202 Homo sapiens cDNA clone IMAGE:853145.3'
1494	10707	19880	2.54	7.0E-03	AW303599.1	EST_HUMAN	xx21b02.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2813739.3'
1715	10927	20111	1	7.0E-03	AW950556.1	EST_HUMAN	EST302828 MAGE resequences, MAGA Homo sapiens cDNA
1715	10927	20112	1	7.0E-03	AW950556.1	EST_HUMAN	EST302828 MAGE resequences, MAGA Homo sapiens cDNA
2222	12013	20845	1.48	7.0E-03	P04929	SWISSPROT	HISTIDINE-RICH GLYCOPROTEIN PRECURSOR
3533	12758	21888	1	7.0E-03	AI150273.1	EST_HUMAN	qf34h02.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1751955.3'
3749	12969	22084	0.87	7.0E-03	AW444463.1	EST_HUMAN	UI-H-B13-akb-c-10-Q-U1.s1 NCI_CGAP_Sub5 Homo sapiens cDNA clone IMAGE:2733691.3'
3800	13018	22131	0.81	7.0E-03	AF198344.1	NT	Rattus norvegicus neuronal nicotinic acetylcholine receptor subunit (Alpha10) mRNA, complete cds
3995	12969	22084	0.84	7.0E-03	AW444463.1	EST_HUMAN	UI-H-B13-akb-c-10-Q-U1.s1 NCI_CGAP_Sub5 Homo sapiens cDNA clone IMAGE:2733691.3'
4332	13533		1.12	7.0E-03	U60086.1	NT	Dicystosellium discoideum multidrug resistance transporter/Ser protease (tagC) mRNA, complete cds
4532	13728		1.04	7.0E-03	AW117711.1	EST_HUMAN	xx34f09.x1 NCI_CGAP_U11 Homo sapiens cDNA clone IMAGE:2608033.3' similar to TR:Q12987 Q12987
4599	13793		1.38	7.0E-03	AW630888.1	EST_HUMAN	ACIDIC 82 KDA PROTEIN.
5010	14197		2.53	7.0E-03	AL163278.2	NT	hh89a05.y1 NCI_CGAP_GU1 Homo sapiens cDNA clone IMAGE:2869936.5'
5713	18083		4.99	7.0E-03	AW661059.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C078
5795	15012	24416	1.73	7.0E-03	W68251.1	EST_HUMAN	RC1-CT0286-050400-018-c08 CT0286 Homo sapiens cDNA
5896	15113	24524	3.19	7.0E-03	A4327129.1	EST_HUMAN	xx33f10.r1 Soares_fetal_heart_NbHH19W Homo sapiens cDNA clone IMAGE:342475.5'
6115	15228	24647	1.92	7.0E-03	BE928133.1	EST_HUMAN	EST30674 Cden1 Homo sapiens cDNA 5' end
							CM2-CT0478-230800-347-b11 CT0478 Homo sapiens cDNA

Table 4

## Single Exon Probes Expressed in HELA Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6299	15480	24923	5.21	7.0E-03	Z35838.1	NT	S.cerevisiae chromosome II reading frame ORF YBL077w
6299	15480	24924	5.21	7.0E-03	Z35838.1	NT	S.cerevisiae chromosome II reading frame ORF YBL077w
6498	15695	25159	4.1	7.0E-03	BE175687.1	EST_HUMAN	RC5-HT0582-160300-011-D02 HT0582 Homo sapiens cDNA
7403	16616	26106	3.29	7.0E-03	AB008852.1	NT	Bos taurus mRNA for NDP52, complete cds
8904	18370		1.5	7.0E-03	H94065.1	EST_HUMAN	y15h01.s1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:242833 3' similar to contains Alu repetitive element
8911	17800		2.34	7.0E-03	BE263253.1	EST_HUMAN	601145154F2 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3160476 5'
9006	17864		1.59	7.0E-03	Y17455.1	NT	Homo sapiens LSFR2 gene, penultimate exon
9147	18367		1.41	7.0E-03	AL163300.2	NT	Homo sapiens chromosome 21 segment HS21C100
9278	18040		1.4	7.0E-03	AW868110.1	EST_HUMAN	RC0-SN0052-110400-021-a04 SN0052 Homo sapiens cDNA
1247	10464	19824	10.61	6.0E-03	AW511148.1	EST_HUMAN	hd22a05.x1 Soares NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2810224 3' similar to SW_PXR_HUMAN 075469 ORPHAN NUCLEAR RECEPTOR PXR ;
1247	10464	19825	10.61	6.0E-03	AW511148.1	EST_HUMAN	hd22a05.x1 Soares NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2810224 3' similar to SW_PXR_HUMAN 075469 ORPHAN NUCLEAR RECEPTOR PXR ;
2727	11808	21121	1.11	6.0E-03	AF112374.1	NT	Danio rerio odorant receptor gene cluster
2843	12082	21207	4.79	6.0E-03	AA759135.1	EST_HUMAN	ah78e11.s1 Soares testis_NHT Homo sapiens cDNA clone 1321772 3'
2843	12082	21208	4.79	6.0E-03	AA759135.1	EST_HUMAN	eh78e11.s1 Soares testis_NHT Homo sapiens cDNA clone 1321772 3'
3213	12447		2.26	6.0E-03	HT5680.1	EST_HUMAN	y77h04.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:211351 5'
3275	12508		0.7	6.0E-03	AF190338.1	NT	Notoncus sp. cytochrome c oxidase subunit II gene, partial cds; mitochondrial gene for mitochondrial product
3360	12588	21727	1.3	6.0E-03	U90880.1	NT	Fugu rubripes zinc finger protein, isotocin, fatty acid binding protein, septiparin reductase and vasotocin genes, complete cds
3360	12588	21728	1.3	6.0E-03	U90880.1	NT	Fugu rubripes zinc finger protein, isotocin, fatty acid binding protein, septiparin reductase and vasotocin genes, complete cds
3521	12745		1.25	6.0E-03	W37985.1	EST_HUMAN	zc13a11.r1 Soares parathyroid_tumor_NbHPA Homo sapiens cDNA clone IMAGE:322172 5'
3640	12861	21979	2.21	6.0E-03	BF510986.1	EST_HUMAN	UI-H-B14-apm-c-08-Q-U1.s1 NCI_CGAP_Sub8 Homo sapiens cDNA clone IMAGE:3087754 3'
3759	12978	22093	1.06	6.0E-03	6754029	NT	Mus musculus glucosamine-6-phosphate deaminase (Gnpl), mRNA
3833	13149		0.99	6.0E-03	BE250108.1	EST_HUMAN	600942904F1 NIH_MGC_15 Homo sapiens cDNA clone IMAGE:2959513 5'
4317	13518		0.95	6.0E-03	N56946.1	EST_HUMAN	y62h10.s1 Soares multiple_sclerosis_2NbHMSP Homo sapiens cDNA clone IMAGE:278179 3'
4358	13560		1.94	6.0E-03	A016833.1	EST_HUMAN	ov33c11.x1 Soares testis_NHT Homo sapiens cDNA clone IMAGE:1639124 3'
4705	13896	22695	7.35	6.0E-03	AA324242.1	EST_HUMAN	EST27118 Cerebellum II Homo sapiens cDNA 5' end similar to EST containing Alu repeat
5273	14445	23517	0.9	6.0E-03	AF050737.1	NT	Homo sapiens dopamine D2 receptor (DRD2) gene, complete cds
6413	15610	25074	13.87	6.0E-03	A1033980.1	EST_HUMAN	ow13a04.x1 Soares parathyroid_tumor_NbHPA Homo sapiens cDNA clone IMAGE:1648670 3' similar to contains MER10.b1 MER10 repetitive element ;

Table 4

## Single Exon Probes Expressed in HELA Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6453	15650	25118	3.3	6.0E-03	AW798337.1	EST_HUMAN	RC0-UM0051-210300-032-g02 UM0051 Homo sapiens cDNA
6937	16081	25551	10.41	6.0E-03	D10548.1	NT	Subacute sclerosing panencephalitis (SSPE) virus mRNA for fusion protein
7330	16546	26036	2.3	6.0E-03	AW962164.1	EST_HUMAN	EST374237 MAGE resequences, MAGG Homo sapiens cDNA
7388	16602		2.24	6.0E-03	11545814	NT	Homo sapiens hypothetical zinc finger protein FLJ14011 (FLJ14011). mRNA
7423	16633	26127	2.03	6.0E-03	AI420786.1	EST_HUMAN	ts91c12.x1 NCL CGAP_P28 Homo sapiens cDNA clone IMAGE:2094070 3' similar to TR:O00519 O00519 FATTY ACID AMIDE HYDROLASE.
7423	16633	26128	2.03	6.0E-03	AI420786.1	EST_HUMAN	ts91c12.x1 NCL CGAP_P28 Homo sapiens cDNA clone IMAGE:2094070 3' similar to TR:O00519 O00519 FATTY ACID AMIDE HYDROLASE.
7555	16760		4.37	6.0E-03	U14568.1	NT	Mus musculus zinc-finger protein mRNA, complete cds
7556	16761	26254	2.64	6.0E-03	BE737895.1	EST_HUMAN	601572746F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:3839747 5'
8262	17389	26921	1.76	6.0E-03	H70298.1	EST_HUMAN	y95101.1 Soares fetal liver spleen 1NFS Homo sapiens cDNA clone IMAGE:213049 5' similar to SP:8PGD_PIG P14332 6-PHOSPHOGLUCONATE DEHYDROGENASE, DECARBOXYLATING;
8449	17508		1.57	6.0E-03	AF010496.1	NT	Rhodobacter capsulatus strain SB1003, partial genome
8559	18198		1.26	6.0E-03	BF671185.1	EST_HUMAN	602151024F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4282212 5'
8595	18130		6.17	6.0E-03	AE000833.1	NT	Methanobacterium thermoautotrophicum from bases 429192 to 450296 (section 39 of 148) of the complete genome
8669	18194		2.42	6.0E-03	U30790.1	NT	Pneumocystis carinii f. sp. ratti guanine nucleotide binding protein alpha subunit (pcg1) gene, complete cds
9022	17873		1.98	6.0E-03	BE788019.1	EST_HUMAN	601482621F1 NIH_MGC_88 Homo sapiens cDNA clone IMAGE:3885388 5'
9045	17868		1.96	6.0E-03	AJ245480.1	NT	Brassica napus sig gene for S-locus glycoprotein, cultivar T2
675	9920	19050	1.9	5.0E-03	L25105.1	NT	Chlamydia trachomatis partial ORFB; aminoacyl-tRNA synthase, complete cds; complete ORFA, and grpE- like protein, complete cds
675	9920	19051	1.9	5.0E-03	L25105.1	NT	Chlamydia trachomatis partial ORFB; aminoacyl-tRNA synthase, complete cds; complete ORFA, and grpE- like protein, complete cds
676	9920	19050	3.67	5.0E-03	L25105.1	NT	Chlamydia trachomatis partial ORFB; aminoacyl-tRNA synthase, complete cds; complete ORFA, and grpE- like protein, complete cds
676	9920	19051	3.67	5.0E-03	L25105.1	NT	Chlamydia trachomatis partial ORFB; aminoacyl-tRNA synthase, complete cds; complete ORFA, and grpE- like protein, complete cds
1120	10344	19495	1.63	5.0E-03	AJ010457.1	NT	Arabidopsis thaliana mRNA for DEAD box RNA helicase, RH3
2841	11824	21039	1.97	5.0E-03	AB033006.1	NT	Homo sapiens mRNA for KIAA1180 protein, partial cds
2866	12124	21257	0.79	5.0E-03	BE266057.1	EST_HUMAN	601194766F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3538799 5'
3101	12337	21465	4.54	5.0E-03	T87623.1	EST_HUMAN	yc81f09.s1 Soares infant brain 1NIB Homo sapiens cDNA clone IMAGE:22395 3'
3118	12353		2.3	5.0E-03	AL161491.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 3
3131	12366	21496	1.13	5.0E-03	R71794.1	EST_HUMAN	y88g02.s1 Soares breast 2NBHBst Homo sapiens cDNA clone IMAGE:155668 3'

Page 115 of 382  
Table 4  
Single Exon Probes Expressed in HELA Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3245	12478		0.65	5.0E-03	AJ287337.1	NT	Homo sapiens partial LMD1 gene for LIM domains containing protein 1 and KIAA0851 gene
3677	12888	22018	4.23	5.0E-03	AF147449.2	NT	Pseudomonas aeruginosa strain PAO1 penicillin-binding protein 1B (ponB) gene, complete cds
3741	12961	22076	0.74	5.0E-03	U38914.1	NT	Citrus sinensis seed storage protein citrin mRNA, complete cds
3948	13164		1.67	5.0E-03	AA298675.1	EST_HUMAN	EST12218 Uterus tumor 1 Homo sapiens cDNA 5' end
4291	13493	22591	0.64	5.0E-03	H78355.1	EST_HUMAN	y479g10.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:240066 5'
4293	12961	22076	0.76	5.0E-03	U38914.1	NT	Citrus sinensis seed storage protein citrin mRNA, complete cds
4609	13803	22893	0.94	5.0E-03	AJ131016.1	NT	Homo sapiens SCL gene locus
4731	13922	23026	1.59	5.0E-03	AJ752367.1	EST_HUMAN	cn15002.x1 Normal Human Trabecular Bone Cells Homo sapiens cDNA clone NHTBC_cn15c02 random
4954	14141	23235	0.97	5.0E-03	P15265	SWISSPROT	SPERM MITOCHONDRIAL CAPSULE SELENOPROTEIN (MCS)
5570	14795	24168	5.73	5.0E-03	P35500	SWISSPROT	SODIUM CHANNEL PROTEIN PARA (PARALYTIC PROTEIN)
							PROBABLE UBIQUITIN CARBOXYL-TERMINAL HYDROLASE FAF-Y (UBIQUITIN THIOLESTERASE FAF-Y) (UBIQUITIN-SPECIFIC PROCESSING PROTEASE FAF-Y) (DEUBIQUITINATING ENZYME FAF-Y) (FAF FACETS PROTEIN RELATED, Y-LINKED) (UBIQUITIN-SPECIFIC PROTEASE 8, Y CHROMOSOME)
5884	14804	24287	2.62	5.0E-03	O00507	SWISSPROT	
5931	15147		7.17	5.0E-03	BE300091.1	EST_HUMAN	800944564T1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:2960871 3'
6016	14508	23574	6.81	5.0E-03	AB025024.1	NT	Mus musculus AMD1 gene for S-adenosylmethionine decarboxylase, complete cds
6402	15583	25040	7.06	5.0E-03	AB018816.1	NT	Homo sapiens MASL1 mRNA, complete cds
6659	15954		9.12	5.0E-03	M61132.1	NT	Mouse complement receptor (CR2) mRNA, 3' end
7308	16528		7.45	5.0E-03	T19586.1	EST_HUMAN	694F Heart Homo sapiens cDNA clone 694
							xn59g05.x1 Soares_NHCCc_cervical_tumor Homo sapiens cDNA clone IMAGE:2698040 3' similar to contains L1 L2 L1 repetitive element ;
7513	16718	26207	2.98	5.0E-03	AW170334.1	EST_HUMAN	xn59g05.x1 Soares_NHCCc_cervical_tumor Homo sapiens cDNA clone IMAGE:2698040 3' similar to contains L1 L2 L1 repetitive element ;
7513	16718	26208	2.98	5.0E-03	AW170334.1	EST_HUMAN	contains L1 L2 L1 repetitive element ;
7811	16814	26310	2.19	5.0E-03	T49153.1	EST_HUMAN	y409g04.r1 Stratagene placenta (#837225) Homo sapiens cDNA clone IMAGE:70686 5'
7876	17084		3.94	5.0E-03	BE049055.1	EST_HUMAN	tz46c04.y1 NC1 CGAP_Bms52 Homo sapiens cDNA clone IMAGE:2291622 5'
8602	18332		5.41	5.0E-03	AF047874.1	NT	Gallus gallus glyceraldehyde-3-phosphate dehydrogenase mRNA, complete cds
8743	17698		10.59	5.0E-03	AF087253.1	NT	Brugia malayi Y chromosome marker
8844	17753		1.75	5.0E-03	L10347.1	NT	Human pro-alpha1 type II collagen (COL2A1) gene exons 1-54, complete cds.
8881	17776						zx75d03.s1 Soares ovary tumor NIHOT Homo sapiens cDNA clone IMAGE:809548 3' similar to SW:DXA2 MOUSE P14685 PROBABLE DIPHENOL OXIDASE A2 COMPONENT ;
8912	18139		5.75	5.0E-03	BF572332.1	EST_HUMAN	60207774F1 NIH_MGC_62 Homo sapiens cDNA clone IMAGE:4252002 5'
9097	17913	23869	2.66	5.0E-03	AW449109.1	EST_HUMAN	UI-H-B13-akf-f-08-Q-UJ.s1 NC1 CGAP_Sub5 Homo sapiens cDNA clone IMAGE:2734215 3'
9118	18211		1.4	5.0E-03	Q02388	SWISSPROT	COLLAGEN ALPHA 1(VII) CHAIN PRECURSOR (LONG-CHAIN COLLAGEN) (LC COLLAGEN)



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## Single Exon Probes Expressed in HELA Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
238	9517	18846	3.28	4.0E-03	AW500186.1	EST_HUMAN	UI-HF-BNO-alc-t-04-0-UI.r1 NIH_MGC 50 Homo sapiens cDNA clone IMAGE:3076831 5'
326	9597	18726	2.1	4.0E-03	R46482.1	EST_HUMAN	y51e04.s1 Soares infant brain 1N1B Homo sapiens cDNA clone IMAGE:35988 3'
449	9702	18840	0.94	4.0E-03	P54875	SWISSPROT	PHOSPHATIDYLINOSITOL 3-KINASE 3 (PI3-KINASE) (PTDINS-3-KINASE) (PI3K)
610	9857	18976	2.44	4.0E-03	AA939339.1	EST_HUMAN	on75g12.s1 Soares NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1562568 3'
887	10122	18286	1.91	4.0E-03	R46482.1	EST_HUMAN	y51e04.s1 Soares infant brain 1N1B Homo sapiens cDNA clone IMAGE:35988 3'
921	10158		4.09	4.0E-03	AW749101.1	EST_HUMAN	RC3-BT0333-110100-012-f01 BT0333 Homo sapiens cDNA
1159	10381	19533	24.64	4.0E-03	AA098777.1	EST_HUMAN	z181a08.r1 Stragene colon (#837204) Homo sapiens cDNA clone IMAGE:510898 5'
1177	10398	19551	1.71	4.0E-03	AW794740.1	EST_HUMAN	RC6-UM0014-170400-023-G01 UM0014 Homo sapiens cDNA
1310	10526	19686	0.86	4.0E-03	AA284374.1	EST_HUMAN	zs59e01.r1 NCI_CGAP_G0B1 Homo sapiens cDNA clone IMAGE:701736 5'
1588	10779		0.95	4.0E-03	AV708305.1	EST_HUMAN	AV708305 ADC Homo sapiens cDNA clone ADCAKB06 5'
1717	10928	20114	2.29	4.0E-03	U93472.1	NT	Rattus norvegicus type 1 astrocyte and olfactory-limbic associated protein AT1-48 mRNA, complete cds
1985	11188	20399	16.08	4.0E-03	AA098777.1	EST_HUMAN	z181a08.r1 Stragene colon (#837204) Homo sapiens cDNA clone IMAGE:510898 5'
2212	11409		1.85	4.0E-03	BE410556.1	EST_HUMAN	801304161F1 NIH_MGC 21 Homo sapiens cDNA clone IMAGE:3638510 5'
2243	11438	20662	1.44	4.0E-03	AW794740.1	EST_HUMAN	RC6-UM0014-170400-023-G01 UM0014 Homo sapiens cDNA
2537	11725	20941	1.4	4.0E-03	U52111.2	NT	Homo sapiens X28 region near ALD locus containing dual specificity phosphatase 9 (DUSP9), ribosomal protein L18a (RPL18a), Ca2+/Calmodulin-dependent protein kinase I (CAMKI), creatine transporter (CRTR), CDM protein (CDM), adrenergic dystrophy protein >
2537	11725	20941	1.4	4.0E-03	U52111.2	NT	Homo sapiens X28 region near ALD locus containing dual specificity phosphatase 9 (DUSP9), ribosomal protein L18a (RPL18a), Ca2+/Calmodulin-dependent protein kinase I (CAMKI), creatine transporter (CRTR), CDM protein (CDM), adrenergic dystrophy protein >
2631	11834	21047	1.92	4.0E-03	AJ277365.1	NT	Homo sapiens polyglutamine-containing C14ORF4 gene
2651	11834	21048	1.92	4.0E-03	AJ277365.1	NT	Homo sapiens polyglutamine-containing C14ORF4 gene
2657	11839	21051	1.09	4.0E-03	AL163284.2	NT	Homo sapiens chromosome 21 segment HS21C084
3191	12426	21560	0.99	4.0E-03	BE154134.1	EST_HUMAN	PM1-HT0340-151299-003-H08 HT0340 Homo sapiens cDNA
3191	12426	21561	0.99	4.0E-03	BE154134.1	EST_HUMAN	PM1-HT0340-151299-003-H08 HT0340 Homo sapiens cDNA
3504	12728	21864	0.98	4.0E-03	AW188426.1	EST_HUMAN	x98104.x1 NCI_CGAP_C018 Homo sapiens cDNA clone IMAGE:2665279 3'
3504	12728	21865	0.96	4.0E-03	AW188426.1	EST_HUMAN	x98104.x1 NCI_CGAP_C018 Homo sapiens cDNA clone IMAGE:2665279 3'
3602	12823	21845	0.69	4.0E-03	Q13606	SWISSPROT	OLFATORY RECEPTOR 5H1 (OLFATORY RECEPTOR-LIKE PROTEIN OLF1)
3612	12833	21954	0.68	4.0E-03	AV646253.1	EST_HUMAN	AV646253 GLC Homo sapiens cDNA clone GLC4D02 3'
3904	13120	22238	0.77	4.0E-03	AF060868.1	NT	Mus musculus tumor susceptibility protein 101 (tsg101) gene, complete cds
3972	13186		1.89	4.0E-03	AJ011712.1	NT	Homo sapiens TNNT1 gene, exons 1-11 (and joined CDS)
4225	13428	22519	5.3	4.0E-03	AJ766727.1	EST_HUMAN	w187a06.x1 NCI_CGAP_Kid12 Homo sapiens cDNA clone IMAGE:2400274 3'
5312	14544	23613	1.71	4.0E-03	AF005859.1	NT	Drosophila melanogaster anon2D7 (anon2D7) mRNA, complete cds

Table 4

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5395	14824	23737	22.47	4.0E-03	AF109825.1	NT	Rattus norvegicus beta-catenin binding protein mRNA, complete cds
5569	14784	24167	2.5	4.0E-03	P04196	SWISSPROT	(HPRG)
5702	14921		3.78	4.0E-03	U22180.1	NT	Rattus norvegicus opsin gene, complete cds
5781	15008	24412	1.85	4.0E-03	BE548453.1	EST_HUMAN	801076015F1 NIH_MGC_12 Homo sapiens cDNA clone IMAGE:3461954 5'
6163	15348	24783	4.05	4.0E-03	Q02817	SWISSPROT	MUCIN 2 PRECURSOR (INTESTINAL MUCIN 2)
6480	15977	25147	5.72	4.0E-03	AF111944.1	NT	Dicystostellium discoidium AX4 development protein DG1122 (DG1122) gene, partial cds
6530	15726	25191	2.26	4.0E-03	7682087	NT	Homo sapiens KIAA0345 gene product (KIAA0345), mRNA
6884	15879	25338	8.28	4.0E-03	AI553983.1	EST_HUMAN	te49b1.1.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2080013 3' similar to contains Alu repetitive element
6743	15938	25399	5.44	4.0E-03	AL163278.2	NT	Homo sapiens chromosome 21 segment HS21C078
7689	16888	26395	6.92	4.0E-03	AL163206.2	NT	Homo sapiens chromosome 21 segment HS21C008
8242	17371	26907	2.1	4.0E-03	AE002102.1	NT	Ureaplasma urealyticum section 3 of 59 of the complete genome
8569	18347		3.68	4.0E-03	BE815173.1	EST_HUMAN	PM4-BN0138-180600-002-b08 BN0138 Homo sapiens cDNA
8592	17601		1.6	4.0E-03	BE298280.1	EST_HUMAN	801116164F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3028095 5'
8676	17648		2.3	4.0E-03	AW504273.1	EST_HUMAN	U1-HF-BN0-elp-g-04-0-U1r1 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3080622 5'
8923	17807		3.28	4.0E-03	BF224125.1	EST_HUMAN	7q74c09.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE: 3' similar to contains Alu repetitive element; contains element MER31 repetitive element;
8965	18253		1.91	4.0E-03	AW614598.1	EST_HUMAN	hh02c07.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2953932 3' similar to contains element LTR5 repetitive element
8978	17845		1.75	4.0E-03	AW619141.1	EST_HUMAN	RC3-ST0281-240400-016-f03 ST0281 Homo sapiens cDNA
3176	9842	18777	2.69	3.0E-03	AF011920.1	NT	Homo sapiens protein kinase CK2 catalytic subunit alpha gene, exon 1
889	10124	19287	7.37	3.0E-03	AF011920.1	NT	Homo sapiens protein kinase CK2 catalytic subunit alpha gene, exon 1
1636	10850	20028	3.13	3.0E-03	AA468110.1	EST_HUMAN	nc73c05.s1 NCI_CGAP_Pr2 Homo sapiens cDNA clone IMAGE:782884 similar to contains Alu repetitive element
2223	11419		1.08	3.0E-03	AF050066.1	NT	Homo sapiens MHG class 1 region
2257	11452		7.21	3.0E-03	Z32521.1	NT	S.cereale (cv. Halo) mRNA for triosephosphate isomerase
2950	12188		0.77	3.0E-03	Y08006.1	NT	Arabidopsis thaliana rpoMt gene
3048	12284	21411	3.88	3.0E-03	BE379298.1	EST_HUMAN	601237982F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3609933 5'
3114	12349	21477	2.89	3.0E-03	AW802687.1	EST_HUMAN	IL2-UM0076-240300-058-D03 UM0076 Homo sapiens cDNA
3395	12622	21753	3.37	3.0E-03	U34606.1	NT	Mus musculus alpha-1(XVIII) collagen (COL18A1) gene, exon 1 and 2
3405	12631		7.36	3.0E-03	Y12500.1	NT	C.elegans samdc gene
3955	13170	22285	7.39	3.0E-03	AV762392.1	EST_HUMAN	AV762392 MDS Homo sapiens cDNA clone MDSBSG01 5'
3955	13170	22286	7.39	3.0E-03	AV762392.1	EST_HUMAN	AV762392 MDS Homo sapiens cDNA clone MDSBSG01 5'
4014	13226	22327	1.73	3.0E-03	AI782278.1	EST_HUMAN	af04f08.y5 Gessler Wilms tumor Homo sapiens cDNA clone IMAGE:1155889 5'

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4132	13338		1.01	3.0E-03	Z32521.1	NT	S.cereale (cv. Halo) mRNA for triosephosphate isomerase
4389	13590	22682	2.97	3.0E-03	AJ011432.1	NT	Rattus norvegicus gdnf gene
4455	13653		0.71	3.0E-03	BE348739.1	EST_HUMAN	h18g08.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3151834 3'
4518	13714	22808	3.35	3.0E-03	AI536141.1	EST_HUMAN	xa8.P10.H3 conorm Homo sapiens cDNA 3'
4850	14039	23132	2.54	3.0E-03	A1732754.1	EST_HUMAN	ab18a08.x5 Strategene lung (#837210) Homo sapiens cDNA clone IMAGE:841142 3' similar to contains Alu repetitive element;
4870	14058	23152	8.15	3.0E-03	BE787945.1	EST_HUMAN	601482716F1 NIH_MGC_88 Homo sapiens cDNA clone IMAGE:3885483 5'
5148	14327		0.66	3.0E-03	BF204360.1	EST_HUMAN	601866437F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4106960 5'
5307	14538	23543	3.87	3.0E-03	B922499	NT	Homo sapiens hypothetical protein FLJ10539 (FLJ10539), mRNA
5902	15119	24530	9.51	3.0E-03	AA456701.1	EST_HUMAN	aa13f10.r1 Soares_NhhMPu_S1 Homo sapiens cDNA clone IMAGE:813163 5'
6300	15481	24925	3.2	3.0E-03	AB021736.1	NT	Oryza sativa gene for bZIP protein, complete cds
6763	15958		10.15	3.0E-03	AW613774.1	EST_HUMAN	h180f10.x1 NCI_CGAP_GU1 Homo sapiens cDNA clone IMAGE:2869131 3' similar to contains L1.11 L1 repetitive element;
6782	15977	25435	3.26	3.0E-03	AL161589.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 85
6783	15988	25449	9.71	3.0E-03	A1016731.1	EST_HUMAN	av03d12.x1 NCI_CGAP_Kid3 Homo sapiens cDNA clone IMAGE:1636247 3' similar to gb:X57138_ma1
6994	16172		3.95	3.0E-03	P08872	SWISSPROT	HISTONE H2B.2 (HUMAN);
7121	16298	25780	5.83	3.0E-03	AL163303.2	NT	CIRCUMSPOROZOITE PROTEIN PRECURSOR (CS)
7425	16635		2.75	3.0E-03	5803028	NT	Homo sapiens chromosome 21 segment HS21C103
7738	15481	24925	1.72	3.0E-03	AB021736.1	NT	Homo sapiens ATP/GTP-binding protein (HEAD), mRNA
7818	17133	26663	2.14	3.0E-03	AF009222.1	NT	Oryza sativa gene for bZIP protein, complete cds
7983	18418	25905	2.09	3.0E-03	AF266285.1	NT	Pneumocystis carinii kexin-like serine endoprotease mRNA, partial cds
8015	17154	26889	3.08	3.0E-03	AF094481.1	NT	Homo sapiens gldin-like protein (GLP) gene, complete cds
8015	17154	26690	3.08	3.0E-03	AF094481.1	NT	Homo sapiens trinucleotide repeat DNA binding protein p20-CGGBP (CGGBP) gene, complete cds
							Homo sapiens trinucleotide repeat DNA binding protein p20-CGGBP (CGGBP) gene, complete cds
							RETROVIRUS-RELATED POL POLYPROTEIN [CONTAINS: REVERSE TRANSCRIPTASE ;
							ENDONUCLEASE]
8088	17223	26759	1.74	3.0E-03	P11369	SWISSPROT	UI-H-B12-shi-d-06-Q-U1.s1 NCI_CGAP_Sub4 Homo sapiens cDNA clone IMAGE:2726842 3'
8248	17377		1.63	3.0E-03	AW294812.1	EST_HUMAN	promnae-5.E07.f bvtumor Homo sapiens cDNA 5'
8330	18153		3.61	3.0E-03	AI525058.1	EST_HUMAN	at77b10.s1 Soares_total_fetus Nb2HF8_9w Homo sapiens cDNA clone IMAGE:1622779 3' similar to contains L1.13 MER28 repetitive element;
8387	17454	26582	1.75	3.0E-03	AA893154.1	EST_HUMAN	Homo sapiens gene for CNP-N-acetylneuraminic acid hydroxylase, partial cds
8424	18286		1.79	3.0E-03	AB009688.1	NT	Rattus norvegicus mRNA for connexin36 (cx36 gene)
8615	17612	23968	1.7	3.0E-03	AJ296282.1	NT	RING CANAL PROTEIN (KELCH PROTEIN)
521	9772	18896	0.69	2.0E-03	Q04652	SWISSPROT	RING CANAL PROTEIN (KELCH PROTEIN)
521	9772	18897	0.69	2.0E-03	Q04652	SWISSPROT	RING CANAL PROTEIN (KELCH PROTEIN)

Page 119 of 382  
Table 4  
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795	11978		11.98	2.0E-03	T70874.1	EST_HUMAN	jd15h03.r1 Soares fetal liver spleen 1NLS Homo sapiens cDNA clone IMAGE:108341 5'
1371	10586	19752	2.08	2.0E-03	M20783.1	NT	Human alpha-2-plasmin inhibitor gene, exons 6 and 7
1374	10588	19754	1.38	2.0E-03	AA661605.1	EST_HUMAN	nu86f01.s1 NCI_CGAP_ALV1 Homo sapiens cDNA clone IMAGE:1217593
1382	10596	19762	13.61	2.0E-03	AF284446.1	NT	Homo sapiens tumor-related protein DRC2 (DRC2) gene, complete cds
1491	10694	19869	0.86	2.0E-03	P48509	SWISSPROT	PLATELET-ENDOTHELIAL TETRASPAN ANTIGEN 3 (PETA-3) (GP27) (MEMBRANE GLYCOPROTEIN SFA-1) (CD151 ANTIGEN)
1505	10718	19889	1.65	2.0E-03	4557836	NT	Homo sapiens procollagen-lysine, 2-oxoglutarate 5-dioxygenase (lysine hydroxylase, Ehlers-Danlos syndrome type VI) (PLOD) mRNA
1505	10718	19890	1.65	2.0E-03	4557836	NT	Homo sapiens procollagen-lysine, 2-oxoglutarate 5-dioxygenase (lysine hydroxylase, Ehlers-Danlos syndrome type VI) (PLOD) mRNA
1571	10784		6.81	2.0E-03	P28400	SWISSPROT	COLLAGEN ALPHA 5(IV) CHAIN PRECURSOR
1741	10953	20138	1.09	2.0E-03	AA450138.1	EST_HUMAN	z42a10.1 Soares_tet1_fetus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:789114 5'
1894	11168	20373	1.15	2.0E-03	AF302691.1	NT	Mus musculus myelin expression factor-3-like protein gene, partial cds
2214	11411	20635	0.91	2.0E-03	AL163302.2	NT	Homo sapiens chromosome 21 segment HS21C102
2543	11731		5.05	2.0E-03	AW137782.1	EST_HUMAN	UI-H-B11-adj-g-10-0-J1.s1 NCI_CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2717010 3'
3394	12621	21752	4.7	2.0E-03	AA450138.1	EST_HUMAN	z42a10.1 Soares_tet1_fetus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:789114 5'
3401	12627	21758	0.79	2.0E-03	BF568955.1	EST_HUMAN	602183560T1 NIH_MGC_42 Homo sapiens cDNA clone IMAGE:4300070 3'
3647	12868	21885	5.81	2.0E-03	X87344.1	NT	H. sapiens DMA, DMB, HLA-Z1, IPP2, LMP2, TAP1, LMP7, TAP2, DOB, DQB2 and RING8, 9, 13 and 14 genes
4081	13289	22398	2.3	2.0E-03	P03374	SWISSPROT	ENV POLYPEPTIDE [CONTAINS: COAT PROTEIN GP52; COAT PROTEIN GP36]
4204	13407		9.81	2.0E-03	U88491.1	NT	Rattus norvegicus 5-Hydroxytryptamine7 receptor gene, partial cds
4405	13605		0.94	2.0E-03	L35079.1	NT	Porcine rotavirus major outer capsid protein (VP7) mRNA, complete cds
4419	13619		1.04	2.0E-03	AW287380.1	EST_HUMAN	UI-H-BW0-air-g-03-Q-U1.s1 NCI_CGAP_Sub6 Homo sapiens cDNA clone IMAGE:2730413 3'
4543	13738	22836	2.05	2.0E-03	L42512.1	NT	Drosophila melanogaster shortighted class 2 (shs) mRNA, complete cds
4543	13738	22837	2.05	2.0E-03	L42512.1	NT	Drosophila melanogaster shortighted class 2 (shs) mRNA, complete cds
4721	13912		1.94	2.0E-03	R87773.1	EST_HUMAN	yo45e02.s1 Soares adult brain N2b4HB55Y Homo sapiens cDNA clone IMAGE:180890 3'
4751	13942	23044	1.3	2.0E-03	AA909466.1	EST_HUMAN	cl14f05.s1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1623457 3'
5044	14228	23310	0.8	2.0E-03	AF003528.1	NT	Homo sapiens X-linked anhidrotic ectodermal dysplasia protein gene (EDA), exon 2 and flanking repeat regions
5071	14251	23334	0.71	2.0E-03	P45969	SWISSPROT	HYPOPHYSICAL 37.4 KD PROTEIN T08A5.9 IN CHROMOSOME III
5245	14418		1.1	2.0E-03	BE019692.1	EST_HUMAN	bb28h05.x1 NIH_MGC_5 Homo sapiens cDNA clone IMAGE:2884249 3'
5503	18057	24091	1.91	2.0E-03	AB014693.1	NT	Homo sapiens mRNA for KIAA0683 protein, partial cds
5541	14765	24131	2.05	2.0E-03	U83711.1	NT	Xenopus laevis xefillin mRNA, complete cds
5712	14931	24326	3.67	2.0E-03	P23477	SWISSPROT	ATP-DEPENDENT NUCLEASE SUBUNIT B

Page 120 of 382  
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5712	14931	24326	3.67	2.0E-03	P23477	SWISSPROT	ATP-DEPENDENT NUCLEASE SUBUNIT B
5809	15028	24426	2.05	2.0E-03	Q95203	SWISSPROT	CARBONIC ANHYDRASE-RELATED PROTEIN 2 PRECURSOR (CARP 2) (CA-RP II) (CA-XI)
5809	15028	24427	2.05	2.0E-03	Q95203	SWISSPROT	CARBONIC ANHYDRASE-RELATED PROTEIN 2 PRECURSOR (CARP 2) (CA-RP II) (CA-XI)
5811	15028	24428	7.05	2.0E-03	BF308187.1	EST_HUMAN	601887434F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4121408 5'
5828	15043	24447	2.07	2.0E-03	Q8JUKP4	SWISSPROT	ADAM-TS 7 PRECURSOR (A DISINTEGRIN AND METALLOPROTEINASE WITH THROMBOSPONDIN MOTIFS 7) (ADAMTS-7) (ADAM-TS7)
5833	15050	24456	1.68	2.0E-03	X94451.1	NT	L. esculentum mRNA for lysyl-tRNA synthetase (LysRS)
6068	14515	23573	1.76	2.0E-03	AB038502.1	NT	Caenorhabditis elegans mRNA for galectin LEC-11, complete cds
6117	15230	24849	2.9	2.0E-03	BE087886.1	EST_HUMAN	CM4-BT0368-061299-054-d01 BT0368 Homo sapiens cDNA
6481	15678	25148	5.15	2.0E-03	AW592004.1	EST_HUMAN	H37b06.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2834035 3' similar to TR:Q60976 Q60976 JERKY. ;
6534	15730	25183	7.65	2.0E-03	N20287.1	EST_HUMAN	yx42g06.s1 Soares melanocyte 2NbhM Homo sapiens cDNA clone IMAGE:264442 3' similar to contains L1.b2 L1 repetitive element ;
6534	15730	25184	7.65	2.0E-03	N20287.1	EST_HUMAN	yx42g06.s1 Soares melanocyte 2NbhM Homo sapiens cDNA clone IMAGE:264442 3' similar to contains L1.b2 L1 repetitive element ;
6941	16085	25553	3.18	2.0E-03	P24821	SWISSPROT	TENASCIN PRECURSOR (TN) (HEXABRACHION) (CYTOTACTIN) (NEURONECTIN) (GMEIN) (J1) (NIOTENDINOUS ANTIGEN) (GLIOMA-ASSOCIATED-EXTRACELLULAR MATRIX ANTIGEN) (GP 150-225) (TENASCIN-C) (TN-C)
7088	16265		5.2	2.0E-03	AA261376.1	EST_HUMAN	zs10a06.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:684754 3'
7685	16760		3.24	2.0E-03	M86524.1	NT	Human dystrophin gene
8022	15522	24970	2.31	2.0E-03	P07354	SWISSPROT	PROTEOLYCAN LINK PROTEIN PRECURSOR (CARTILAGE LINK PROTEIN) (LP)
8076	17211		2.28	2.0E-03	BF330909.1	EST_HUMAN	RC3-BT0333-310800-115-g04 BT0333 Homo sapiens cDNA
8083	17218	26753	15.54	2.0E-03	Z11740.1	NT	H. sapiens variable number tandem repeat (VNTR) locus DNA
8313	17417		2.5	2.0E-03	AB25745.1	EST_HUMAN	iy65h03.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2283989 3' similar to SW:VATG_MANSE Q25532 VACUOLAR ATP SYNTHASE SUBUNIT G ;
8328	17430	26937	2.71	2.0E-03	AF157516.2	NT	Homo sapiens SEL1L (SEL1L) gene, partial cds
8353	17446	26940	1.28	2.0E-03	AB94325.1	EST_HUMAN	oy43g05.s1 Soares_parathyroid_tumor_NbHPA Homo sapiens cDNA clone IMAGE:1668634 3' similar to TR:P97535 P97535 PS-PLA1 PRECURSOR. ;
8376	14500		4.25	2.0E-03	AJ245187.1	NT	Camelus dromedarius cvhp19 gene for immunoglobulin heavy chain variable region
8597	18328		2.72	2.0E-03	AV697966.1	EST_HUMAN	AV697966 GKC Homo sapiens cDNA clone GKCGXD05 5'
8695	17663	23947	1.54	2.0E-03	Y00508.1	NT	H. sapiens M1 gene for muscarinic acetylcholine receptor
8813	17733		1.56	2.0E-03	AL163203.2	NT	Homo sapiens chromosome 21 segment HS21C003
8870	18181		1.24	2.0E-03	AB375037.1	EST_HUMAN	ta66f02.x1 Soares_tetus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:2049051 3' similar to contains Alu repetitive element;

Table 4

## Single Exon Probes Expressed in HELA Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8995	17856		1.34	2.0E-03	AF128756.1	NT	Homo sapiens MSH55 gene, partial cds; and CLIC1, DDAH, G6b, G6c, G6d, G6e, G6f, BAT5, G5b, CSK2B, BAT4, G4, Apo M, BAT3, BAT2, AIF-1, TCT, LST-1, LTB, TNF, and LTA genes, complete cds
9172	18131		2.37	2.0E-03	AV697866.1	EST_HUMAN	AV697866 GK Homo sapiens cDNA clone GKCGX005 5'
445	8699	18835	1.13	1.0E-03	H08471.1	EST_HUMAN	y88c08.t1 Soares_pineal_gland_N3HPG Homo sapiens cDNA clone IMAGE:232334 5'
839	10078	18235	2.02	1.0E-03	A1720263.1	EST_HUMAN	as70b08.x1 Barslead colon HPLRB7 Homo sapiens cDNA clone IMAGE:2334039 3' similar to TR:Q13825
839	10076	19236	2.02	1.0E-03	A1720263.1	EST_HUMAN	Q13825 AU-BINDING PROTEIN/ENYOYL-COA HYDRATASE. ;
1103	10327	19477	2.73	1.0E-03	A1865788.1	EST_HUMAN	Q13825 AU-BINDING PROTEIN/ENYOYL-COA HYDRATASE. ;
1123	10347	19488	1.49	1.0E-03	A1954572.1	EST_HUMAN	wk88a06.x1 NCI_CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2422258 3'
1174	10395	19547	3.1	1.0E-03	A1952618.1	EST_HUMAN	w83a10.x1 NCI_CGAP_Mel15 Homo sapiens cDNA clone IMAGE:2551242 3'
1987	11200	20411	4.06	1.0E-03	P47808	SWISSPROT	wd88a01.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:2338440 3' similar to contains Alu repetitive element;
2122	11321	20539	7.75	1.0E-03	A1131016.1	NT	HIGH MOLECULAR WEIGHT FORM OF MYOSIN I (HMMWI)
2937	12175	21309	1.43	1.0E-03	AB033117.1	NT	Homo sapiens SCL gene locus
3154	12389	21521	1.49	1.0E-03	P18915	SWISSPROT	Homo sapiens mRNA for KIAA1281 protein, partial cds
3154	12389	21522	1.49	1.0E-03	P18915	SWISSPROT	CARBONIC ANHYDRASE VI PRECURSOR (CARBONATE DEHYDRATASE VI) (CA-VI) (SECRETED)
3271	12504	21635	0.84	1.0E-03	P08547	SWISSPROT	CARBONIC ANHYDRASE (SALIVARY CARBONIC ANHYDRASE)
3646	12867		1.34	1.0E-03	AB044400.1	NT	CARBONIC ANHYDRASE VI PRECURSOR (CARBONATE DEHYDRATASE VI) (CA-VI) (SECRETED)
3908	13124	22242	0.63	1.0E-03	Z49649.1	NT	CARBONIC ANHYDRASE VI PRECURSOR (CARBONATE DEHYDRATASE VI) (CA-VI) (SECRETED)
4427	13627	22721	3.45	1.0E-03	BE839162.1	EST_HUMAN	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG
4471	13669	22780	5.28	1.0E-03	BE246536.1	EST_HUMAN	Homo sapiens SYMT gene for synaptic vesicle monoamine transporter, exons 14, 15
4840	14028	23121	2.09	1.0E-03	A1073485.1	EST_HUMAN	S. cerevisiae chromosome X reading frame ORF YJR149w
4840	14029	23122	2.09	1.0E-03	A1073485.1	EST_HUMAN	RC1-TN0128-160800-021-g01 TN0128 Homo sapiens cDNA
4841	14030		4.02	1.0E-03	BE154087.1	EST_HUMAN	TCBAP1D4909 Pediatric pre-B cell acute lymphoblastic leukemia Baylor-HGSC project=TCBA Homo sapiens cDNA clone TCBAP4909
5107	14287	23372	7.76	1.0E-03	O48409	SWISSPROT	sapiens cDNA clone IMAGE:1640262 3'
5396	14587	23641	1.91	1.0E-03	AA280951.1	EST_HUMAN	ov45c04.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1640262 3'
5396	14625	23738	3.07	1.0E-03	A1008345.1	NT	ov45c04.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1640262 3'
5422	14649	23783	1.99	1.0E-03	K03332.1	NT	PMO-HT0339-200400-010-D02 HT0339 Homo sapiens cDNA
5422	14649	23784	1.99	1.0E-03	K03332.1	NT	APOLIPOPROTEIN A-IV PRECURSOR (APO-AIV)
							zs44f01.t1 NCI_CGAP_GCBT1 Homo sapiens cDNA clone IMAGE:700345 5'
							Homo sapiens KVLQ11 gene
							Epstein-Barr virus (AG876 isolate) U2-IR2 domain encoding nuclear protein EBNA2, complete cds
							Epstein-Barr virus (AG876 isolate) U2-IR2 domain encoding nuclear protein EBNA2, complete cds

Table 4  
Single Exon Probes Expressed in HELA Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5479	14706	24080	1.85	1.0E-03	Q02388	SWISSPROT	COLLAGEN ALPHA 1(VII) CHAIN PRECURSOR (LONG-CHAIN COLLAGEN) (LC COLLAGEN)
5667	14889		2.54	1.0E-03	X07699.1	NT	Mouse nucleolin gene
5692	14912	24306	3.07	1.0E-03	BE983939.2	EST_HUMAN	601857519R1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3875693 3'
5750	14969		9.14	1.0E-03	11526178	NT	Homo sapiens T-cell lymphoma invasion and metastasis 1 (TIAM1), mRNA
6141	15325	24760	2.83	1.0E-03	D16828.1	NT	Human gene for fourth somatostatin receptor subtype
6352	15532	24984	1.65	1.0E-03	U52111.2	NT	Homo sapiens X28 region near ALD locus containing dual specificity phosphatase 8 (DUSP8), ribosomal protein L18a (RPL18a), Ca2+/Calmodulin-dependent protein kinase 1 (CAMK1), creatine transporter (CRTR), CDM protein (CDM), adrenoleukodystrophy protein >
6379	15559	25015	3.58	1.0E-03	M63376.1	NT	Human TRPM-2 protein gene, exons 1,2 and 3
6442	15639	25108	8.04	1.0E-03	AJ251973.1	NT	Homo sapiens partial steerin-1 gene
6541	15737	25198	2.89	1.0E-03	AF153980.1	NT	Homo sapiens exostosin-like protein 1 (EXTL1) gene, exons 2 through 11, and complete cds
6813	16008	25470	3	1.0E-03	M30471.1	NT	Human class III alcohol dehydrogenase (ADH5) chi subunit mRNA, complete cds
6813	16008	25471	3	1.0E-03	M30471.1	NT	Human class III alcohol dehydrogenase (ADH5) chi subunit mRNA, complete cds
6966	16144	25613	2.52	1.0E-03	AF011400.1	NT	Thermoboga neapolitana alpha-1,6-galactosidase (aglA) gene, complete cds
6966	16144	25614	2.52	1.0E-03	AF011400.1	NT	Thermoboga neapolitana alpha-1,6-galactosidase (aglA) gene, complete cds
7258	16478	25969	1.89	1.0E-03	AW362393.1	EST_HUMAN	RC1-CT0279-181099-011-a09 CT0279 Homo sapiens cDNA
7258	16478	25970	1.89	1.0E-03	AW362393.1	EST_HUMAN	RC1-CT0279-181099-011-a09 CT0279 Homo sapiens cDNA
7336	16552	26041	3.07	1.0E-03	BE170859.1	EST_HUMAN	QV3-HT0543-220300-130-a03 HT0543 Homo sapiens cDNA
7400	16613		3.38	1.0E-03	AJ583847.1	EST_HUMAN	IR73a12.x1 NCI_CGAP_HSC3 Homo sapiens cDNA clone IMAGE:2248448 3' similar to TR:Q26195 Q26195
7468	16676	26159	1.64	1.0E-03	AW237482.1	EST_HUMAN	PVA1 GENE. ;
7717	16916		4.02	1.0E-03	AV759949.1	EST_HUMAN	xm72d12.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2688751 3'
8307	17413	26935	5.13	1.0E-03	BE5894488.1	EST_HUMAN	AV759949 MDS Homo sapiens cDNA clone MDSDDF11 5'
8778	17708	23956	1.55	1.0E-03	9507208	NT	601433087F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3918524 5'
8803	18308		3.08	1.0E-03	AJ347355.1	EST_HUMAN	Rattus norvegicus transcription related protein 63 (Trp63), mRNA
8921	18330	23602	4.03	1.0E-03	BE780572.1	EST_HUMAN	tc05h11.x1 NCI_CGAP_Co16 Homo sapiens cDNA clone IMAGE:2063013 3' similar to contains Alu repetitive element;
5225	14399	23482	1.31	9.0E-04	L11910.1	NT	601468878F1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3872035 5'
5527	14751		1.66	9.0E-04	P06727	SWISSPROT	Human retinoblastoma susceptibility gene exons 1-27, complete cds
4161	13355		5.66	8.0E-04	P08547	SWISSPROT	APOLIPOPROTEIN A-IV PRECURSOR (APO-AIV)
4776	13665	23068	2.33	8.0E-04	U29185.1	NT	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG
7705	16904		2.61	8.0E-04	AA77084.1	EST_HUMAN	Homo sapiens prion protein (PrP) gene, complete cds
7843	17035		2.58	8.0E-04	AJ571099.1	EST_HUMAN	z24c10.s1 Soares_fetal_NH19W Homo sapiens cDNA clone IMAGE:377874 3'
1795	11094	20189	1.5	7.0E-04	L41825.1	NT	tr85a08.x1 NCI_CGAP_U2 Homo sapiens cDNA clone IMAGE:2176310 3'
							Homo sapiens CYP17 gene, 5' end

Page 123 of 382  
Table 4  
Single Exon Probes Expressed in HELA Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2363	11556	20778	0.99	7.0E-04	U28185.1	NT	Homo sapiens prion protein (PrP) gene, complete cds
2874	11856	21071	1.13	7.0E-04	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C010
3248	12481	21813	1.3	7.0E-04	4885170	NT	Homo sapiens chromosome X open reading frame 9 (CXORF9) mRNA
5980	15097		2.17	7.0E-04	AI769331.1	EST_HUMAN	wg3669.x1 Soares NSF_E8_9W_OT_PA_P_ST Homo sapiens cDNA clone IMAGE:2367209 3'
8100	17234		3.32	7.0E-04	U78027.1	NT	Homo sapiens Bruton's tyrosine kinase (BTK), alpha-D-galactosidase A (GLA), L44-like ribosomal protein (L44L) and FTP3 (FTP3) genes, complete cds
8120	17254	28795	2.18	7.0E-04	Z40581.1	EST_HUMAN	HSC28A072 normalized infant brain cDNA Homo sapiens cDNA clone c-28a07 3'
8847	17755		3.68	7.0E-04	BE077941.1	EST_HUMAN	CM1-BT0814-110300-142-b12 BT0814 Homo sapiens cDNA
8098	17912		3.4	7.0E-04	RI7338.1	EST_HUMAN	Yp13c08.r1 Soares infant brain 1N1B Homo sapiens cDNA clone IMAGE:32288 5'
9125	17938		3.87	7.0E-04	6005855	NT	Homo sapiens Retina-derived POU-domain factor-1 (RPF-1), mRNA
2656	11838		1.75	6.0E-04	BF341380.1	EST_HUMAN	602013339F1 NCI_CGAP_Bim64 Homo sapiens cDNA clone IMAGE:4149287 5'
3836	13152	22288	1.76	6.0E-04	AI862525.1	EST_HUMAN	Wj15a11.x1 NCI_CGAP_Kid12 Homo sapiens cDNA clone IMAGE:2402876 3'
4065	13275	22375	1.44	6.0E-04	K01315.1	NT	Homo sapiens epsilon-1 pseudogene (IGHEP1) gene, 5' flanking region
4085	13275	22378	1.44	6.0E-04	K01315.1	NT	Homo sapiens epsilon-1 pseudogene (IGHEP1) gene, 5' flanking region
4166	13370	22489	3.95	6.0E-04	U45983.1	NT	Homo sapiens CCR8 chemokine receptor (CMKBR8) gene, complete cds
7066	16243		5.71	6.0E-04	AL048507.2	EST_HUMAN	DKFZp586M2024_r1 588 (synonym: hute1) Homo sapiens cDNA clone DKFZp586M2024
7101	16278	25758	2.59	6.0E-04	BE005850.1	EST_HUMAN	RC2-BN0120-250400-012-h11 BN0120 Homo sapiens cDNA
8019	17158	26694	2.73	6.0E-04	AJ228042.1	NT	Homo sapiens 959 kb contig between AML1 and CBR1 on chromosome 21q22, segment 2/3
8101	17235	26771	3.28	6.0E-04	AW013847.1	EST_HUMAN	UI-H-Bio-aab-e-09-0-UI.s1 NCI_CGAP_Sub1 Homo sapiens cDNA clone IMAGE:2708825 3'
8152	17284		2.49	6.0E-04	Q01768	SWISSPROT	NUCLEOSIDE DIPHOSPHATE KINASE B (NDK B) (NDP KINASE B) (NM23-M2) (P18)
8498	18208		2.39	6.0E-04	AW380519.1	EST_HUMAN	RC1-HT0269-261199-012-ab8 HT0269 Homo sapiens cDNA
657	9903	19028	7.85	5.0E-04	O10341	SWISSPROT	HYPOPHOSPHATE KINASE 2B (H2B) (ORF92)
1493	10706		1.5	5.0E-04	AW851844.1	EST_HUMAN	QV0-CT0225-021099-030-a07 CT0225 Homo sapiens cDNA
3391	12618	21749	1.57	5.0E-04	AA548931.1	EST_HUMAN	nK27e11.s1 NCI_CGAP_Cot11 Homo sapiens cDNA clone IMAGE:1014784 3' similar to contains Alu repetitive element;
5428	14856	23794	2.85	5.0E-04	AF248054.1	NT	Bos taurus micromolar calcium activated neutral protease 1 (CAPN1) gene, exons 11-20, and partial cds
5947	15163	24577	4.71	5.0E-04	AA156080.1	EST_HUMAN	20333b08.r1 Stratiogene colon (#937204) Homo sapiens cDNA clone IMAGE:589863 5'
6246	15427	24867	12.76	5.0E-04	M23604.1	NT	Gorilla gorilla involucrin gene medium allele, complete cds
6444	15641	25107	6.01	5.0E-04	AI188382.1	EST_HUMAN	qd13f06.x1 Soares placenta, 8to9weeks, 2NbhIP8b9W Homo sapiens cDNA clone IMAGE:1723619 3' similar to gp.X51602_cds1 VASCULAR ENDOTHELIAL GROWTH FACTOR RECEPTOR 1 (HUMAN); contains Alu repetitive element;
6968	16146	25817	5.62	5.0E-04	AW270938.1	EST_HUMAN	xs06a02.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2768858 3'
7649	18754		4.31	5.0E-04	AL048507.2	EST_HUMAN	DKFZp586M2024_r1 588 (synonym: hute1) Homo sapiens cDNA clone DKFZp586M2024



Page 124 of 382  
Table 4  
Single Exon Probes Expressed in HELA Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8203	14656	23794	12.77	5.0E-04	AF248054.1	NT	Bos taurus micromolar calcium activated neutral protease 1 (CAPN1) gene, exons 11-20, and partial cds
8428	18140		2.42	5.0E-04	AA588513.1	EST_HUMAN	h15h02.s1 NCI_CGAP_P11 Homo sapiens cDNA clone IMAGE:913875
879	8823	19054	1.37	4.0E-04	U32748.1	NT	Haemophilus influenzae Rd section 63 of 183 of the complete genome
857	10093	19255	1.36	4.0E-04	A1720263.1	EST_HUMAN	as70b08.x1 Barstead colon HPLRB7 Homo sapiens cDNA clone IMAGE:2334039 3' similar to TR:Q13825
857	10093	19256	1.38	4.0E-04	A1720263.1	EST_HUMAN	as70b08.x1 Barstead colon HPLRB7 Homo sapiens cDNA clone IMAGE:2334039 3' similar to TR:Q13825
1461	10674	19847	2.48	4.0E-04	AW753356.1	EST_HUMAN	Q13825 AU-BINDING PROTEINENOL-COA HYDRATASE. ;
2052	11253	20467	1.21	4.0E-04	AL163278.2	NT	as70b08.x1 Barstead colon HPLRB7 Homo sapiens cDNA clone IMAGE:2334039 3' similar to TR:Q13825
2103	11303		0.9	4.0E-04	AL046704.1	EST_HUMAN	Q13825 AU-BINDING PROTEINENOL-COA HYDRATASE. ;
2590	11776	20995	2.53	4.0E-04	O98615	SWISSPROT	RC3-CT0254-130100-023-401 CT0254 Homo sapiens cDNA
3128	12363	21483	1.41	4.0E-04	AF281074.1	NT	Homo sapiens chromosome 21 segment HS21C078
3335	12564	21702	0.61	4.0E-04	AV696824.1	EST_HUMAN	DKFZp434D059_r1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434D059 5'
4314	13515	22608	3.3	4.0E-04	AA576331.1	EST_HUMAN	SERICIN-2 (SILK GUM PROTEIN 2)
4314	13515	22609	3.3	4.0E-04	AA576331.1	EST_HUMAN	Homo sapiens neuropilin 2 (NRP2) gene, complete cds, alternatively spliced
4534	13730	22827	2.26	4.0E-04	AA086324.1	EST_HUMAN	nh10a10.s1 NCI_CGAP_Co1 Homo sapiens cDNA clone IMAGE:562870 3'
5119	14298	23386	2.96	4.0E-04	BE560680.1	EST_HUMAN	SPECIFIC RANTES PROTEIN PRECURSOR (HUMAN);
5190	14368		0.86	4.0E-04	BE178680.1	EST_HUMAN	nh10a10.s1 NCI_CGAP_Co1 Homo sapiens cDNA clone IMAGE:562870 3'
6637	15832	25293	2.98	4.0E-04	N25507.1	EST_HUMAN	PM4-HT0608-030400-001-h11 HT0608 Homo sapiens cDNA
8814	18112		1.78	4.0E-04	AF254822.1	NT	yx39e12.r1 Soares melanocyte 2NblHM Homo sapiens cDNA clone IMAGE:264142 5'
8974	18085		1.81	4.0E-04	Q05860	SWISSPROT	Homo sapiens SMARCA4 isoform (SMARCA4) gene, complete cds, alternatively spliced
159	8441	18574	3.52	3.0E-04	AL119426.1	EST_HUMAN	FORMIN (LMB DEFORMITY PROTEIN)
200	9480	18613	2.15	3.0E-04	P49259	SWISSPROT	DKFZp78J221_r1 761 (synonym: hamy2) Homo sapiens cDNA clone DKFZp78J221 5'
890	10125	19288	2.39	3.0E-04	U83991.1	NT	180 KD SECRETORY PHOSPHOLIPASE A2 RECEPTOR PRECURSOR (PLA2-R)
1807	11016	20208	1.27	3.0E-04	AL262100.1	EST_HUMAN	Human short chain acyl CoA dehydrogenase gene, exons 1 and 2
1821	11029		1.12	3.0E-04	A1989674.1	EST_HUMAN	qz28d03.y1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2028197 5'
3279	12511	21641	3.59	3.0E-04	P25147	SWISSPROT	h23a02.y1 NCI_CGAP_P228 Homo sapiens cDNA clone IMAGE:2119082 3'
3941	13157	22274	3.38	3.0E-04	P49448	SWISSPROT	INTERNALIN B PRECURSOR
4033	13243		1.73	3.0E-04	A1271735.1	NT	GLUTAMATE DEHYDROGENASE 2 PRECURSOR (GDH)
4069	13279		1.92	3.0E-04	BE140609.1	EST_HUMAN	Homo sapiens Xq pseudautosomal region, segment 1/2
4831	14020		5.35	3.0E-04	BE153778.1	EST_HUMAN	RCO-HT0014-310599-028 HT0014 Homo sapiens cDNA
						EST_HUMAN	PM0-HT0339-180200-007-g12 HT0339 Homo sapiens cDNA

Page 125 of 382  
Table 4  
Single Exon Probes Expressed in HELA Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4903	14091	23184	0.85	3.0E-04	AW937723.1	EST_HUMAN	QV3-DT0045-221289-046-d09 DT0045 Homo sapiens cDNA
5289	14460	23528	1.22	3.0E-04	L78833.1	NT	Human BRCA1, Rho7 and veil genes, complete cds, and jpr35 gene, partial cds
5732	14951		5.43	3.0E-04	AL163281.2	NT	Homo sapiens chromosome 21 segment HS21C081
6006	15256	24680	1.93	3.0E-04	AL163278.2	NT	Homo sapiens chromosome 21 segment HS21C078
6546	15742	25203	6.87	3.0E-04	P22607	SWISSPROT	FIBROBLAST GROWTH FACTOR RECEPTOR 3 PRECURSOR (FGFR-3)
7202	16379	25860	7.45	3.0E-04	AA761201.1	EST_HUMAN	g124g05.s1 Soares, testis, NHT Homo sapiens cDNA clone 1391288 3' similar to gb:M36072 60S
8380	18348	23606	2.85	3.0E-04	AA228301.1	EST_HUMAN	RIBOSOMAL PROTEIN L7A (HUMAN); repetitive element;
8770	18188	23758	2.87	3.0E-04	AB018292.1	NT	Homo sapiens mRNA for KIAA0749 protein, partial cds
9191	17979		2.55	3.0E-04	AL134483.1	EST_HUMAN	DKFZ547L185_r1 547 (synonym: hibr1) Homo sapiens cDNA clone DKFZp547L185 5'
179	9459	18591	1.76	2.0E-04	AF217796.1	NT	Homo sapiens SCG10 like-protein, helicase-like protein NHL, M88, and ADP-ribosylation factor related protein 1 (ARFRP1) genes, complete cds
485	9737	18870	3.52	2.0E-04	AU148707.1	EST_HUMAN	AU148707 HEMBB1 Homo sapiens cDNA clone HEMBB1001253 3'
917	10152	18312	10.64	2.0E-04	M86524.1	NT	Human dystrophin gene
917	10152	18313	10.64	2.0E-04	M86524.1	NT	Human dystrophin gene
1187	10408		4.9	2.0E-04	AI286021.1	EST_HUMAN	qh98a11.x1 Soares, NFL_I_GBC_S1 Homo sapiens cDNA clone IMAGE:1855052 3' similar to contains
1194	10414		2.28	2.0E-04	AL183203.2	NT	MER3.b2 MER3 repetitive element;
1800	11009		1.44	2.0E-04	AF224288.1	NT	Homo sapiens chromosome 21 segment HS21C003
2150	11348		1.37	2.0E-04	AA478980.1	EST_HUMAN	Mus musculus 5' flanking region of Pitx3 gene zu39p05.s1 Soares ovary tumor NbHOT Homo sapiens cDNA clone IMAGE:740337 3' similar to contains Alu repetitive element;
2539	11727	20944	2.71	2.0E-04	U86081.1	NT	Human germline T-cell receptor beta chain TCRBV17S1A1T, TCRBV2S1, TCRBV10S1P, TCRBV28S1P, TCRBV18S1P, TCRBV15S1, TCRBV11S1A1T, HVB relic, TCRBV28S1P, TCRBV34S1, TCRBV14S1, TCRBV3S1, TCRBV4S1A1T, TRY4, TRY6, TRY7, TRY8, TCRBD1, TCRBJ1S1, TCRBJ1S2.>
2944	12182	21315	1.02	2.0E-04	AI124529.1	EST_HUMAN	am58c09.x1 Johnston frontal cortex Homo sapiens cDNA clone IMAGE:1539760 3'
3308	12538	21672	0.74	2.0E-04	5174736	NT	Homo sapiens tubulin, beta, 4 (TUBB4) mRNA
3414	12640	21769	2.01	2.0E-04	BE082317.1	EST_HUMAN	QV2-BT0636-070500-194-b07 B10636 Homo sapiens cDNA
3890	13106	22224	0.7	2.0E-04	AW978441.1	EST_HUMAN	EST390550 IMAGE resequences, MAGP Homo sapiens cDNA
4125	13331		6.15	2.0E-04	U01028.1	NT	Phaseolus vulgaris nitrate reductase (PVNR2) gene, complete cds
4672	13866	22867	1.32	2.0E-04	H96285.1	EST_HUMAN	y01e11.1 Soares, pineal_gland_N3HPG Homo sapiens cDNA clone IMAGE:232556 5'
4672	13866	22868	1.32	2.0E-04	H96285.1	EST_HUMAN	y01e11.1 Soares, pineal_gland_N3HPG Homo sapiens cDNA clone IMAGE:232556 5'
4807	13996		1.61	2.0E-04	U09226.1	NT	Gallus gallus proteasome 28 kDa subunit homolog mRNA, complete cds

Table 4  
Single Exon Probes Expressed in HELA Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5090	14270	23354	1.31	2.0E-04	AB037897.1	NT	Danio rerio hector gene, exons 1 to 6, partial cds
5470	14698	24049	1.85	2.0E-04	AI600862.1	EST_HUMAN	U03b11.x1 NCI_CGAP_U13 Homo sapiens cDNA clone IMAGE:2207709 3'
6178	15360		2.39	2.0E-04	AU121712.1	EST_HUMAN	AU121712 MAMMA1 Homo sapiens cDNA clone MAMMA1000798 5'
6343	15524		13.77	2.0E-04	P08548	SWISSPROT	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG
7428	16638	26131	6.33	2.0E-04	AV730373.1	EST_HUMAN	AV730373 HTF Homo sapiens cDNA clone HTFAA01 5'
7853	17043	26560	6.28	2.0E-04	AI440282.1	EST_HUMAN	U01111.x1 NCI_CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2140269 3' similar to contains Alu repetitive element;
7864	17143	26676	3.15	2.0E-04	AW136740.1	EST_HUMAN	U11-B11-adm-c-04-Q-U1.s1 NCI_CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2717190 3'
8267	17394	26924	7.66	2.0E-04	AA320338.1	EST_HUMAN	EST22678 Adiposa tissue, white II Homo sapiens cDNA 5' end similar to EST containing Alu repeat
776	10015	19163	1.88	1.0E-04	H88846.1	EST_HUMAN	y26c09.s1 Soares melanocyte 2NbhM Homo sapiens cDNA clone IMAGE:262864 3' similar to contains L1.1 L1 repetitive element ;
1082	10307	18458	2.39	1.0E-04	P11369	SWISSPROT	RETROVIRUS-RELATED POL POLYPROTEIN [CONTAINS: REVERSE TRANSCRIPTASE ;
1122	10346	19496	3.89	1.0E-04	AW013947.1	EST_HUMAN	U11-B10-aab-e-09-Q-U1.s1 NCI_CGAP_Sub1 Homo sapiens cDNA clone IMAGE:2708825 3'
1122	10346	19497	3.89	1.0E-04	AW013947.1	EST_HUMAN	U11-B10-aab-e-09-Q-U1.s1 NCI_CGAP_Sub1 Homo sapiens cDNA clone IMAGE:2708825 3'
1340	10554		3.92	1.0E-04	U62918.1	NT	Anguilla anguilla dopaminergic D1A1 receptor (d1A1) gene, complete cds
1605	10819	19894	3.55	1.0E-04	AF148805.1	NT	Kaposi's sarcoma-associated herpesvirus ORF 68 gene, partial cds; and ORF 68, kaposin, v-FLIP, v-cyclin, latent nuclear antigen, ORF K14, v-GPCR, putative phosphoribosylformylglycinamide synthase, and LAMP (LAMP) genes, complete cds
1605	10819	19995	3.55	1.0E-04	AF148805.1	NT	Kaposi's sarcoma-associated herpesvirus ORF 68 gene, partial cds; and ORF 68, kaposin, v-FLIP, v-cyclin, latent nuclear antigen, ORF K14, v-GPCR, putative phosphoribosylformylglycinamide synthase, and LAMP (LAMP) genes, complete cds
1828	11037	20233	1.75	1.0E-04	AB048342.1	NT	Equus caballus DNA, chromosome 24q14, microsatellite TKY36
2648	11831	21044	0.91	1.0E-04	BE218833.1	EST_HUMAN	h45c08.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3176368 3'
2648	11831	21045	0.91	1.0E-04	BE218833.1	EST_HUMAN	h45c08.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3176368 3'
3252	12485	21617	0.95	1.0E-04	Q62203	SWISSPROT	SPLICEOSOME ASSOCIATED PROTEIN 62 (SAP 62) (SPLICING FACTOR 3A SUBUNIT 2) (SF3A60)
3716	12936	22054	0.82	1.0E-04	AI440282.1	EST_HUMAN	U01111.x1 NCI_CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2140269 3' similar to contains Alu repetitive element;
4037	13247	22350	2.01	1.0E-04	MT14042.1	NT	Mouse alpha 1 type-IV collagen mRNA
4058	13269	22371	1.16	1.0E-04	AV647727.1	EST_HUMAN	AV647727 GLC Homo sapiens cDNA clone GLC88D04 3'
4460	13658	22752	1.09	1.0E-04	P08547	SWISSPROT	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG
6159	15342	24779	9.99	1.0E-04	A1251800.1	EST_HUMAN	q57d10.x1 NCI_CGAP_Ov62 Homo sapiens cDNA clone IMAGE:1985683 3'
6322	15342	24779	12.88	1.0E-04	A1251800.1	EST_HUMAN	q57d10.x1 NCI_CGAP_Ov62 Homo sapiens cDNA clone IMAGE:1985683 3'
6863	16053	25521	3.89	1.0E-04	AI606220.1	EST_HUMAN	wf26c09.x1 Soares NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2356742 3'

Page 127 of 382  
Table 4  
Single Exon Probes Expressed in HELA Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7128	16305		5.3	1.0E-04	P08547	SWISSPROT	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG
7881	17059		2.28	1.0E-04	M28587.1	NT	Mouse alpha leukocyte interferon gene, complete cds
8159	17291	26832	1.93	1.0E-04	AB032968.1	NT	Homo sapiens mRNA for KIAA1142 protein, partial cds
8189	17321	26884	1.97	1.0E-04	AW269061.1	EST_HUMAN	xx49g12.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2816518 3'
8214	17345	26884	1.65	1.0E-04	Q03696	SWISSPROT	NEURONAL-GLIAL CELL ADHESION MOLECULE PRECURSOR (NG-CAM)
8214	17345	26885	1.65	1.0E-04	Q03686	SWISSPROT	NEURONAL-GLIAL CELL ADHESION MOLECULE PRECURSOR (NG-CAM)
8549	18158		1.5	1.0E-04	BE676396.1	EST_HUMAN	7f28a10.x1 NCI_CGAP_CLL1 Homo sapiens cDNA clone IMAGE:3298058 3' similar to contains L1.13 L1 repetitive element
705	6947	19083	2.76	9.0E-05	AA718933.1	EST_HUMAN	ah45c11.s1 Soares_testis_NHT Homo sapiens cDNA clone 1282488 3'
6905	16062		2.6	9.0E-05	D85606.1	NT	Homo sapiens gene for cholesteryltransferin type-A receptor, complete cds
7697	16898	26405	2.85	9.0E-05	AW073078.1	EST_HUMAN	xa3-4g05.x1 NCI_CGAP_Br18 Homo sapiens cDNA clone IMAGE:2568728 3' similar to contains L1.12 L1 repetitive element
7784	16987	26501	1.84	9.0E-05	AI287878.1	EST_HUMAN	q23f06.x1 NCI_CGAP_Lym8 Homo sapiens cDNA clone IMAGE:1982435 3' similar to contains element
8139	14862	24247	4.58	9.0E-05	Q60716	SWISSPROT	MIR repetitive element ; PROLYL 4-HYDROXYLASE ALPHA-2 SUBUNIT PRECURSOR
8604	18218		3.76	9.0E-05	AF128756.1	NT	Homo sapiens MSH55 gene, partial cds; and CLIC1, DDAH, G6b, G6c, G5b, G6d, G6e, G6f, BAT5, G5b, CSK2B, BAT4, G4, Apo M, BAT3, BAT2, AIF-1, 1C7, LST-1, LTB, TNF, and LTA genes, complete cds
831	10069	18224	1.8	8.0E-05	AJ251648.1	NT	Pisum sativum mRNA for beta-1,3 glucanase (gns2 gene)
874	10110		7.89	8.0E-05	AJ251646.1	NT	Pisum sativum mRNA for beta-1,3 glucanase (gns2 gene)
4477	13675	22764	0.69	8.0E-05	AW044905.1	EST_HUMAN	wy78e04.x1 Soares_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:2554638 3'
7710	16809	26419	2.06	8.0E-05	M69197.1	NT	Human haptoglobin and haptoglobin-related protein (HP and HPR) genes, complete cds
9229	18201		2.43	8.0E-05	AA279333.1	EST_HUMAN	zs88h01.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:704593 3' similar to contains Alu repetitive element ; contains element MSR1 repetitive element ;
352	9620	18747	7.26	7.0E-05	AW847445.1	EST_HUMAN	RC3-CT0208-220989-011-E04 CT0208 Homo sapiens cDNA
352	9620	18748	7.26	7.0E-05	AW847446.1	EST_HUMAN	RC3-CT0208-220989-011-E04 CT0208 Homo sapiens cDNA
574	9824	18943	1.33	7.0E-05	L49075.1	EST_HUMAN	HUM072014F Human fovea cDNA Homo sapiens cDNA clone EST HFD072014
574	9824	18944	1.33	7.0E-05	L49075.1	EST_HUMAN	HUM072014F Human fovea cDNA Homo sapiens cDNA clone EST HFD072014
1082	10288	19439	1.12	7.0E-05	Q22949	SWISSPROT	PROBABLE GLYCEROL-3-PHOSPHATE ACYLTRANSFERASE, MITOCHONDRIAL PRECURSOR (GPAT)
2678	11860	21074	4.06	7.0E-05	AL163278.2	NT	Homo sapiens chromosome 21 segment HS21C078
3122	12357	21486	5.35	7.0E-05	AB009080.1	NT	Dicystostellum discoideum gene for TRFA, complete cds
3679	12900		0.97	7.0E-05	AI432413.1	EST_HUMAN	tg73c09.x1 Soares_NhHMPu_S1 Homo sapiens cDNA clone IMAGE:2114416 3'
4366	13588	22684	1.5	7.0E-05	AL163201.2	NT	Homo sapiens chromosome 21 segment HS21C001

Page 128 of 382  
Table 4  
Single Exon Probes Expressed in HELA Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4440	13640	22731	0.61	7.0E-05	U00980.1	NT	Caenorhabditis elegans Skip'p homolog mRNA, complete cds
4947	14134	23228	0.85	7.0E-05	9845300	NT	Rat cytomegalovirus Measuricht, complete genome
6936	16080	25550	5.65	7.0E-05	T07095.1	EST_HUMAN	EST04984 Fetal brain, Stralagene (cat#839208) Homo sapiens cDNA clone HFBED60
7720	16919		6.81	7.0E-05	10895048	NT	Homo sapiens sarcoglycan, epsilon (SGCE), mRNA
1996	11199	20409	1.41	6.0E-05	4885170	NT	Homo sapiens chromosome X open reading frame 6 (CXORF6) mRNA
1996	11199	20410	1.41	6.0E-05	4885170	NT	Homo sapiens chromosome X open reading frame 6 (CXORF6) mRNA
2549	11737	20955	1.06	6.0E-05	A1655241.1	EST_HUMAN	W554H08.x1 NCI_CGAP_G08 Homo sapiens cDNA clone IMAGE:2309531 3' similar to gb:J03250 DNA TOPOISOMERASE I (HUMAN);
2766	8928	18059	2.78	6.0E-05	AF053630.1	NT	Homo sapiens monocyte/neutrophil elastase inhibitor gene, complete cds
5622	14845	24225	3.42	6.0E-05	Q12860	SWISSPROT	CONTACTIN PRECURSOR (GLYCOPROTEIN GP135)
5622	14845	24226	3.42	6.0E-05	Q12860	SWISSPROT	CONTACTIN PRECURSOR (GLYCOPROTEIN GP135)
6614	15810	25266	3.79	6.0E-05	AW896629.1	EST_HUMAN	P144-NN0050-310300-001-f10 NN0050 Homo sapiens cDNA yf59d08.s1 Scores placenta Nb2HP Homo sapiens cDNA clone IMAGE:143535 3' similar to contains Alu repetitive element; contains LTR7 repetitive element;
7334	16950	26040	4.35	6.0E-05	R75639.1	EST_HUMAN	2k59f02.r1 Scores_pregnant_uterus_Nb2HPU Homo sapiens cDNA clone IMAGE:487035 5'
8050	17186	26725	4.17	6.0E-05	AA044015.1	EST_HUMAN	MRO-NT0038-250400-001-f09 NT0038 Homo sapiens cDNA
8922	18169	23762	8.56	6.0E-05	AW890110.1	EST_HUMAN	QV4-ST0234-241199-040-h11 ST0234 Homo sapiens cDNA
1407	10620	19784	59.64	5.0E-05	AW392086.1	EST_HUMAN	Homo sapiens 22kDa peroxidomal membrane protein-like (LOC55895), mRNA
1831	11039		1.35	5.0E-05	8923891	NT	Homo sapiens partial SL C22A3 gene for extraneuronal monoamine transporter (EMT), exon 1
3957	13172	22287	3.89	5.0E-05	AJ251884.1	NT	Homo MLC1emb gene for embryonic myosin alkaline light chain, 3'UTR
5453	14679	23839	11.84	5.0E-05	X58855.1	NT	Human MLC1emb gene for embryonic myosin alkaline light chain, 3'UTR
5651	14874	24261	3.01	5.0E-05	AV653544.1	EST_HUMAN	AV653544 GLC Homo sapiens cDNA clone GLCDMA06 3'
8601	17775		3.79	5.0E-05	P49193	SWISSPROT	RETINAL-BINDING PROTEIN (RALBP)
8879	17775		4.46	5.0E-05	P49193	SWISSPROT	RETINAL-BINDING PROTEIN (RALBP)
2759	9511		3.93	4.0E-05	U12821.1	NT	Human renin (REN) gene, 5' flanking region
4479	13677	22766	0.73	4.0E-05	P49193	SWISSPROT	RETINAL-BINDING PROTEIN (RALBP)
4479	13677	22767	0.73	4.0E-05	P49193	SWISSPROT	RETINAL-BINDING PROTEIN (RALBP)
4892	14080		0.95	4.0E-05	AF164488.1	NT	Cryptosporidium parvum isolate Zaire 15 kDa glycoprotein gp15 gene, partial cds
5042	14226	23309	0.66	4.0E-05	AF212313.1	NT	Drosophila melanogaster senseless protein (sense) gene, complete cds
6923	16116		5.98	4.0E-05	AF202635.1	NT	Homo sapiens PP1200 mRNA, complete cds
7352	16568	26058	5.03	4.0E-05	AW627946.1	EST_HUMAN	h36c07.x1 Scores_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2874380 3' similar to contains element MIR repetitive element;
8471	17524	24025	1.47	4.0E-05	AL163252.2	NT	Homo sapiens chromosome 21 segment HS21C052
8500	17581		1.54	4.0E-05	AW117580.1	EST_HUMAN	xd83c09.x1 Scores_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2605192 3'
9256	18024		1.29	4.0E-05	AA417756.1	EST_HUMAN	z01e11.s1 NCI_CGAP_G081 Homo sapiens cDNA clone IMAGE:746252 3'

Page 129 of 382  
Table 4  
Single Exon Probes Expressed in HELA Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
687	8630	19061	0.64	3.0E-05	AI248061.1	EST_HUMAN	qh84c10.x1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:1849458 3' similar to contains Alu repetitive element; contains element KER repetitive element;
1066	10292	19443	0.87	3.0E-05	AW273851.1	EST_HUMAN	XV24g03.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2814100 3'
1139	10362	19511	2.89	3.0E-05	BF037898.1	EST_HUMAN	601461463F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3865142 5'
1139	10362	18512	2.89	3.0E-05	BF037898.1	EST_HUMAN	601461463F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3865142 5'
3261	12494		0.87	3.0E-05	AI288919.1	EST_HUMAN	qi91g11.x1 Soares_NHMPu_S1 Homo sapiens cDNA clone IMAGE:1879748 3' similar to TR:O08632
4376	13578	22676	5.19	3.0E-05	BE169211.1	EST_HUMAN	O08632 GLYCINE TYROSINE-RICH HAIR PROTEIN;
4376	13578	22677	5.19	3.0E-05	BE169211.1	EST_HUMAN	PM1-HT0521-120200-001-e10 HT0521 Homo sapiens cDNA
4462	13660	22753	0.9	3.0E-05	AA368679.1	EST_HUMAN	PM1-HT0521-120200-001-e10 HT0521 Homo sapiens cDNA
4462	13660	22754	0.9	3.0E-05	AA368679.1	EST_HUMAN	EST79696 Placenta I Homo sapiens cDNA similar to similar to p53-associated protein
4589	13763		0.89	3.0E-05	AL163302.2	NT	EST79696 Placenta I Homo sapiens cDNA similar to similar to p53-associated protein
4621	13815	22905	0.83	3.0E-05	AF149773.1	NT	Homo sapiens chromosome 21 segment HS21C102
4855	8630	19061	0.83	3.0E-05	AI248061.1	EST_HUMAN	Homo sapiens NOD1 protein (NOD1) gene, exons 1, 2, and 3
5471	14697	24050	1.83	3.0E-05	11072102	NT	qh84c10.x1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:1849458 3' similar to contains Alu repetitive element; contains element KER repetitive element;
6081	16159		4.49	3.0E-05	AF769331.1	EST_HUMAN	Mus musculus myosin light chain 2, precursor lymphocyte-specific (Mylc2pl), mRNA
8484	17532		1.67	3.0E-05	L77570.1	NT	wg36f09.x1 Soares_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:2367209 3'
2262	11487	20707	2.08	2.0E-05	AI286021.1	EST_HUMAN	Homo sapiens DiGeorge syndrome critical region, centromeric and
2545	11733	20950	4.57	2.0E-05	MT13792.1	NT	qh86e11.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1855052 3' similar to contains MER3.b2 MER3 repetitive element;
2673	11855		6.59	2.0E-05	AA160562.1	EST_HUMAN	Human adenosine deaminase (ADA) gene, complete cds
3102	12338	21466	1.78	2.0E-05	BE066036.1	EST_HUMAN	zq46a12.r1 Stratagene hNT neuron (#837233) Homo sapiens cDNA clone IMAGE:632734 5' similar to contains Alu repetitive element; contains element L1 repetitive element;
3322	12551	21685	0.96	2.0E-05	AF184614.1	NT	RC3-BT0319-120200-014-h08 BT0319 Homo sapiens cDNA
3348	12576	21717	0.93	2.0E-05	X89211.1	NT	Homo sapiens p47-phox (NCF1) gene, complete cds
3469	12684		0.69	2.0E-05	X95465.1	NT	H. sapiens DNA for endogenous retroviral like element
3795	13013		1.31	2.0E-05	AL039107.1	EST_HUMAN	S cerevisiae 12.8 Kbp fragment of the left arm of chromosome XV
4902	14090	23183	0.77	2.0E-05	AJ131016.1	NT	DKFZp5661064.r1 566 (synonym: htkd2) Homo sapiens cDNA clone DKFZp5661064 5'
5287	14440	23513	32.31	2.0E-05	AA084052.1	EST_HUMAN	Homo sapiens SCL gene locus
5555	14779	24147	1.75	2.0E-05	AJ011712.1	NT	zn18b10.s1 Stratagene neuroepithelium NT2RAM1 937234 Homo sapiens cDNA clone IMAGE:547579 3' similar to contains L1.11 L1 repetitive element;
5944	15160	24573	2.4	2.0E-05	AA714330.1	EST_HUMAN	Homo sapiens TNNT1 gene, exons 1-11 (and joined CDS)
6042	15210	24630	1.9	2.0E-05	Y08926.1	NT	nm06d12.s1 NCI CGAP_SS1 Homo sapiens cDNA clone IMAGE:1238519 3'
							P. falciparum mRNA for AARP1 protein, partial

Table 4  
Single Exon Probes Expressed in HELA Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6052	15220		9.31	2.0E-05	AI891025.1	EST_HUMAN	wu35h07.x1 Soares Dieckgraefe_colon_NHCO Homo sapiens cDNA clone IMAGE:2522077 3'
6142	15328	24761	2.26	2.0E-05	AF224282.1	NT	Heterodontus francisci HoxA10 (HoxA10), HoxA9 (HoxA9), HoxA7 (HoxA7), HoxA6 (HoxA6), HoxA5 (HoxA5), HoxA4 (HoxA4), HoxA3 (HoxA3), HoxA2 (HoxA2), and HoxA1 (HoxA1) genes, complete cds
6142	15328	24762	2.26	2.0E-05	AF224282.1	NT	Heterodontus francisci HoxA10 (HoxA10), HoxA9 (HoxA9), HoxA7 (HoxA7), HoxA6 (HoxA6), HoxA5 (HoxA5), HoxA4 (HoxA4), HoxA3 (HoxA3), HoxA2 (HoxA2), and HoxA1 (HoxA1) genes, complete cds
7223	16400	25885	5.08	2.0E-05	N41751.1	EST_HUMAN	yw91a08.r1 Soares placenta_8to9weeks_2NbHP8b0W Homo sapiens cDNA clone IMAGE:259570 5'
7223	16400	25886	5.08	2.0E-05	N41751.1	EST_HUMAN	yw91a08.r1 Soares placenta_8to9weeks_2NbHP8b0W Homo sapiens cDNA clone IMAGE:259570 5'
7238	15220		2.39	2.0E-05	AI891025.1	EST_HUMAN	wu35h07.x1 Soares Dieckgraefe_colon_NHCO Homo sapiens cDNA clone IMAGE:2522077 3'
7988	16423	25910	3.15	2.0E-05	BE175801.1	EST_HUMAN	RCS-HT0582-280300-012-E12 HT0582 Homo sapiens cDNA
8610	18125		5.29	2.0E-05	BE348228.1	EST_HUMAN	hw21a03.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:3183532 3' similar to TR:Q12832 Q12832 GLYCOPHORIN HEP2;
8723	18298		5.07	2.0E-05	AW074604.1	EST_HUMAN	xa89a03.x1 NCI_CGAP_Cot17 Homo sapiens cDNA clone IMAGE:2573832 3' similar to contains L1.b3 L1 repetitive element;
8773	18110		1.62	2.0E-05	AF275948.1	NT	Homo sapiens ABCA1 (ABCA1) gene, complete cds
8935	17816	23928	1.39	2.0E-05	AU131513.1	EST_HUMAN	AU131513 NT2RP3 Homo sapiens cDNA clone NT2RP3002707 5'
2655	12023	21050	1.24	1.0E-05	AL163282.2	NT	Homo sapiens chromosome 21 segment HS21C082
3628	12850	21869	1.97	1.0E-05	AF088273.1	NT	Drosophila melanogaster strain Lambo 120 Suppressor of Hairless (Su(H)) gene, partial cds
3801	13019		1.02	1.0E-05	AF223391.1	NT	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced
3944	13160	22276	11.49	1.0E-05	P81274	SWISSPROT	MOSAIC PROTEIN LGN
4262	13465	22556	1.56	1.0E-05	AA431119.1	EST_HUMAN	zw68g04.r1 Soares Testis_NHT Homo sapiens cDNA clone IMAGE:781494 5'
4967	14055	23149	1.7	1.0E-05	AW419134.1	EST_HUMAN	xy49g11.x1 NCI_CGAP_Lu34.1 Homo sapiens cDNA clone IMAGE:2856548 3'
4966	14173	23263	0.67	1.0E-05	AL163246.2	NT	Homo sapiens chromosome 21 segment HS21C046
6116	15228	24648	2.6	1.0E-05	AA641846.1	EST_HUMAN	ns18g02.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1184114 3' similar to contains L1.t1 L1 L1 repetitive element;
6118	15302	24734	12.58	1.0E-05	4505844	NT	Homo sapiens phospholipase A2, group X (PLA2G10) mRNA, and translated products
6750	15945		3.79	1.0E-05	AL163227.2	NT	Homo sapiens chromosome 21 segment HS21C027
6789	15984	25444	2.49	1.0E-05	AA452578.1	EST_HUMAN	zz35h12.s1 Soares total_fetus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:788519 3' similar to gb:L02632 PEROXISOME PROLIFERATOR ACTIVATED RECEPTOR ALPHA (HUMAN);

Table 4

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6851	16040	25504	15.7	1.0E-05	AA236110.1	EST_HUMAN	zs05a11.1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:68432 5' similar to contains Alu repetitive element; contains element TAR1 repetitive element;
7493	16700	26185	2.48	1.0E-05	U91328.1	NT	Human hereditary haemochromatosis region, histone 2A-like protein gene, hereditary haemochromatosis (HLA-H) gene, RoRet gene, and sodium phosphate transporter (NP-T3) gene, complete cds
7493	16700	26185	2.48	1.0E-05	U91328.1	NT	Human hereditary haemochromatosis region, histone 2A-like protein gene, hereditary haemochromatosis (HLA-H) gene, RoRet gene, and sodium phosphate transporter (NP-T3) gene, complete cds
2632	11815	21034	5.8	9.0E-06	AI583811.1	EST_HUMAN	173a08.x1 NCI_CGAP_HSC3 Homo sapiens cDNA clone IMAGE:2246386 3'
3081	12267	21421	5.75	9.0E-06	AI218983.1	EST_HUMAN	qg11b08.x1 Soares_placenta_8to8weeks_2Nbl-P8to9W Homo sapiens cDNA clone IMAGE:1759191 3'
3588	12809	25493	3.58	9.0E-06	M61755.1	NT	Human alanine:glyoxylate aminotransferase (AGXT) gene, exons 1 and 2
5617	14840	24218	2.48	9.0E-06	L23416.1	NT	Homo sapiens differentiation antigen CD20 gene, exons 5, 8
6408	15587	25046	11.37	9.0E-06	AI034370.1	EST_HUMAN	alpha20g01.x1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:1656812 3' similar to contains Alu repetitive element;
6833	16027	25493	4.11	9.0E-06	U35114.1	NT	Human apolipoprotein E (APOE) gene, hepatic control region HCR-2
7512	16717	26208	3.57	9.0E-06	Q10364	SWISSPROT	PUTATIVE SERINE/THREONINE-PROTEIN KINASE C22E12.14C
2495	12017	20902	2.21	8.0E-08	AW362538.1	EST_HUMAN	RC3-CT0283-201199-011-111 CT0283 Homo sapiens cDNA
988	10217		2.15	7.0E-06	AA669729.1	EST_HUMAN	ab90110.s1 Stratiens lung (#837210) Homo sapiens cDNA clone IMAGE:854251 3' similar to contains MER20.11 MER20 repetitive element;
1440	10654	19828	2.53	7.0E-06	7682177	NT	Homo sapiens KIAA0555 gene product (KIAA0555), mRNA
2825	12084		5.04	7.0E-06	AI368252.1	EST_HUMAN	qw16g09.x1 NCI_CGAP_U3 Homo sapiens cDNA clone IMAGE:1991298 3' similar to contains Alu repetitive element;
3538	12761		0.76	7.0E-06	AA385542.1	EST_HUMAN	EST89205 Thyroid Homo sapiens cDNA 5' and similar to EST containing L1 repeat
5533	14757		5.93	7.0E-06	AW883141.1	EST_HUMAN	QV2-OT0082-250400-173-H01 OT0082 Homo sapiens cDNA
8333	18321	25597	2.35	7.0E-06	BF215972.1	EST_HUMAN	601881522F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4083972 5'
2868	12106	21235	1.48	6.0E-06	BE069189.1	EST_HUMAN	QV3-BT0379-010300-105-411 BT0379 Homo sapiens cDNA
4764	12130	21265	2.05	6.0E-06	Q01456	SWISSPROT	OVARIAN ABUNDANT MESSAGE PROTEIN (OAM PROTEIN)
4771	13960	23061	2.03	6.0E-06	AI040089.1	EST_HUMAN	alpha20g02.x1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:1655738 3' similar to contains MER8.12 MER8 repetitive element;
7025	16202		2.62	6.0E-06	AW801912.1	EST_HUMAN	IL5-UM0070-110400-063-g02 UM0070 Homo sapiens cDNA
9220	17999	23867	2.28	6.0E-06	11418157	NT	Homo sapiens calcium channel, voltage-dependent, alpha 1I subunit (CACNA1I), mRNA
5694	14914	24308	4.05	5.0E-06	AL163246.2	NT	Homo sapiens chromosome 21 segment HS21C046



Page 132 of 382  
Table 4  
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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5805	15022	24423	1.98	5.0E-06	U07561.1	NT	Human ABL gene, exon 1b and intron 1b, and putative M8604 Met protein (M8604 Met) gene, complete cds
7113	16280	25771	10.33	5.0E-06	AA313620.1	EST_HUMAN	EST185486 Colon carcinoma (HCC) cell line Homo sapiens cDNA 5' end
9104	17928	23878	3.8	5.0E-06	AI065045.1	EST_HUMAN	HA0877 Human fetal liver cDNA library Homo sapiens cDNA
653	9899	19024	6.68	4.0E-06	R18267.1	EST_HUMAN	ye48c03.r1 Soares infant brain 1N1B Homo sapiens cDNA clone IMAGE:53254 5' similar to contains Alu repetitive element; contains L1 repetitive element;
856	10092	19254	11.86	4.0E-06	AW103354.1	EST_HUMAN	xc68g12.x1 NCI_CGAP_Eso2 Homo sapiens cDNA clone IMAGE:2589574 3' similar to contains Alu repetitive element; contains element MER21 repetitive element;
1342	10556	19721	4.4	4.0E-06	AI334928.1	EST_HUMAN	tb33e09.x1 NCI_CGAP_HSC2 Homo sapiens cDNA clone IMAGE:2056168 3'
1342	10556	19722	4.4	4.0E-06	AI334928.1	EST_HUMAN	tb33e09.x1 NCI_CGAP_HSC2 Homo sapiens cDNA clone IMAGE:2056168 3'
1469	10882	19856	5.73	4.0E-06	BF365612.1	EST_HUMAN	QV2-NT0048-200600-260-H07 NT0048 Homo sapiens cDNA
2230	11428	20652	1.39	4.0E-06	AW015401.1	EST_HUMAN	U1-H-B10-act-f05-0-U1.s1 NCI_CGAP_Sub1 Homo sapiens cDNA clone IMAGE:2710425 3'
3028	12264	21392	1	4.0E-06	AF198349.1	NT	Gallus gallus Dech2 protein (Dech2) mRNA, complete cds
3872	13088	22204	1.34	4.0E-06	AW048295.1	EST_HUMAN	IL3-CT0214-150200-074-B03 CT0214 Homo sapiens cDNA
4821	14010	23108	1.81	4.0E-06	AI868939.1	EST_HUMAN	wf94c10.x1 NCI_CGAP_Bm25 Homo sapiens cDNA clone IMAGE:2432562 3' similar to contains element MER22 repetitive element;
6716	15911	25369	2.61	4.0E-06	AF009660.1	NT	Homo sapiens T cell receptor beta locus, TCRBV7S3A2 to TCRBV12S2 region
7985	16420	25907	4.04	4.0E-06	AB007855.1	NT	Homo sapiens mRNA, chromosome 1 specific transcript KIAA0488
2129	11328	20546	1.11	3.0E-06	AA700562.1	EST_HUMAN	z34b08.s1 Soares_fetal_liver_spleen_INFLS_S1 Homo sapiens cDNA clone IMAGE:432663 3' similar to contains L1.11 L1 repetitive element;
2129	11328	20547	1.11	3.0E-06	AA700562.1	EST_HUMAN	z34b08.s1 Soares_fetal_liver_spleen_INFLS_S1 Homo sapiens cDNA clone IMAGE:432663 3' similar to contains L1.11 L1 repetitive element;
2232	11427		2.13	3.0E-06	AF202635.1	NT	Homo sapiens PP1200 mRNA, complete cds
2872	12110	21238	1.04	3.0E-06	AA868218.1	EST_HUMAN	ak48g11.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1409252 3' similar to contains LTR1.13 LTR1 repetitive element;
3232	12468		2.55	3.0E-06	AI857779.1	EST_HUMAN	w22a05.x1 NCI_CGAP_U1 Homo sapiens cDNA clone IMAGE:2425616 3' similar to TR:O60734 O60734 LINE-1 LIKE PROTEIN; contains L1.12 L1 repetitive element;
3766	12984	22099	1.35	3.0E-06	BE047094.1	EST_HUMAN	hg64d12.x1 NCI_CGAP_HN13 Homo sapiens cDNA clone IMAGE:3124151 3'
3766	12984	22100	1.35	3.0E-06	BE047094.1	EST_HUMAN	hg64d12.x1 NCI_CGAP_HN13 Homo sapiens cDNA clone IMAGE:3124151 3'
4560	13754	22852	3.87	3.0E-06	X54816.1	NT	Homo sapiens gene for alpha-1-microglobulin-bikunin, exons 1-5 (encoding alpha-1-microglobulin, N-terminus.)
6177	15359		2.52	3.0E-06	P08548	SWISSPROT	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG
8781	17710		7.4	3.0E-06	AW385262.1	EST_HUMAN	RCQ1-T0001-281189-011-A03 LT0001 Homo sapiens cDNA
207	9487		2.17	2.0E-06	P54368	SWISSPROT	HOMEBOX PROTEIN GOOSECOID

Page 133 of 382  
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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1549	10763		4.53	2.0E-06	P21414	SWISSPROT	POL POLYPROTEIN [CONTAINS: PROTEASE ; REVERSE TRANSCRIPTASE; ENDONUCLEASE] w804a03.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2287068 3' similar to contains MER30 b1 MER30 repetitive element ;
2344	11537	20761		2.0E-06	A1672138.1	EST_HUMAN	
2428	11920	20841	1.48	2.0E-06	P04929	SWISSPROT	HISTIDINE-RICH GLYCOPROTEIN PRECURSOR
2632	11720	20837	1.7	2.0E-06	P06719	SWISSPROT	KNOB-ASSOCIATED HISTIDINE-RICH PROTEIN PRECURSOR (KAHRP)
3492	12716	21852	1.07	2.0E-06	AV657555.1	EST_HUMAN	AV657555 GLC Homo sapiens cDNA clone GLCFDB05 3'
3744	12664	22079	1.19	2.0E-06	AA173518.1	EST_HUMAN	402a05.r1 Stragene ovarian cancer (#837219) Homo sapiens cDNA clone IMAGE:595232 5'
3752	12971	22086	0.62	2.0E-06	AW450215.1	EST_HUMAN	UIH-B13-4ky-g-05-O-U1.s1 NCI_CGAP_Sub5 Homo sapiens cDNA clone IMAGE:2736178 3'
3758	12977	22092	1.66	2.0E-06	AB030896.1	NT	Mus musculus gene for odorant receptor A16, complete cds
5945	15062	24470	5.38	2.0E-06	AB18424.1	EST_HUMAN	wj90b04.x1 NCI_CGAP_Lym12 Homo sapiens cDNA clone IMAGE:2410063 3'
8663	18322	23598	1.53	2.0E-06	P23249	SWISSPROT	PROTEIN MOV-10
8837	17747		2.74	2.0E-06	BE328232.1	EST_HUMAN	hs92702.x1 NCI_CGAP_Kid13 Homo sapiens cDNA clone IMAGE:3144698 3' similar to contains L1.12 L1 repetitive element ;
35	9331	18436	2.01	1.0E-06	O76082	SWISSPROT	ORGANIC CATION/CARNITINE TRANSPORTER 2 (SOLUTE CARRIER FAMILY 22, MEMBER 5) (HIGH- AFFINITY SODIUM-DEPENDENT CARNITINE COTRANSPORTER)
663	9909	19038	1.28	1.0E-06	AF084394.1	NT	Mus musculus D8MM5E protein (D8MM5e) mRNA, complete cds
1452	10865	19839	1.48	1.0E-06	P09125	SWISSPROT	MEROZOITE SURFACE PROTEIN CMZ-8
1510	10724	19898	1.14	1.0E-06	AL163278.2	NT	Homo sapiens chromosome 21 segment HS21C078
1552	10768	19839	0.95	1.0E-06	AA034141.1	EST_HUMAN	z106a12.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:429982 3' similar to contains Alu repetitive element;
1552	10768	19940	0.95	1.0E-06	AA034141.1	EST_HUMAN	z106a12.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:429982 3' similar to contains Alu repetitive element;
1563	10777		1.12	1.0E-06	P27826	SWISSPROT	DNA-DIRECTED RNA POLYMERASE III LARGEST SUBUNIT
1983	11167	20371	10.85	1.0E-06	AF184614.1	NT	Homo sapiens p47-phox (NCF1) gene, complete cds
1983	11167	20372	10.85	1.0E-06	AF184614.1	NT	Homo sapiens p47-phox (NCF1) gene, complete cds
4363	13565	22660	13.16	1.0E-06	U07561.1	NT	Human ABL gene, exon 1b and intron 1b, and putative M8604 Met protein (M8604 Met) gene, complete cds
5268	14439	23512	2.15	1.0E-06	U07561.1	NT	Human ABL gene, exon 1b and intron 1b, and putative M8604 Met protein (M8604 Met) gene, complete cds
5288	14459		0.61	1.0E-06	U61297.1	NT	Human progesterone receptor (PGR) gene, far 5' flanking region
5320	14552	23622	5.34	1.0E-06	BF333015.1	EST_HUMAN	MRI-BT0800-030700-002-c06 BT0800 Homo sapiens cDNA
6028	15236	24659	5.56	1.0E-06	P02671	SWISSPROT	FIBRINOGEN ALPHA1/ALPHA-E CHAIN PRECURSOR
6985	16163	25634	2.58	1.0E-06	U82698.1	NT	Homo sapiens shox gene, alternatively spliced products, complete cds
6985	16163	25635	2.58	1.0E-06	U82698.1	NT	Homo sapiens shox gene, alternatively spliced products, complete cds

Page 134 of 382  
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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7011	16189		4.26	1.0E-06	AA449257.1	EST_HUMAN	z04d11.s1 Scores: total_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:785493 3' similar to gb:D28129 RIBONUCLEASE PANCREATIC PRECURSOR (HUMAN);
8158	17260		5.02	1.0E-06	AW890941.1	EST_HUMAN	RC4-NT0054-120500-012-603 NT0054 Homo sapiens cDNA
8721	17674	23949	3.45	1.0E-06	L78910.1	NT	Homo sapiens ADP/ATP carrier protein (ANT-2) gene, complete cds
8824	11167	20371	1.86	1.0E-06	AF184614.1	NT	Homo sapiens p47-phox (NCF1) gene, complete cds
8824	11167	20372	1.86	1.0E-06	AF184614.1	NT	Homo sapiens p47-phox (NCF1) gene, complete cds
365	9632	18784	2.24	9.0E-07	AF003528.1	NT	Homo sapiens p47-phox (NCF1) gene, complete cds
365	9632	18785	2.24	9.0E-07	AF003528.1	NT	Homo sapiens glycylc 3 (GPC3) gene, partial cds and flanking repeat regions
5223	14397		1.4	9.0E-07	AW971932.1	EST_HUMAN	Homo sapiens glycylc 3 (GPC3) gene, partial cds and flanking repeat regions
7789	16982	26505	2.85	9.0E-07	AL163281.2	NT	EST384021 MAGE resequences, MAGI Homo sapiens cDNA
4781	13970	23072	4.52	8.0E-07	A1288596.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C081
4781	13970	23073	4.52	8.0E-07	A1288596.1	EST_HUMAN	q182g07.x1 Scores: NHMPu_S1 Homo sapiens cDNA clone IMAGE:1878876 3'
5608	14832		8.53	8.0E-07	P21414	SWISSPROT	q182g07.x1 Scores: NHMPu_S1 Homo sapiens cDNA clone IMAGE:1878876 3'
6485	15662		14.61	8.0E-07	AF135410.1	NT	POLYPROTEIN [CONTAINS: PROTEASE; REVERSE TRANSCRIPTASE; ENDONUCLEASE]
8142	17274		8.94	8.0E-07	T07770.1	EST_HUMAN	Homo sapiens UDP-glucuronosyltransferase gene, complete cds
8316	17420		5.59	8.0E-07	AL163280.2	NT	EST056660 Fetal brain, Stratiogene (cat#9393206) Homo sapiens cDNA clone HFBEN89
1877	11084	20274	2.64	6.0E-07	AW855558.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C080
							OM3-CT0277-221099-024-e11 CT0277 Homo sapiens cDNA
							Homo sapiens HLA class III region containing tenascin X (tenascin-X) gene, partial cds: cytochrome P450 21-hydroxylase (CYP21B), complement component C4 (C4B) G11, helicase (SKI2W), RD, complement factor B (Bf), and complement component C2 (C2) genes.>
2455	11846	20867	2.48	6.0E-07	AF019413.1	NT	HYPOTHETICAL 24.1 KD PROTEIN IN LEF-4-P33 INTERGENIC REGION
3949	13165		2.04	6.0E-07	P41479	SWISSPROT	OM4-NN1029-250300-121-h12 NN1029 Homo sapiens cDNA
8578	18287		2.08	6.0E-07	AW603222.1	EST_HUMAN	wh64f10.x1 NCI CGAP_K1d11 Homo sapiens cDNA clone IMAGE:2385547 3'
331	9601		1.48	5.0E-07	A1831883.1	EST_HUMAN	EST93915 Supt cells Homo sapiens cDNA 5' end
1084	10290		2.65	5.0E-07	AA380630.1	EST_HUMAN	wh64f10.x1 NCI CGAP_K1d11 Homo sapiens cDNA clone IMAGE:2385547 3'
2897	12233		0.8	5.0E-07	A1831883.1	EST_HUMAN	Homo sapiens NOD1 protein (NOD1) gene, exons 4 through 14 and complete cds
4847	13841	22831	1.29	5.0E-07	AF149774.1	NT	xx31a02.x1 NCI CGAP_B118 Homo sapiens cDNA clone IMAGE:2568362 3' similar to gb:X15341
6230	15411	24852	19.2	5.0E-07	AW070985.1	EST_HUMAN	CYTOCHROME C OXIDASE POLYPEPTIDE VIA-LIVER (HUMAN);
7183	16390	25839	5.84	5.0E-07	A1808587.1	EST_HUMAN	CM-BT178-220499-014 BT178 Homo sapiens cDNA
8048	17184	26723	4.83	5.0E-07	P11087	SWISSPROT	COLLAGEN ALPHA 1(I) CHAIN PRECURSOR
8110	17244		2.42	5.0E-07	AJ271735.1	NT	Homo sapiens Xq pseudautosomal region, segment 1/2
9013	18167		2.19	5.0E-07	AW862537.1	EST_HUMAN	QV0-CT0383-210400-204-b12 CT0383 Homo sapiens cDNA
3976	13180	22289	1.79	4.0E-07	AW009802.1	EST_HUMAN	ws94h05.x1 NCI CGAP_Co3 Homo sapiens cDNA clone IMAGE:2504697 3'
6786	15981	25441	3.15	4.0E-07	AW419134.1	EST_HUMAN	xy49g11.x1 NCI CGAP_Lu34.1 Homo sapiens cDNA clone IMAGE:2656548 3'

Page 135 of 382  
Table 4  
Single Exon Probes Expressed in HELA Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7511	16716	26204	4.29	4.0E-07	A1765528.1	EST_HUMAN	w181b08.x1 NCL_CGAP_Kid12 Homo sapiens cDNA clone IMAGE:2399703 3'
7511	16716	26205	4.29	4.0E-07	A1765528.1	EST_HUMAN	w181b08.x1 NCL_CGAP_Kid12 Homo sapiens cDNA clone IMAGE:2399703 3'
7774	16969		2.08	4.0E-07	BE001828.1	EST_HUMAN	PM1-BN0083-030300-003-e12 BN0083 Homo sapiens cDNA
447	9701	18837	4.33	3.0E-07	U19719.1	NT	Human microfibril-associated glycoprotein (MFAP2) gene, putative promoter region and alternatively spliced untranslated exons
590	9838	18957	2.19	3.0E-07	AJ271735.1	NT	Homo sapiens Xq pseudautosomal region, segment 1/2
1361	10595	19761	2.2	3.0E-07	M96149.1	NT	Human polymorphic microsatellite DNA
1603	10817		3.12	3.0E-07	M84857.1	NT	Human IgK subgroup I germline gene, exons 1 and 2, V-region 018 allele
2013	11215		3.54	3.0E-07	AA526763.1	EST_HUMAN	ni56b09.s1 NCL_CGAP_Ov2 Homo sapiens cDNA clone IMAGE:980825 similar to contains Alu repetitive element; contains L1 L3 L1 repetitive element
2252	11447	20668	1.24	3.0E-07	M96149.1	NT	Human polymorphic microsatellite DNA
2432	11623	20845	11.76	3.0E-07	BE005077.1	EST_HUMAN	MRO-BN0115-020300-001-f11 BN0115 Homo sapiens cDNA
2432	11623	20846	11.76	3.0E-07	BE005077.1	EST_HUMAN	MRO-BN0115-020300-001-f11 BN0115 Homo sapiens cDNA
3000	12236	21366	1.23	3.0E-07	T64704.1	EST_HUMAN	Y50F12.1 Soares fetal liver spleen 1NLS Homo sapiens cDNA clone IMAGE:116895 5'
3123	12358	21497	1.82	3.0E-07	P38739	SWISSPROT	HYPOTHETICAL 63.8 KD PROTEIN IN GUT1-RIM1 INTERGENIC REGION PRECURSOR
4738	13929	23033	8.7	3.0E-07	AV650201.1	EST_HUMAN	AV650201 GLC Homo sapiens cDNA clone GLCCDD01 3'
4774	13963	23065	0.78	3.0E-07	A1797236.1	EST_HUMAN	w68b12.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2347867 3'
5086	14276	23359	1.39	3.0E-07	T57850.1	EST_HUMAN	yc14h09.s1 Stratagene lung (#837210) Homo sapiens cDNA clone IMAGE:80705 3' similar to similar to
5096	14276	23360	1.39	3.0E-07	T57850.1	EST_HUMAN	gb:M62982 ARACHIDONATE 12-LIPOXYGENASE (HUMAN)
5241	14415	23496	1.06	3.0E-07	BE072335.1	EST_HUMAN	yc14h09.s1 Stratagene lung (#837210) Homo sapiens cDNA clone IMAGE:80705 3' similar to similar to
5520	14745	24113	11.02	3.0E-07	O88807	SWISSPROT	gb:M62982 ARACHIDONATE 12-LIPOXYGENASE (HUMAN)
5965	15180		4.7	3.0E-07	AA815175.1	EST_HUMAN	QV3-BT0537-221289-048-e07 BT0537 Homo sapiens cDNA
6293	15474	24916	3.2	3.0E-07	AW797168.1	EST_HUMAN	PROTEIN-ARGININE DEIMINASE TYPE IV (PEPTIDYLARGININE DEIMINASE IV) (PAD-R4)
9258	18026		4.29	3.0E-07	AJ132352.1	NT	(PEPTIDYLARGININE DEIMINASE TYPE ALPHA)
30	8326	18430	2.76	2.0E-07	AF262898.1	NT	cc04c10.s1 NCL_CGAP_G0B1 Homo sapiens cDNA clone IMAGE:1339890 3'
157	9439	18572	7.69	2.0E-07	L77569.1	NT	QV1-UM0036-200300-115-q02 UM0036 Homo sapiens cDNA
157	9439	18573	7.69	2.0E-07	L77569.1	NT	Ratfus nonvagus mRNA for 45 kDa secretory protein, partial
188	9465	18596	76.92	2.0E-07	U38849.1	NT	Homo sapiens TRF2-interacting telomeric RAP1 protein (RAP1) mRNA, complete cds
756	9997	19142	2.28	2.0E-07	AF003530.1	NT	Homo sapiens DiGeorge syndrome critical region, telomeric end
756	9997	19143	2.28	2.0E-07	AF003530.1	NT	Homo sapiens DiGeorge syndrome critical region, telomeric end
							Fugu rubripes beta-cytoplasmic (vesicular) actin gene, complete cds
							Homo sapiens homeobox protein CDX4 (CDX4) gene, complete cds and flanking repeat regions
							Homo sapiens homeobox protein CDX4 (CDX4) gene, complete cds and flanking repeat regions

Page 136 of 382  
Table 4  
Single Exon Probes Expressed in HELA Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
768	10008		1.13	2.0E-07	P11369	SWISSPROT	RETROVIRUS-RELATED POL POLYPROTEIN [CONTAINS: REVERSE TRANSCRIPTASE ; ENDONUCLEASE]
951	10184	19340	3.36	2.0E-07	AA223280.1	EST_HUMAN	zr08b07.s1 Stratagene NT2 neuronal precursor 937230 Homo sapiens cDNA clone IMAGE:650869 3' similar to gb:L31860 GLYCOPHORIN A PRECURSOR (HUMAN); contains Alu repetitive element
952	10185	19341	12.92	2.0E-07	T63042.1	EST_HUMAN	yc15g04.s1 Stratagene lung (#937210) Homo sapiens cDNA clone IMAGE:80780 3' similar to contains L1 repetitive element;
1171	10392	19544	1.22	2.0E-07	Q26768	SWISSPROT	IIG AUTOANTIGEN
1580	10793	19970	1.82	2.0E-07	Q09701	SWISSPROT	HYPOTHETICAL 72.5 KD PROTEIN C2F7.10 IN CHROMOSOME 1
3597	12818		0.6	2.0E-07	BF131397.1	EST_HUMAN	601818916F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:4044891 5'
3668	12889	22010	22.49	2.0E-07	AF125348.1	NT	Homo sapiens cavedin 1 (CAV1) gene, exon 3 and partial cds
5282	14463	23531	9.22	2.0E-07	P23269	SWISSPROT	OLFACTORY RECEPTOR-LIKE PROTEIN I3
5957	15173	24588	1.77	2.0E-07	AI208715.1	EST_HUMAN	qg56d05.x1 Soares testis, NHT Homo sapiens cDNA clone IMAGE:1839177 3'
7005	16183		2.32	2.0E-07	AL163303.2	NT	Homo sapiens chromosome 21 segment HS21C103
7157	16334	25817	8.58	2.0E-07	AW892507.1	EST_HUMAN	CM4-NN0003-280300-124-e08 NN0003 Homo sapiens cDNA
8269	17917		1.69	2.0E-07	BE153717.1	EST_HUMAN	PMO-HT0339-260100-008-H07 HT0339 Homo sapiens cDNA
8357	18168		1.95	2.0E-07	AI732462.1	EST_HUMAN	zr85h11.x5 Stratagene lung carcinoma 937218 Homo sapiens cDNA clone IMAGE:565029 3' similar to contains THR.b2 THR repetitive element;
1110	10334		1.83	1.0E-07	AL163282.2	NT	Homo sapiens chromosome 21 segment HS21C082
1940	11144	20342	0.95	1.0E-07	AL163213.2	NT	Homo sapiens chromosome 21 segment HS21C013
1940	11144	20343	0.95	1.0E-07	AL163213.2	NT	Homo sapiens chromosome 21 segment HS21C013
2416	11607	20829	0.91	1.0E-07	7549818	NT	Homo sapiens RAB, member of RAS oncogene family-like 2A (RABL2A), transcript variant 2, mRNA
2779	10723	18895	1.75	1.0E-07	P08256	SWISSPROT	GLYCOPROTEIN GPV
3725	10334		1.43	1.0E-07	AL163282.2	NT	Homo sapiens chromosome 21 segment HS21C082
4280	13483	22580	3.17	1.0E-07	AV718682.1	EST_HUMAN	AV718682 GLC Homo sapiens cDNA clone GLCFNF04 5'
4280	13483	22581	3.17	1.0E-07	AV718682.1	EST_HUMAN	AV718682 GLC Homo sapiens cDNA clone GLCFNF04 5'
6024	15232	24652	4.61	1.0E-07	BE047871.1	EST_HUMAN	tz43d06.y1 NCI CGAP Brn52 Homo sapiens cDNA clone IMAGE:2281339 5'
6024	15232	24653	4.61	1.0E-07	BE047871.1	EST_HUMAN	tz43d06.y1 NCI CGAP Brn52 Homo sapiens cDNA clone IMAGE:2281339 5'
6287	15488	24910	8.24	1.0E-07	N55081.1	EST_HUMAN	y43c07.s1 Soares fetal liver, spleen, INFLS S1 Homo sapiens cDNA clone IMAGE:245484 3'
6755	15950	25407	4.48	1.0E-07	AA693576.1	EST_HUMAN	z51e10.s1 Soares fetal liver, spleen, INFLS S1 Homo sapiens cDNA clone IMAGE:434348 3'
7051	16228	25704	4.17	1.0E-07	BF674524.1	EST_HUMAN	602137714F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4274428 5'
7204	16361		2.32	1.0E-07	AL163282.2	NT	Homo sapiens chromosome 21 segment HS21C082

Table 4

## Single Exon Probes Expressed in HELA Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8641	18143	23750	3.09	1.0E-07	BE048770.1	EST_HUMAN	h53c11.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:3132212 3' similar to TR:O95722 O95722
8784	17713		1.55	1.0E-07	X64467.1	NT	DJ1163.11.1;
8958	17831		1.35	1.0E-07	X51755.1	NT	H. sapiens ALAD gene for porphobilinogen synthase
7038	18213	25690	2.9	9.0E-08	AV734819.1	EST_HUMAN	Human lambda-immunoglobulin constant region complex (germline)
7737	16934	28442	3.19	9.0E-08	AI891052.1	EST_HUMAN	AV734819 cdA Homo sapiens cDNA clone cDABFB06 5'
8171	17303	26848	4.6	9.0E-08	AL163301.2	NT	wn30a07.x1 NCI_CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2446832 3' similar to contains OFR.12
8591	17600		3.94	9.0E-08	AJ251973.1	NT	OFR repetitive element;
613	11972		3.63	8.0E-08	AI911352.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C101
1057	10283		0.66	8.0E-08	BE795489.1	EST_HUMAN	Homo sapiens partial steen-1 gene
3519	12743		1.84	8.0E-08	BE795489.1	EST_HUMAN	wd16b05.x1 Soares_NFL_I_GBC_S1 Homo sapiens cDNA clone IMAGE:2328273 3'
8695	15690	25351	4.48	8.0E-08	AI752387.1	EST_HUMAN	601590133F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3943976 5'
6695	15690	25352	4.48	8.0E-08	AI752387.1	EST_HUMAN	601590133F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3943976 5'
6972	16150	25621	4.01	8.0E-08	AW970689.1	EST_HUMAN	cn15c02.x1 Normal Human Trabecular Bone Cells Homo sapiens cDNA clone NHTBC_cn15c02 random
7797	16990		2.74	8.0E-08	AF253417.1	NT	cn15c02.x1 Normal Human Trabecular Bone Cells Homo sapiens cDNA clone NHTBC_cn15c02 random
80	9373	18503	2.46	7.0E-08	Q02357	SWISSPROT	EST382776 IMAGE resequences, MAGK Homo sapiens cDNA
1369	10583	19750	38.64	7.0E-08	X04809.1	NT	Homo sapiens microsomal epoxide hydrolase (EPHX1) gene, complete cds
3551	12774	21902	1.31	7.0E-08	P15305	SWISSPROT	ANKYRIN 1 (ERYTHROCYTE ANKYRIN)
3551	12774	21903	1.31	7.0E-08	P15305	SWISSPROT	Rat mRNA for ribosomal protein L31
7391	16805		7.93	7.0E-08	AI535743.1	EST_HUMAN	DYNEIN HEAVY CHAIN (DYHC)
8175	17307	28850	6.73	7.0E-08	U24070.1	NT	DYNEIN HEAVY CHAIN (DYHC)
9075	12774	21902	3.5	7.0E-08	P15305	SWISSPROT	cong3.P11.A5 conorm Homo sapiens cDNA 3'
9075	12774	21903	3.5	7.0E-08	P15305	SWISSPROT	Rattus norvegicus Munc13-1 mRNA, complete cds
9146	17951		1.31	7.0E-08	AJ131016.1	NT	DYNEIN HEAVY CHAIN (DYHC)
827	10065	19217	2.5	6.0E-08	AL163248.2	NT	Homo sapiens SCL gene locus
827	10065	19218	2.5	6.0E-08	AL163248.2	NT	Homo sapiens chromosome 21 segment HS21C048
2331	11524	20747	1.98	6.0E-08	BE144398.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C048
3026	12262	21390	0.83	6.0E-08	7662473	NT	MRO-HT0166-191169-004-g09 HT0166 Homo sapiens cDNA
4234	13437	22530	1.15	6.0E-08	AL163248.2	NT	Homo sapiens KIAA1074 protein (KIAA1074), mRNA
7953	17092	26622	2.48	6.0E-08	P11369	SWISSPROT	Homo sapiens chromosome 21 segment HS21C048
							RETROVIRUS-RELATED POL POLYPROTEIN [CONTAINS: REVERSE TRANSCRIPTASE ; ENDONUCLEASE]

Table 4

## Single Exon Probes Expressed in HELA Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8084	17189		1.82	6.0E-08	AL163209.2	NT	Homo sapiens chromosome 21 segment HS21C009
84	8377	18507	2.87	5.0E-08	AL163303.2	NT	Homo sapiens chromosome 21 segment HS21C103
2202	11399	20824	2.84	5.0E-08	AA483851.1	EST_HUMAN	h03b09.s1 NCI_CGAP_Thy1 Homo sapiens cDNA clone IMAGE:943193 similar to contains Alu repetitive element
8318	17421		3.74	5.0E-08	P06681	SWISSPROT	COMPLEMENT C2 PRECURSOR (C3/C5 CONVERTASE)
8515	17549	23986	1.26	5.0E-08	AW851878.1	EST_HUMAN	QV0-CT0225-131089-034-at12 CT0225 Homo sapiens cDNA
1731	10943	20125	0.92	4.0E-08	P25723	SWISSPROT	DORSAL-VENTRAL PATTERNING TOLLOID PROTEIN PRECURSOR
1731	10943	20126	0.92	4.0E-08	P25723	SWISSPROT	DORSAL-VENTRAL PATTERNING TOLLOID PROTEIN PRECURSOR
3891	13107	22225	0.72	4.0E-08	U82668.1	NT	Homo sapiens shox gene, alternatively spliced products, complete cds
7185	16362	25942	2.55	4.0E-08	AID50027.1	EST_HUMAN	an22d10.x1 Gessler Wilms tumor Homo sapiens cDNA clone IMAGE:169411 3' similar to contains Alu repetitive element; contains element MER22 repetitive element
7477	16885		1.77	4.0E-08	AJ238617.1	NT	Homo sapiens mRNA for UGA suppressor tRNA-associated antigenic protein (tRNA48 gene)
7658	16856	26356	4.35	4.0E-08	BF692493.1	EST_HUMAN	602248024F1 NIH_MGC_92 Homo sapiens cDNA clone IMAGE:4333300 5'
7658	16856	26357	4.35	4.0E-08	BF692493.1	EST_HUMAN	602248024F1 NIH_MGC_92 Homo sapiens cDNA clone IMAGE:4333300 5'
8323	18300		2.4	4.0E-08	W76159.1	EST_HUMAN	zd65g03.r1 Scores_fetal_heart_NbHH19W Homo sapiens cDNA clone IMAGE:345556 5' similar to contains L1.1 L1 repetitive element
9002	17861		2.01	4.0E-08	A1343353.1	EST_HUMAN	b95a11.x1 NCI_CGAP_Co18 Homo sapiens cDNA clone IMAGE:2062076 3' similar to contains MER18.b3
5496	14722	24080	2.66	3.0E-08	BE018348.1	EST_HUMAN	bb79a10.y1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3048570 5' similar to TR:Q9Z158 Q9Z158
6075	14521	23564	3.72	3.0E-08	A1792737.1	EST_HUMAN	SYNTAXIN 17.1
6397	15578		3.43	3.0E-08	A1436352.1	EST_HUMAN	qs76f11.y5 NCI_CGAP_P128 Homo sapiens cDNA clone IMAGE:1944045 5'
8288	17402		13.41	3.0E-08	R18420.1	EST_HUMAN	h93h09.x1 Scores_NSF_F8_gw_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:2128273 3' similar to TR:Q13537 Q13537 MER37 TRANSPOSABLE ELEMENT, COMPLETE CONSENSUS SEQUENCE. ;
211	9491		12.34	2.0E-08	AV302898.1	EST_HUMAN	y90204.r1 Scores Infant brain 1N1B Homo sapiens cDNA clone IMAGE:30948 5' similar to contains Alu repetitive element
233	9512		6.42	2.0E-08	AA425598.1	EST_HUMAN	xb7f06.x1 NCI_CGAP_Lu26 Homo sapiens cDNA clone IMAGE:2767139 3'
503	9755	18883	3.37	2.0E-08	AF108349.1	NT	zw48f07.r1 Scores_tal_fetus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:773317 5' similar to contains Alu repetitive element; contains element MER15 repetitive element ;
666	9912	18040	10.21	2.0E-08	AW886438.1	EST_HUMAN	Gallus gallus Daeh2 protein (Daeh2) mRNA, complete cds
666	9912	19041	10.21	2.0E-08	AW886438.1	EST_HUMAN	MRO-OT0080-240200-001-g08 OT0080 Homo sapiens cDNA
897	10229		35.03	2.0E-08	BE280477.1	EST_HUMAN	MRO-OT0080-240200-001-g08 OT0080 Homo sapiens cDNA
1350	10565	19730	95.22	2.0E-08	AL163247.2	NT	601155321F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3138883 5'
							Homo sapiens chromosome 21 segment HS21C047

Page 139 of 382  
Table 4  
Single Exon Probes Expressed in HELA Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1714	10628		1.55	2.0E-08	BE734871.1	EST_HUMAN	601570463F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3845199 5'
1822	11030		4.08	2.0E-08	AW270271.1	EST_HUMAN	XP4311.X1 NCI_CGAP_HN11 Homo sapiens cDNA clone IMAGE:2743149 3'
2508	11697		1.91	2.0E-08	K00216.1	NT	Sheep His-rRNA-GUG
3174	12409	21544	6.99	2.0E-08	O42280	SWISSPROT	WNT-14 PROTEIN PRECURSOR
3174	12409	21545	6.99	2.0E-08	O42280	SWISSPROT	WNT-14 PROTEIN PRECURSOR
3842	13059		1.59	2.0E-08	AW813620.1	EST_HUMAN	RC3-ST0197-161099-012-803 ST0197 Homo sapiens cDNA
4399	13600		1.47	2.0E-08	AA459040.1	EST_HUMAN	aa28c07.r1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:814380 5' similar to contains L1.12 L1 repetitive element;
4977	14184		2.92	2.0E-08	AW572881.1	EST_HUMAN	he17h08.x2 NCI_CGAP_CML1 Homo sapiens cDNA clone IMAGE:2918327 3' similar to contains Alu repetitive element
1745	10957	20140	1.06	1.0E-08	AF125348.1	NT	Homo sapiens cavedin 1 (CAV1) gene, exon 3 and partial cde
2018	11219		2.7	1.0E-08	BE141859.1	EST_HUMAN	PM2-HT0130-150999-001-f12 HT0130 Homo sapiens cDNA
3155	12390	21523	1.07	1.0E-08	BE246844.1	EST_HUMAN	TCBAP1D5232 Pediatric pre-B cell acute lymphoblastic leukemia Baylor-HGSC project=TCBA Homo sapiens cDNA clone TCBAP5232
3155	12390	21524	1.07	1.0E-08	BE246844.1	EST_HUMAN	TCBAP1D5232 Pediatric pre-B cell acute lymphoblastic leukemia Baylor-HGSC project=TCBA Homo sapiens cDNA clone TCBAP5232
5480	14716	24073	4.44	1.0E-08	AJ010770.1	NT	Homo sapiens hyperton gene, exons 1-50
6639	15834	25298	2.75	1.0E-08	AJ016304.1	EST_HUMAN	cd35a05.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1618736 3'
7882	17052	26573	4.24	1.0E-08	AF044083.1	NT	Homo sapiens major histocompatibility locus class III region
8715	17671		2.18	1.0E-08	X51755.1	NT	Human lambda8-immunoglobulin constant region complex (germline)
4228	13431	22524	2.66	9.0E-09	AL163279.2	NT	Homo sapiens chromosome 21 segment HS21C079
4228	13431	22525	2.66	9.0E-09	AL163279.2	NT	Homo sapiens chromosome 21 segment HS21C079
6193	15375	24815	7.03	8.0E-09	AH183500.1	EST_HUMAN	qd42e07.x1 Soares_fetal_heart_NBHH19W Homo sapiens cDNA clone IMAGE:1732164 3' similar to contains MSR1.11 MSR1 repetitive element;
6484	15661	25133	3.54	8.0E-09	AW900159.1	EST_HUMAN	CMO-NN1004-100300-273-e08 NN1004 Homo sapiens cDNA
6761	15966		3.3	8.0E-09	AA938892.1	EST_HUMAN	op74d08.s1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1582575 3'
3585	12806		2.2	7.0E-09	D88842.1	NT	Homo sapiens DNA for 3-ketacyl-CoA thiolase beta-subunit of mitochondrial trifunctional protein, exon 2, 3
7265	16484		3.06	7.0E-09	T97950.1	EST_HUMAN	ye58a12.s1 Soares_fetal_liver_spleen_INFLS Homo sapiens cDNA clone IMAGE:121918 3'
5000	14187	23277	6.35	6.0E-09	BE169421.1	EST_HUMAN	PM1-HT0527-160200-001-f05 HT0527 Homo sapiens cDNA
5386	14875	23728	6.98	6.0E-09	AW185784.1	EST_HUMAN	xa85h08.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2701311 3'
6823	16017	25482	2.71	6.0E-09	4503710	NT	Homo sapiens fibroblast growth factor receptor 3 (achondroplasia, thanatophoric dwarfism) (FGFR3) mRNA
7161	16338		4.91	6.0E-09	AF200923.2	NT	Homo sapiens testis-specific kinase substrate (TSKS) gene, complete cde



Table 4

## Single Exon Probes Expressed in HELA Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1418	10832	18800	3.26	5.0E-09	BE149284.1	EST_HUMAN	RC2-H10252-120200-014-h10 HT0252 Homo sapiens cDNA
1820	11028	20223	1.02	5.0E-09	AL163284.2	NT	Homo sapiens chromosome 21 segment HS21C084
5830	15047	24451	1.78	5.0E-09	AA359454.1	EST_HUMAN	EST168748 Fetal lung II Homo sapiens cDNA 5' end
7108	18285	25766	2.57	5.0E-09	AW796687.1	EST_HUMAN	PM2-UM0053-240300-005-c09 UM0053 Homo sapiens cDNA
9028	18224		1.24	5.0E-09	BE963272.2	EST_HUMAN	601658707R1 NIH_MGC_87 Homo sapiens cDNA clone IMAGE:3965897 3'
527	9778		1.75	4.0E-09	AL163282.2	NT	Homo sapiens chromosome 21 segment HS21C082
972	10204		2.43	4.0E-09	AL163285.2	NT	Homo sapiens chromosome 21 segment HS21C085
1465	10878	19851	1.81	4.0E-09	9588718	NT	Homo sapiens hypothetical protein (AF038169), mRNA
2393	11588	20804	37.61	4.0E-09	AA350878.1	EST_HUMAN	EST58385 Infant brain Homo sapiens cDNA 5' and similar to heat shock protein, 90 kDa
7641	16841	26339	3.63	4.0E-09	AI888401.1	EST_HUMAN	wn94f10.x1 NCI_CGAP_U12 Homo sapiens cDNA clone IMAGE:2443627 3'
2320	11513	20734	4.11	3.0E-09	BE222239.1	EST_HUMAN	hu09e09.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3168120 3' similar to contains MER18.13
2519	11707	20922	0.91	3.0E-09	BE222239.1	EST_HUMAN	MER18 repetitive element; hu09e09.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3168120 3' similar to contains MER18.13
3302	12533	21665	3.20	3.0E-09	BE222239.1	EST_HUMAN	MER18 repetitive element; hu09e09.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3168120 3' similar to contains MER18.13
3355	12583		0.66	3.0E-09	AA442272.1	EST_HUMAN	z654a04.r1 Scores_testis_NHT Homo sapiens cDNA clone IMAGE:757422 5'
4074	13284		0.69	3.0E-09	X16674.1	NT	H. sapiens PADPRP-I gene for NAD(+) ADP-ribosyltransferase
4418	13818	22714	10.9	3.0E-09	AF175325.1	NT	Homo sapiens eukaryotic initiation factor 4A1 (EIF4A1) gene, partial cds
4513	13709	22802	1.53	3.0E-09	Q9Y3R5	SWISSPROT	258.1 KDA PROTEIN C21ORF5 (KIAA0933)
7151	16328	25811	2.31	3.0E-09	AL163247.2	NT	Homo sapiens chromosome 21 segment HS21C047
7591	16795	26287	3.99	3.0E-09	BF109943.1	EST_HUMAN	7172c08.x1 Scores_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:3527030 3'
7591	16795	26288	3.99	3.0E-09	BF109943.1	EST_HUMAN	7172c08.x1 Scores_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:3527030 3'
822	10060		0.78	2.0E-09	X16674.1	NT	H. sapiens PADPRP-I gene for NAD(+) ADP-ribosyltransferase
1265	10480	19641	5.78	2.0E-09	AL163284.2	NT	Homo sapiens chromosome 21 segment HS21C084
1634	10848		11.84	2.0E-09	AL118573.1	EST_HUMAN	DKFZp781B1710_r1 781 (synonym: hamy2) Homo sapiens cDNA clone DKFZp781B1710 5'
2285	11490	20710	4.74	2.0E-09	Q9Y3R5	SWISSPROT	258.1 KDA PROTEIN C21ORF5 (KIAA0933)
3911	13127	22244	3.74	2.0E-09	O60241	SWISSPROT	BRAIN-SPECIFIC ANGIOGENESIS INHIBITOR 2 PRECURSOR
6274	15454	24895	7.44	2.0E-09	AA461430.1	EST_HUMAN	z63h06.r1 Scores_total_fetus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:798187 5' similar to contains Alu repetitive element
8263	17390		1.79	2.0E-09	AF111168.2	NT	Homo sapiens serine palmitoyl transferase, subunit II gene, complete cds; and unknown genes
8984	10060		14.46	2.0E-09	X16674.1	NT	H. sapiens PADPRP-I gene for NAD(+) ADP-ribosyltransferase
8939	18369		1.35	2.0E-09	AA228070.1	EST_HUMAN	nc11c02.r1 NCI_CGAP_P1 Homo sapiens cDNA clone IMAGE:1007810 similar to contains Alu repetitive element

Table 4

## Single Exon Probes Expressed in HELA Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1002	10233		2.24	1.0E-09	W78152.1	EST_HUMAN	zsf78d03.s1 Soares_fetal_heart_NHH19W Homo sapiens cDNA clone IMAGE:346853 3' similar to
1117	10341	19491	5.1	1.0E-09	5031824	NT	gb:U02832 PEROXISOME PROLIFERATOR ACTIVATED RECEPTOR ALPHA (HUMAN);
1117	10341	19492	5.1	1.0E-09	5031824	NT	Homo sapiens CCAAT-box-binding transcription factor (CBF2) mRNA
2842	12081	21208	1.57	1.0E-09	U80017.1	NT	Homo sapiens CCAAT-box-binding transcription factor (CBF2) mRNA
2878	12114	21242	12.67	1.0E-09	M28699.1	NT	Homo sapiens basic transcription factor 2 p44 (btf2p44) gene, partial cds, neuronal apoptosis inhibitory
2878	12114	21243	12.67	1.0E-09	M28699.1	NT	protein (hnp) and survival motor neuron protein (smn) genes, complete cds
3003	12239	21369	0.72	1.0E-09	BE535440.1	EST_HUMAN	Homo sapiens nucleolar phosphoprotein B23 (NPM1) mRNA, complete cds
4811	14000		6.59	1.0E-09	AA718287.1	EST_HUMAN	Homo sapiens nucleolar phosphoprotein B23 (NPM1) mRNA, complete cds
5258	14431	23508	0.68	1.0E-09	U80017.1	NT	601058602F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3445177 5'
5733	14952	24350	3.36	1.0E-09	P28694	SWISSPROT	zh35x03.s1 Soares_pineal_gland_N3HPG Homo sapiens cDNA clone IMAGE:414028 3' similar to contains
7171	16348		2.4	1.0E-09	AL163283.2	NT	Alu repetitive element contains element MER22 repetitive element;
8255	17382		1.72	1.0E-09	AL163283.2	NT	Homo sapiens basic transcription factor 2 p44 (btf2p44) gene, partial cds, neuronal apoptosis inhibitory
8650	17633		2.2	1.0E-09	P08547	SWISSPROT	Homo sapiens CIRCUMSPOROZOITE PROTEIN PRECURSOR (CS)
8766	18310	23691	2.32	1.0E-09	11418127	NT	Homo sapiens chromosome 21 segment HS21C083
1316	10532	19694	2.22	9.0E-10	AW867740.1	EST_HUMAN	Homo sapiens LINE-1 REVERSE TRANSCRIPTASE HOMOLOG
2787	12027	21154	7.73	9.0E-10	A1870071.1	EST_HUMAN	Homo sapiens GTP binding protein 1 (GTPBP1), mRNA
6012	15262	24686	5.41	9.0E-10	A1452982.1	EST_HUMAN	MRO-SN0040-050500-002-c07 SN0040 Homo sapiens cDNA
149	9431	18565	12.37	8.0E-10	U63630.2	NT	we78h03.x1 Soares_Dieckgraefe_colon_NHCD Homo sapiens cDNA clone IMAGE:2347253 3' similar to
3316	12546	21079	0.68	8.0E-10	BE080748.1	EST_HUMAN	SW-RL29_HUMAN P47914 60S RIBOSOMAL PROTEIN L29 contains element PTR5 repetitive element;
4183	13367	22485	4.81	8.0E-10	AA376832.1	EST_HUMAN	q46509.x1 Soares_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:2144537 3' similar to
7050	16237		3	8.0E-10	U36308.2	NT	TR:O00372 O00372 PUTATIVE P150.1
708	9950	18088	23.91	7.0E-10	7706225	NT	Homo sapiens MCM4 (MCM4) and DNA-PKcs (PRKDC) genes, partial cds
708	9950	18088	23.91	7.0E-10	7706225	NT	QV1-BT0031-150200-071-01 BT0031 Homo sapiens cDNA
1599	10813	19990	3.1	7.0E-10	Q13342	SWISSPROT	EST789564 Small intestine I Homo sapiens cDNA 5' end
1989	11192		1.2	7.0E-10	P08548	SWISSPROT	Homo sapiens lens major intrinsic protein (MIP) gene, complete cds
2525	11713		13.32	7.0E-10	P08547	SWISSPROT	Homo sapiens TPA inducible protein (LOC51586), mRNA
3053	12289	21414	2.97	7.0E-10	X00856.1	NT	Homo sapiens TPA inducible protein (LOC51586), mRNA
							LYSP100 PROTEIN (LYMPHOID-RESTRICTED HOMOLOG OF SP100)
							LINE-1 REVERSE TRANSCRIPTASE HOMOLOG
							LINE-1 REVERSE TRANSCRIPTASE HOMOLOG
							H sapiens DHFR gene, exon 3

Table 4

## Single Exon Probes Expressed in HELA Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5747	14958	24365	3.58	7.0E-10	A4345220.1	EST_HUMAN	EST51247 Gall bladder II Homo sapiens cDNA 5' end
923	10158	18315	3.29	6.0E-10	AJ400877.1	NT	Homo sapiens ASCL3 gene, CEGP1 gene, C11orf14 gene, C11orf15 gene, C11orf16 gene and C11orf17 gene
2637	11820	21036	1.54	6.0E-10	A424405.1	EST_HUMAN	
4750	13941		2.51	6.0E-10	AW653719.1	EST_HUMAN	RC3-CT0254-031089-012-g12 CT0254 Homo sapiens cDNA
8354	17447		1.64	6.0E-10	AW971923.1	EST_HUMAN	EST384012 MAGE resequences, MAGL Homo sapiens cDNA
769	10009		5.57	5.0E-10	AL046804.1	EST_HUMAN	DKFZp434N219_1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434N219 5'
6012	14189	23286	1.35	5.0E-10	AF181897.1	NT	Homo sapiens WRN (WRN) gene, complete cds
6219	15400		1.71	5.0E-10	BF105159.1	EST_HUMAN	601822184F1 NIH_MGC_79 Homo sapiens cDNA clone IMAGE:4042413 5'
111	9389		1.63	4.0E-10	A1221083.1	EST_HUMAN	qg09f09.x1 Soares placenta_8tc6weeks_2NbhP8tc6w Homo sapiens cDNA clone IMAGE:1758049 3'
598	9836	18955	1.89	4.0E-10	AA515260.1	EST_HUMAN	similar to contains LTR8 b2 LTR8 repetitive element
1065	11169	20374	1.75	4.0E-10	AW594709.1	EST_HUMAN	nf64e01.s1 NCL_CGAP_Cc3 Homo sapiens cDNA clone IMAGE:924648 3'
2538	11726	20943	4.74	4.0E-10	AL163303.2	NT	hg58g03.x1 NCL_CGAP_GC6 Homo sapiens cDNA clone IMAGE:2849844 3' similar to contains Alu repetitive element
6155	15339	24778	14.13	4.0E-10	AF224669.1	NT	Homo sapiens chromosome 21 segment HS21C103
925	10159	18317	1.78	3.0E-10	N36113.1	EST_HUMAN	Homo sapiens mannosidase, beta A, lysosomal (MANBA) gene, and ubiquitin-conjugating enzyme E2D 3 (UBE2D3) genes, complete cds
1359	10574		4.66	3.0E-10	A7005150.1	NT	Y3206.s1 Soares melanocyte 2NbhM Homo sapiens cDNA clone IMAGE:272863 3' similar to contains L1.11 L1 repetitive element
5755	14974	24373	1.92	3.0E-10	P20350	SWISSPROT	Homo sapiens extracellular glycoprotein lacritin precursor, gene, complete cds
5813	15030	24431	3.41	3.0E-10	BE302870.1	EST_HUMAN	RHOMBOLD PROTEIN (VEINLET PROTEIN)
6784	15979	25438	2.33	3.0E-10	AW850731.1	EST_HUMAN	ba76d08.y1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:2906319 5'
6784	15979	25439	2.33	3.0E-10	AW850731.1	EST_HUMAN	IL3-CT0219-160200-084-B08 CT0219 Homo sapiens cDNA
7224	18401		2.23	3.0E-10	AA769294.1	EST_HUMAN	IL3-CT0219-160200-084-B08 CT0219 Homo sapiens cDNA
9041	17883	23896	2.19	3.0E-10	BE179517.1	EST_HUMAN	n38g03.s1 NCL_CGAP_GC81 Homo sapiens cDNA clone IMAGE:1289608 3'
37	9333	18438	1.24	2.0E-10	P48988	SWISSPROT	IL3-HT0618-110500-136-E07 HT0618 Homo sapiens cDNA
37	9333	18439	1.24	2.0E-10	P48988	SWISSPROT	MAJOR CENTROMERE AUTOANTIGEN B (CENTROMERE PROTEIN B) (CENP-B)
1862	11059		3.01	2.0E-10	U80017.1	NT	MAJOR CENTROMERE AUTOANTIGEN B (CENTROMERE PROTEIN B) (CENP-B)
2943	12181		0.75	2.0E-10	BF675047.1	EST_HUMAN	Homo sapiens basic transcription factor 2 p44 (btf2p44) gene, partial cds, neuronal apoptosis inhibitory protein (naip) and survival motor neuron protein (smn) genes, complete cds
5574	14798		2.78	2.0E-10	Q28640	SWISSPROT	802138640F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4273377 5' (HPRG)

Table 4

## Single Exon Probes Expressed in HELA Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5772	14990	24390	2.13	2.0E-10	AF280107.1	NT	Homo sapiens cytochrome P450 polypeptide 43 (CYP3A43) gene, partial cds; cytochrome P450 polypeptide 4 (CYP3A4) and cytochrome P450 polypeptide 7 (CYP3A7) genes, complete cds; and cytochrome P450 polypeptide 5 (CYP3A5) gene, partial cds
6247	15428	24868	5.7	2.0E-10	BE791082.1	EST_HUMAN	601588208F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3940824 5'
1498	10711		13.64	1.0E-10	AW867767.1	EST_HUMAN	MFO-SN0038-280300-001-f01 SN0038 Homo sapiens cDNA
1586	10769	18975	2.68	1.0E-10	AV652123.1	EST_HUMAN	AV652123 GLC Homo sapiens cDNA clone GLCXA11 3'
2544	11732		1.66	1.0E-10	AW852001.1	EST_HUMAN	QV0-CT0225-191189-058-e08 CT0225 Homo sapiens cDNA
3473	12697	21833	0.87	1.0E-10	AW832612.1	EST_HUMAN	QV2-TT0003-161189-013-g10 TT0003 Homo sapiens cDNA
3515	12739		0.68	1.0E-10	AL041685.1	EST_HUMAN	DKFZp434N1317_r1 434 (synonym: hies3) Homo sapiens cDNA clone DKFZp434N1317 5'
3829	12739		0.88	1.0E-10	AL041685.1	EST_HUMAN	DKFZp434N1317_r1 434 (synonym: hies3) Homo sapiens cDNA clone DKFZp434N1317 5'
3991	13205		7	1.0E-10	AF213884.1	NT	Homo sapiens nuclear factor of kappa light polypeptide gene enhancer in B-cells 1 (NFKB1) gene, complete cds
4109	13316	22414	6.01	1.0E-10	U52111.2	NT	Homo sapiens X28 region near ALD locus containing dual specificity phosphatase 9 (DUSP9), ribosomal protein L18a (RPL18a), Ca2+/Calmodulin-dependent protein kinase I (CAMKI), creatine transporter (CRTR), CDM protein (CDM), adrenoleukodystrophy protein >
4109	13316	22415	6.01	1.0E-10	U52111.2	NT	Homo sapiens X28 region near ALD locus containing dual specificity phosphatase 9 (DUSP9), ribosomal protein L18a (RPL18a), Ca2+/Calmodulin-dependent protein kinase I (CAMKI), creatine transporter (CRTR), CDM protein (CDM), adrenoleukodystrophy protein >
4116	13323	22424	1.91	1.0E-10	AB031089.1	NT	Homo sapiens PCCX1 mRNA for protein containing CXXC domain 1, complete cds
4152	13358		2.45	1.0E-10	M30829.1	NT	Human pregnancy-specific glycoprotein beta-1 (SP1) mRNA, last exon
5191	14367		0.99	1.0E-10	A1797745.1	EST_HUMAN	we82f04.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2347615 3' similar to contains MER31.t1 MER31 repetitive element;
7134	16311		8.18	1.0E-10	AA081888.1	EST_HUMAN	zn23g08.r1 Strabagene neuroepithelium NT2RAMI 937234 Homo sapiens cDNA clone IMAGE:548314 5'
7488	16695	26179	3.77	1.0E-10	AI038280.1	EST_HUMAN	cy85h03.x1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:1672661 3'
8287	14504		1.53	1.0E-10	X87344.1	NT	H. sapiens DMA, DMB, HLA-Z1, IPP2, LMP2, TAP2, DOB, DQB2 and RING8, 9, 13 and 14 genes
268	8541	18671	1.07	9.0E-11	BE145600.1	EST_HUMAN	IL2-HT0203-291099-016-c08 HT0203 Homo sapiens cDNA
2074	11274	20489	5.61	9.0E-11	AL134395.1	EST_HUMAN	DKFZp547D225_r1 547 (synonym: hfrb1) Homo sapiens cDNA clone DKFZp547D225 5'
2074	11274	20489	5.61	9.0E-11	AL134395.1	EST_HUMAN	DKFZp547D225_r1 547 (synonym: hfrb1) Homo sapiens cDNA clone DKFZp547D225 5'
3361	12589	21728	2.52	9.0E-11	AL134395.1	EST_HUMAN	DKFZp547D225_r1 547 (synonym: hfrb1) Homo sapiens cDNA clone DKFZp547D225 5'
3361	12589	21730	2.52	9.0E-11	AL134395.1	EST_HUMAN	DKFZp547D225_r1 547 (synonym: hfrb1) Homo sapiens cDNA clone DKFZp547D225 5'
4503	13700	22794	0.94	9.0E-11	AA775985.1	EST_HUMAN	ae78f01.s1 Strabagene schizo brain S11 Homo sapiens cDNA clone IMAGE:970287 3'
5477	14704		4.92	9.0E-11	BE076780.1	EST_HUMAN	RC8-BT0627-140200-011-E06 BT0627 Homo sapiens cDNA

Page 144 of 382  
Table 4  
Single Exon Probes Expressed in HELA Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8990	17658	23981	3.31	9.0E-11	C16835.1	EST_HUMAN	C16835 Clontech human aorta polyA+ mRNA (H6572) Homo sapiens cDNA clone GEN:508808 5'
3080	12316		9.13	8.0E-11	H19971.1	EST_HUMAN	yn53f11.s1 Soares adult brain N2b5HB55Y Homo sapiens cDNA clone IMAGE:172173 3' similar to contains L1 repetitive element
3940	13156	22273	0.61	8.0E-11	AI478617.1	EST_HUMAN	tm54c09.x1 NCL_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2161936 3'
4020	13232	22335	5.63	8.0E-11	N23712.1	EST_HUMAN	yy46c08.s1 Weizmann Offactory Epithelium Homo sapiens cDNA clone IMAGE:255288 3'
1449	10662	19837	1.67	7.0E-11	AA330842.1	EST_HUMAN	EST34392 Embryo, 6 week 1 Homo sapiens cDNA 5' end
6825	15821	25281	3.07	7.0E-11	AF163884.1	NT	Homo sapiens SNCA isoform (SNCA) gene, complete cds, alternatively spliced
8835	17745		1.38	7.0E-11	AV701656.1	EST_HUMAN	AV701656 ADB Homo sapiens cDNA clone ADBABC09 5'
418	9871	18812	6.1	6.0E-11	M55270.1	NT	Human matrix Gla protein (MGP) gene, complete cds
418	9871	18813	6.1	6.0E-11	M55270.1	NT	Human matrix Gla protein (MGP) gene, complete cds
6373	15553	25010	3.18	6.0E-11	P08547	SWISSPROT	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG
6584	15760	25240	9.08	6.0E-11	AV727859.1	EST_HUMAN	AV727859 HTC Homo sapiens cDNA clone HTCASC08 5'
11	9307	18409	1.36	5.0E-11	AL163283.2	NT	Homo sapiens chromosome 21 segment HS21C083
3342	9307	18409	1.91	5.0E-11	AL163283.2	NT	Homo sapiens chromosome 21 segment HS21C083
4213	13416	22512	1.55	5.0E-11	P48034	SWISSPROT	ALDEHYDE OXIDASE
5983	15100	24511	1.94	5.0E-11	AL163213.2	NT	Homo sapiens chromosome 21 segment HS21C013
6303	15484	24928	13.54	5.0E-11	11410789	NT	Homo sapiens protocadherin beta 3 (PCDH3), mRNA
1405	10618		1.26	4.0E-11	AA436042.1	EST_HUMAN	zu01b12.r1 Soares testis NHT Homo sapiens cDNA clone IMAGE:730559 5'
2743	11922	21138	7.91	4.0E-11	BE886900.1	EST_HUMAN	60150731F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3809295 5'
2924	12162	21297	1.04	4.0E-11	AL163247.2	NT	Homo sapiens chromosome 21 segment HS21C047
4620	13814	22904	1.18	4.0E-11	D44666.1	EST_HUMAN	HUMSUPY069 Human brain cDNA Homo sapiens cDNA clone 069
5860	15078	24491	3.34	4.0E-11	P20095	SWISSPROT	PRE-MRNA SPLICING FACTOR RNA HELICASE PRP2
							Homo sapiens mannosidase, beta A, lysosomal (MANBA) gene, and ubiquitin-conjugating enzyme E2D 3
6244	15425		3.88	4.0E-11	AF224689.1	NT	(UBE2D3) genes, complete cds
8008	17797	23928	1.42	4.0E-11	11545732	NT	Homo sapiens SH3-domain binding protein 1 (SH3BP1), mRNA
1483	10696	19871	14.62	3.0E-11	6878077	NT	Mus musculus expressed in non-metastatic cells 2, protein (NM23B) (Nme2), mRNA
4261	13464		1.48	3.0E-11	AA308248.1	EST_HUMAN	EST180120 Liver, hepatocellular carcinoma Homo sapiens cDNA 5' end
							qt36c04.x1 Soares testis NHT Homo sapiens cDNA clone IMAGE:1752102 3' similar to contains MER10.13
967	10200	19355	1.59	2.0E-11	AI150302.1	EST_HUMAN	MER10 repetitive element
1193	10413	19568	5.2	2.0E-11	R24807.1	EST_HUMAN	yg43e12.r1 Soares infant brain 1N1B Homo sapiens cDNA clone IMAGE:35144 5'
1193	10413	19569	5.2	2.0E-11	R24807.1	EST_HUMAN	yg43e12.r1 Soares infant brain 1N1B Homo sapiens cDNA clone IMAGE:35144 5'
1592	10805	19980	10.06	2.0E-11	L17432.1	NT	Gallus gallus rho-globin, beta-H globin, beta-A globin, epsilon-globin, and olfactory receptor-like protein COR3/beta (COR3/beta) genes, complete cds

Page 145 of 382  
Table 4  
Single Exon Probes Expressed in HELA Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1592	10805	19981	10.06	2.0E-11	L17432.1	NT	Gallus gallus rho-globin, beta-H globin, beta-A globin, epsilon-globin, and olfactory receptor-like protein COR3beta (COR3beta) genes, complete cds
1594	10808	18984	0.95	2.0E-11	A1126371.1	EST_HUMAN	gc51c10.x1 Soares_pregnant_uterus_NbHPU Homo sapiens cDNA clone IMAGE:1713138 3' similar to gb:L02832 PEROXISOME PROLIFERATOR ACTIVATED RECEPTOR ALPHA (HUMAN); contains L1.11 L1 repetitive element ;
2720	11889	21115	0.93	2.0E-11	AF087813.1	NT	Human endogenous retrovirus HERV-P-T47D
3160	12395	21531	4.04	2.0E-11	P10263	SWISSPROT	RETROVIRUS-RELATED GAG POLYPROTEIN (VERSION 1)
3288	12529	21660	1.62	2.0E-11	A1478617.1	EST_HUMAN	hm54c09.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2161838 3'
3339	12568	21706	0.68	2.0E-11	Q10473	SWISSPROT	POLYPEPTIDE N-ACETYL GALACTOSAMINYLTRANSFERASE (PROTEIN UDP ACETYL GALACTOSAMINYLTRANSFERASE) (UDP-GALNAc:POLYPEPTIDE, N-ACETYL GALACTOSAMINYLTRANSFERASE) (GALNAc-T1)
4438	13638		0.85	2.0E-11	BE065537.1	EST_HUMAN	RC3-BT0318-170200-014-e05 BT0318 Homo sapiens cDNA
4806	13900		0.65	2.0E-11	AL163227.2	NT	Homo sapiens chromosome 21 segment HS21C027
4955	14142		1.38	2.0E-11	BE082558.1	EST_HUMAN	QV2-9T0258-261099-014-a01 BT0258 Homo sapiens cDNA
5028	14214	23288	3.62	2.0E-11	AL163279.2	NT	Homo sapiens chromosome 21 segment HS21C079
5792	15009	24413	1.68	2.0E-11	AA581028.1	EST_HUMAN	nc83h05.r1 NCI_CGAP_GC1 Homo sapiens cDNA clone IMAGE:787433 5' similar to SW:PR16_YEAST P15938 PRE-MRNA SPLICING FACTOR RNA HELICASE PRP16 ;
6834	16028		2.21	2.0E-11	AF028308.1	NT	Homo sapiens chromosome 9 duplication of the T cell receptor beta locus and tyrosinogen gene families
7164	16341	25820	6.37	2.0E-11	Q13606	SWISSPROT	OLFACTORY RECEPTOR 511 (OLFACTORY RECEPTOR-LIKE PROTEIN OLF1)
7674	16873	26377	2.84	2.0E-11	AA035369.1	EST_HUMAN	z427g02.s1 Soares_pregnant_uterus_NbHPU Homo sapiens cDNA clone IMAGE:471784 3'
7674	16873	26378	2.64	2.0E-11	AA035369.1	EST_HUMAN	z427g02.s1 Soares_pregnant_uterus_NbHPU Homo sapiens cDNA clone IMAGE:471784 3'
7702	16901	26409	2.16	2.0E-11	AA281956.1	EST_HUMAN	zs18b04.r1 NCI_CGAP_GC81 Homo sapiens cDNA clone IMAGE:685519 5'
8456	17513		2.3	2.0E-11	AW842143.1	EST_HUMAN	RC0-CN0027-210100-011-c01 CN0027 Homo sapiens cDNA
8485	17533	24027	1.65	2.0E-11	BF377859.1	EST_HUMAN	CM2-TN0140-070900-372-g01 TN0140 Homo sapiens cDNA
8765	17703		1.99	2.0E-11	D25217.2	NT	Homo sapiens mRNA for KIAA0027 protein, partial cds
8922	17808		1.93	2.0E-11	P08547	SWISSPROT	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG
9248	18018		2.34	2.0E-11	11417966	NT	Homo sapiens SEC14 (S. cerevisiae)-like 2 (SEC14L2), mRNA
682	8925	18056	1.26	1.0E-11	AJ131016.1	NT	Homo sapiens SCL gene locus
793	10033	19182	1.21	1.0E-11	AL163209.2	NT	Homo sapiens chromosome 21 segment HS21C009
1225	10443	18598	2.73	1.0E-11	AL163279.2	NT	Homo sapiens chromosome 21 segment HS21C079
1480	10703		1.61	1.0E-11	AF119914.1	NT	Homo sapiens PRO3078 mRNA, complete cds
2086	11296	20508	2.95	1.0E-11	AF000573.1	NT	Homo sapiens homogenisate 1,2-dioxygenase gene, complete cds
3472	12886	21832	1.08	1.0E-11	BE004315.1	EST_HUMAN	CM0-BN0105-170300-292-d12 BN0105 Homo sapiens cDNA

Page 146 of 382  
Table 4  
Single Exon Probes Expressed in HELA Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4944	14131	23228	0.91	1.0E-11	AI168625.1	EST_HUMAN	cd5h05.s1 Soares_NthMPu_S1 Homo sapiens cDNA clone IMAGE:1661243 3'
5354	14584	23680	13.76	1.0E-11	AL163247.2	NT	Homo sapiens chromosome 21 segment HS21C047
6848	15843	25304	7.4	1.0E-11	R131174.1	EST_HUMAN	y73d08.r1 Soares Infant brain 1NIB Homo sapiens cDNA clone IMAGE:28168 5'
7835	17027	26544	1.73	1.0E-11	BF680078.1	EST_HUMAN	602154807F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4295977 5'
8001	18089		1.62	1.0E-11	Z20377.1	EST_HUMAN	HSAACADHP_Human foetal Brain Whole tissue Homo sapiens cDNA
2804	12142	21278	1.11	9.0E-12	P20742	SWISSPROT	PREGNANCY ZONE PROTEIN PRECURSOR
8540	17565		4.76	8.0E-12	AJ271736.1	NT	Homo sapiens Xq pseudautosomal region; segment 2/2
4684	13958	22957	1.62	7.0E-12	Q05904	SWISSPROT	34 KD SPICULE MATRIX PROTEIN PRECURSOR (LSM34)
7889	17105	26635	12.51	7.0E-12	AA704735.1	EST_HUMAN	z123g01.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:451152 3'
3522	12746		0.73	8.0E-12	AV730554.1	EST_HUMAN	AV730554 HTF Homo sapiens cDNA clone HTFAWF06 5'
4341	13543	22634	8.71	8.0E-12	AA732516.1	EST_HUMAN	n288f11.s1 NCL_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1302573 3' similar to contains Alu repetitive element
6903	16060		2.9	6.0E-12	AA847868.1	EST_HUMAN	cd10g11.s1 NCL_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1367588 similar to contains MER29.12
1050	10276	19429	3.79	5.0E-12	T06573.1	EST_HUMAN	MER29 repetitive element ;
3708	12928	22046	6.27	5.0E-12	AJ271736.1	NT	EST04462 Fetal brain, Stratagene (cat#936206) Homo sapiens cDNA clone HFBDV33
5688	14890	24280	5.11	5.0E-12	AL163278.2	NT	Homo sapiens Xq pseudautosomal region; segment 2/2
5688	14890	24281	5.11	5.0E-12	AL163278.2	NT	Homo sapiens chromosome 21 segment HS21C078
5871	15089	24502	10.34	5.0E-12	AW974760.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C078
6810	16005	25466	3.01	5.0E-12	AJ271735.1	NT	EST386850 IMAGE resequences, MAGN Homo sapiens cDNA
7160	16337		6.25	5.0E-12	AL163303.2	NT	Homo sapiens Xq pseudautosomal region; segment 1/2
248	9525	18655	5.28	4.0E-12	AA700326.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C103
249	9525	18655	6.58	4.0E-12	AA700326.1	EST_HUMAN	z174g11.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:460876 3'
4622	13816	22906	0.88	4.0E-12	AI689984.1	EST_HUMAN	z174g11.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:460876 3'
6540	15736		2.37	4.0E-12	AF109607.1	NT	b28h05.x1 NCL_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:2270745 3' similar to TR:Q13539 Q13539
7848	16848	26346	4.08	4.0E-12	AJ228043.1	NT	MARINER TRANSPOSASE ;
8908	17730		1.89	4.0E-12	U78027.1	NT	Homo sapiens S184 gene, partial cds; PS1 and hypothetical protein genes, complete cds; and S171 gene, partial cds
622	9887	18988	4.22	3.0E-12	AW341683.1	EST_HUMAN	Homo sapiens 859 kb contig between AVL1 and CBR1 on chromosome 21q22, segment 3/3
822	9887	18989	4.22	3.0E-12	AW341683.1	EST_HUMAN	Homo sapiens Bruton's tyrosine kinase (BTK), alpha-D-galactosidase A (GLA), L44-like ribosomal protein (L44L) and FTP3 (FTP3) genes, complete cds
							hd13c01.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2808377 3' similar to TR:O14517
							O14517 SMRP ;
							hd13c01.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2808377 3' similar to TR:O14517
							O14517 SMRP ;

Table 4

## Single Exon Probes Expressed in HELA Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7248	18468	25959	3.45	3.0E-12	U37672.1	NT	Human prostate specific antigen gene, 5' flanking region
7248	18468	25960	3.45	3.0E-12	U37672.1	NT	Human prostate specific antigen gene, 5' flanking region
1629	10842	20019	1.81	2.0E-12	AW802131.1	EST_HUMAN	ILS-UM0071-120400-065-a05 UN0071 Homo sapiens cDNA
3443	12668	21803	0.75	2.0E-12	6754495	NT	Mus musculus keratin-associated protein 6.2 (Krtap6-2), mRNA
4092	13300	22399	1.19	2.0E-12	J01884.1	NT	Rat U3A small nuclear RNA
4092	13300	22400	1.19	2.0E-12	J01884.1	NT	Rat U3A small nuclear RNA
4413	13813		2.27	2.0E-12	BE063509.1	EST_HUMAN	CMD-BT0281-031189-087-a03 BT0281 Homo sapiens cDNA
4919	14107	23201	0.59	2.0E-12	O70306	SWISSPROT	TBX15 PROTEIN (T-BOX PROTEIN 15)
4919	14107	23202	0.59	2.0E-12	O70306	SWISSPROT	TBX15 PROTEIN (T-BOX PROTEIN 15)
5861	15079		1.87	2.0E-12	AW971857.1	EST_HUMAN	EST348946 MAGE resequences, MAGL Homo sapiens cDNA
6154	15338	24775	3.16	2.0E-12	T08169.1	EST_HUMAN	EST08060 Infant Brain, Bemto Soares Homo sapiens cDNA clone HIBBA13 5' end
6362	15542	24997	2.07	2.0E-12	11422228	NT	Homo sapiens Ac-like transposable element (ALTE), mRNA
7069	16246		17.58	2.0E-12	BE165980.1	EST_HUMAN	MR3-HT0487-150200-113-g01 HT0487 Homo sapiens cDNA
8440	17503		2.41	2.0E-12	AL163283.2	NT	Homo sapiens chromosome 21 segment HS21C083
8654	17834		1.49	2.0E-12	11418248	NT	Homo sapiens chromosome 21 segment HS21C083
121	9407	18540	3.27	1.0E-12	AW627674.1	EST_HUMAN	hh90a09.x1 NCI CGAP GU1 Homo sapiens cDNA clone IMAGE:2870040 3' similar to contains MER18.11
1956	11160		1.52	1.0E-12	AW627674.1	EST_HUMAN	MER18 repetitive element;
3035	12271	21388	1.76	1.0E-12	AF000991.1	NT	wns5107.x1 NCI CGAP U12 Homo sapiens cDNA clone IMAGE:2438493 3' similar to contains L1.b3 L1
3035	12271	21399	1.76	1.0E-12	AF000991.1	NT	repetitive element;
3955	13071	22185	41.19	1.0E-12	AU132248.1	EST_HUMAN	Homo sapiens testis-specific Testis Transcript Y 2 (TTY2) mRNA, partial cds
3955	13071	22186	41.19	1.0E-12	AU132248.1	EST_HUMAN	Homo sapiens testis-specific Testis Transcript Y 2 (TTY2) mRNA, partial cds
5639	14963		1.92	1.0E-12	U82828.1	NT	AU132248 NT2RP3 Homo sapiens cDNA clone NT2RP3004070 5'
5681	14901		1.82	1.0E-12	Q8Y2G7	SWISSPROT	AU132248 NT2RP3 Homo sapiens cDNA clone NT2RP3004070 5'
6127	15311	24745	1.76	1.0E-12	AF196864.1	NT	Homo sapiens ataxia telangiectasia (ATM) gene, complete cds
6139	15323	24757	9.56	1.0E-12	AF196864.1	EST_HUMAN	HYPOTHETICAL ZINC FINGER PROTEIN KIA00861
6139	15323	24758	9.56	1.0E-12	AF196864.1	EST_HUMAN	Homo sapiens putative BPES syndrome breakpoint region protein gene, complete cds
8348	17441	26839	4.2	1.0E-12	AW062164.1	EST_HUMAN	qh68a04.x1 Soares fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:1849614 3' similar to
8729	18268		1.63	1.0E-12	AL163288.2	NT	gb:M19503 LINE-1 REVERSE TRANSCRIPTASE HOMOLOG (HUMAN);contains MER10.11 MER10
							repetitive element;
							qh68a04.x1 Soares fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:1849614 3' similar to
							gb:M19503 LINE-1 REVERSE TRANSCRIPTASE HOMOLOG (HUMAN);contains MER10.11 MER10
							repetitive element;
							EST374237 MAGE resequences, MAGG Homo sapiens cDNA
							Homo sapiens chromosome 21 segment HS21C068



Page 148 of 382  
Table 4  
Single Exon Probes Expressed in HELA Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3922	13138	22257	0.83	9.0E-13	AB028900.1	NT	Homo sapiens CST gene for cerobroside sulfotransferase, exon 1, 2, 3, 4, 5
6862	16140		2.29	9.0E-13	N69553.1	EST_HUMAN	z26b05.s1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:283651 3'
724	9966	19104	6.37	8.0E-13	U29185.1	NT	Homo sapiens prion protein (PrP) gene, complete cds
724	9966	19105	6.37	8.0E-13	U29185.1	NT	Homo sapiens prion protein (PrP) gene, complete cds
1806	11015	20208	1.99	8.0E-13	U80017.1	NT	Homo sapiens basic transcription factor 2 p44 (btf2p44) gene, partial cds, neuronal apoptosis inhibitory protein (hnp) and survival motor neuron protein (smn) genes, complete cds
7123	16300		2.56	8.0E-13	U78027.1	NT	Homo sapiens Bruton's tyrosine kinase (BTK), alpha-D-galactosidase A (GLA), L44-like ribosomal protein (L44L) and FTP3 (FTP3) genes, complete cds
8244	17373	26908	2.52	8.0E-13	U66060.1	NT	Human germline T-cell receptor beta chain TCRBV13S1, TCRBV6S8A2T, TCRBV5S6A3N2T, TCRBV13S6A2T, TCRBV6S8P, TCRBV5S3A2T, TCRBV13S8P, TCRBV6S3A1N1T, TCRBV5S2, TCRBV6S6A2T, TCRBV5S7P, TCRBV13S4, TCRBV6S2A1N1T, TCRBV6S4A2T, TCRBV6S4A1, TCRBV23S1A2T, TCRBV12>
8838	17748		13.42	7.0E-13	BE778223.1	EST_HUMAN	601463285F1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3866613 5'
8073	17869		19.47	7.0E-13	Q10473	SWISSPROT	POLYPEPTIDE N-ACETYL GALACTOSAMINYL TRANSFERASE (PROTEIN UDP ACETYL GALACTOSAMINYL TRANSFERASE) (UDP-GALNAC:POLYPEPTIDE, N-ACETYL GALACTOSAMINYL TRANSFERASE) (GALNAC-T1)
2071	11271	20486	5.65	6.0E-13	AL163207.2	NT	Homo sapiens chromosome 21 segment HS21C007
3284	12525		0.77	5.0E-13	R78338.1	EST_HUMAN	y82f04.r1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:145759 5'
3375	12603		1.63	5.0E-13	AA435773.1	EST_HUMAN	z77a12.s1 Soares testis_NHT Homo sapiens cDNA clone IMAGE:728350 3' similar to contains Alu repetitive element contains element MER22 repetitive element
7436	16845	26137	2.89	5.0E-13	P07313	SWISSPROT	MYOSIN LIGHT CHAIN KINASE, SKELETAL MUSCLE (MLCK)
1833	11041		8.48	4.0E-13	AW378614.1	EST_HUMAN	PM2-HT0224-221099-001-e11 HT0224 Homo sapiens cDNA
2423	11614		3.52	4.0E-13	AF003529.1	NT	Homo sapiens glypican 3 (GPC3) gene, partial cds and flanking repeat regions
5484	14710	24086	4.77	4.0E-13	BE169131.1	EST_HUMAN	PM3-HT0520-230200-002-c08 HT0520 Homo sapiens cDNA
7080	16257	25731	3.25	4.0E-13	AI289831.1	EST_HUMAN	qn32c05.x1 NCI_CGAP_Kid5 Homo sapiens cDNA clone IMAGE:1898945 3' similar to contains Alu repetitive element
7728	16924	26433	2.08	4.0E-13	AA435819.1	EST_HUMAN	z77g10.s1 Soares testis_NHT Homo sapiens cDNA clone IMAGE:728514 3'
7728	16924	26434	2.08	4.0E-13	AA435819.1	EST_HUMAN	z77g10.s1 Soares testis_NHT Homo sapiens cDNA clone IMAGE:728514 3'
184	8463		5.11	3.0E-13	AF003528.1	NT	Homo sapiens X-linked anhidrotic ectodermal dysplasia protein gene (EDA), exon 2 and flanking repeat regions
875	10111		5.46	3.0E-13	AA430310.1	EST_HUMAN	zv68g08.r1 Soares testis_NHT Homo sapiens cDNA clone IMAGE:781406 5'
2338	11531	20754	1.62	3.0E-13	AJ217735.1	NT	Homo sapiens Xq pseudautosomal region, segment 2/2
2441	11832		2.58	3.0E-13	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C010
2626	11810	21026	2.58	3.0E-13	BF372862.1	EST_HUMAN	CM3-FT0100-140700-242-H08 FT0100 Homo sapiens cDNA

Table 4

## Single Exon Probes Expressed in HELA Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3150	12385		2.42	3.0E-13	AA745844.1	EST_HUMAN	ab18402.s1 NCI_CGAP_K1d5 Homo sapiens cDNA clone IMAGE:1324035 3'
6422	15819	25083	8.11	3.0E-13		NT	Homo sapiens X28 region near ALD locus containing dual specificity phosphatase 9 (DUSP9), ribosomal protein L18a (RPL18a), Ca2+/Calmodulin-dependent protein kinase I (CAMKI), creatine transporter (CRTTR), CDM protein (CDM), adrenoleukodystrophy protein >
7268	16487		3.69	3.0E-13	U52111.2	EST_HUMAN	HAD536 Human fetal liver cDNA library Homo sapiens cDNA
7616	16819	26314	3.1	3.0E-13	BE083509.1	EST_HUMAN	CMO-BT0281-031199-087-403 BT0281 Homo sapiens cDNA
8126	17260	26803	2.87	3.0E-13	AL163248.2	NT	Homo sapiens chromosome 21 segment HS21C048
152	9434	18568	2.21	2.0E-13	U52111.2	NT	Homo sapiens X28 region near ALD locus containing dual specificity phosphatase 9 (DUSP9), ribosomal protein L18a (RPL18a), Ca2+/Calmodulin-dependent protein kinase I (CAMKI), creatine transporter (CRTTR), CDM protein (CDM), adrenoleukodystrophy protein >
243	9521	18652	1.34	2.0E-13	U23839.1	NT	Danio rerio fibroblast growth factor receptor 4 mRNA, complete cds
1277	10492	19851	5.93	2.0E-13	AF239710.1	NT	Homo sapiens DNA polymerase delta small subunit (POLD2) gene, exons 1 through 11 and complete cds
2965	12203	21338	0.79	2.0E-13	8924119	NT	Homo sapiens hypothetical protein PRO2130 (PRO2130), mRNA
2965	12203	21339	0.79	2.0E-13	8924119	NT	Homo sapiens hypothetical protein PRO2130 (PRO2130), mRNA
3249	12482	21614	1.03	2.0E-13	BF431899.1	EST_HUMAN	nab7605.x1 Soares_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE: 3'
3481	12705	21841	1.04	2.0E-13	AF109907.1	NT	Homo sapiens S164 gene, partial cds; PS1 and hypothetical protein genes, complete cds; and S171 gene, partial cds
4086	13295		1.92	2.0E-13	AL163278.2	NT	Homo sapiens chromosome 21 segment HS21C078
5270	14443		2.68	2.0E-13	BE256449.1	EST_HUMAN	601111249F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3351829 5'
5718	14936	24332	4.51	2.0E-13	Q06852	SWISSPROT	CELL SURFACE GLYCOPROTEIN 1 PRECURSOR (OUTER LAYER PROTEIN B) (S-LAYER PROTEIN 1)
6004	15286	24718	6.58	2.0E-13	X16912.1	NT	Human PFKL gene for liver-type 8-phosphofructokinase (EC 2.7.1.11) exon 2
7201	16378	25859	3.55	2.0E-13	5031898	NT	Homo sapiens mab-21 (C. elegans)-like 1 (MAB21L1) mRNA
8521	17552		10.13	2.0E-13	AW892155.1	EST_HUMAN	CMO-NH0001-100300-274-e11 NN0001 Homo sapiens cDNA
296	8569	18701	1.54	1.0E-13	ST4129.1	NT	FGF-1-fibroblast growth factor 1 [human, kidney, Genomic, 342 nt, segment 2 of 2]
898	10133	19295	4.82	1.0E-13	AJ007973.1	NT	Homo sapiens LGMD2B gene
1344	10558	19724	1.38	1.0E-13	X87344.1	NT	H. sapiens DMA, DMB, HLA-Z1, IPP2, LMP2, TAP1, LMP7, TAP2, DOB, DQB2 and RING8, 9, 13 and 14 genes
1991	11194	20404	1.95	1.0E-13	AA720574.1	EST_HUMAN	hw21g02.s1 NCI_CGAP_GCB0 Homo sapiens cDNA clone IMAGE:1241138 3' similar to contains THR.13 THR repetitive element;
4593	13787	22878	1.19	1.0E-13	BF340987.1	EST_HUMAN	602038009F1 NCI_CGAP_Bm64 Homo sapiens cDNA clone IMAGE:4185868 5'
7917	17132	26862	15.9	1.0E-13	BF108755.1	EST_HUMAN	7145e10.x1 Soares_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:3524443 3' similar to contains MER29.b2 MER29 repetitive element;

Page 150 of 382  
Table 4  
Single Exon Probes Expressed in HELA Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8337	17435		1.5	1.0E-13	AV715377.1	EST_HUMAN	AV715377 DCB Homo sapiens cDNA clone DCBAIE03 5'
9015	17887		2.04	1.0E-13	AJ271735.1	NT	Homo sapiens Xq pseudautosomal region, segment 1/2
9161	17860		1.75	1.0E-13	X87579.1	NT	H. sapiens CD4 gene
338	9608	18734	3.04	9.0E-14	AA781159.1	EST_HUMAN	aj24c01.s1 Soares_testis_NHT Homo sapiens cDNA clone 1391232 3' similar to contains MER19.11 MER19 repetitive element:
339	9607	18735	3.14	9.0E-14	AA781159.1	EST_HUMAN	aj24c01.s1 Soares_testis_NHT Homo sapiens cDNA clone 1391232 3' similar to contains MER19.11 MER19 repetitive element:
2484	11655		3.37	9.0E-14	AW861577.1	EST_HUMAN	RC4-CT0322-080100-013-d09 CT0322 Homo sapiens cDNA
2710	11889	21106	6.2	9.0E-14	AB038182.1	NT	Homo sapiens TFF gene cluster for trefol factor, complete cds
3075	12311	21432	5.07	9.0E-14	AW513286.1	EST_HUMAN	xs54h05.x1 NCI_CGAP_U11 Homo sapiens cDNA clone IMAGE:2707833 3'
3204	9606	18734	1.01	9.0E-14	AA781159.1	EST_HUMAN	aj24c01.s1 Soares_testis_NHT Homo sapiens cDNA clone 1391232 3' similar to contains MER19.11 MER19 repetitive element:
3780	12698	22114	7.13	9.0E-14	D14547.1	NT	Human DNA, SINE repetitive element
4768	13957	23058	1.61	9.0E-14	AJ002153.1	NT	Sequins oedipus gene for seminal vesicle secreted protein semenogelin I
3932	13148		3.6	8.0E-14	R76269.1	EST_HUMAN	y72e03.r1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:144796 3'
6893	15599	25065	67.72	8.0E-14	X69211.1	NT	H. sapiens DNA for endogenous retroviral like element
6943	16087	25555	2.85	8.0E-14	AA219316.1	EST_HUMAN	zq17c10.s1 Stratiagene fetal retina 837202 Homo sapiens cDNA clone IMAGE:829670 3'
7971	17150		5.08	8.0E-14	BE062598.1	EST_HUMAN	QV2-BT0268-281099-014-a01 BT0259 Homo sapiens cDNA
8738	17684	23954	1.58	8.0E-14	AI888118.1	EST_HUMAN	wc92h08.x1 NCI_CGAP_Co3 Homo sapiens cDNA clone IMAGE:2326143 3'
1606	11989		4.08	7.0E-14	AW151673.1	EST_HUMAN	x67e10.x1 NCI_CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2623146 3' similar to contains MER10.12 MER10 repetitive element:
372	9638	18771	11.58	6.0E-14	AF020503.1	NT	Homo sapiens FRA3B common fragile region, diadenosine triphosphate hydrolase (FHT) gene, exon 5
7018	16195	25670	3.82	6.0E-14	AF020503.1	NT	Homo sapiens FRA3B common fragile region, diadenosine triphosphate hydrolase (FHT) gene, exon 5
7018	16195	25671	3.82	6.0E-14	AF020503.1	NT	Homo sapiens FRA3B common fragile region, diadenosine triphosphate hydrolase (FHT) gene, exon 5
824	9869	18991	4.42	5.0E-14	Q83120	SWISSPROT	CANALICULAR MULTISPECIFIC ORGANIC ANION TRANSPORTER 1 (MULTIDRUG RESISTANCE-ASSOCIATED PROTEIN 2) (CANALICULAR MULTIDRUG RESISTANCE PROTEIN)
5088	14268	23353	1.24	5.0E-14	AW073791.1	EST_HUMAN	xb03b05.x1 NCI_CGAP_GU1 Homo sapiens cDNA clone IMAGE:2575185 3' similar to contains L1 L2 L1 repetitive element:
5458	14684	24034	5.3	5.0E-14	P08547	SWISSPROT	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG
1131	11988		2.92	4.0E-14	P04928	SWISSPROT	S-ANTIGEN PROTEIN PRECURSOR
1843	11051	20242	5.65	4.0E-14	AJ007973.1	NT	Homo sapiens LGMD2B gene

Page 151 of 382  
Table 4  
Single Exon Probes Expressed in HELA Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3794	12954		0.88	4.0E-14	AA048502.1	EST_HUMAN	zk67a08.r1 Scores_pregnant_uterus_NbHPU Homo sapiens cDNA clone IMAGE:487858 5'
4278	13482	22579	2.22	4.0E-14	N46328.1	EST_HUMAN	y73c12.s1 Scores_multiple_sclerosis_2NbHMSP Homo sapiens cDNA clone IMAGE:279180 3' similar to contains L1.13 L1 repetitive element;
8082	18381		3.28	4.0E-14	AI896224.1	EST_HUMAN	wm08c03.x1 NCI_CGAP_U14 Homo sapiens cDNA clone IMAGE:2435332 3' similar to contains Alu repetitive element;
957	10190	18344	0.85	3.0E-14	X95488.1	NT	R.horvegicus mRNA for CP62 protein
7788	14498	23585	9.96	3.0E-14	AW265354.1	EST_HUMAN	ap45f12.x1 NCI_CGAP_HN11 Homo sapiens cDNA clone IMAGE:2743343 3' similar to contains Alu repetitive element; contains element MER9 repetitive element;
8992	18243		1.51	3.0E-14	AL163285.2	NT	Homo sapiens chromosome 21 segment HS21C085
395	9850	18785	3.21	2.0E-14	AJ271738.1	NT	Homo sapiens Xq pseudautosomal region; segment 2/2
395	9850	18786	3.21	2.0E-14	AJ271738.1	NT	Homo sapiens Xq pseudautosomal region; segment 2/2
697	11974	19072	8.95	2.0E-14	AL163303.2	NT	Homo sapiens chromosome 21 segment HS21C103
2351	11544		1.78	2.0E-14	AW372868.1	EST_HUMAN	RC5-BT0377-091289-031-D12 BT0377 Homo sapiens cDNA
2427	11818		1.48	2.0E-14	7657528	NT	Homo sapiens rhabdoid tumor deletion region protein 1 (RTDR1), mRNA
2492	11862	20898	2.43	2.0E-14	AL163208.2	NT	Homo sapiens chromosome 21 segment HS21C009
2505	11693		1.08	2.0E-14	BE222432.1	EST_HUMAN	hy90g10.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3180738 3' similar to contains Alu repetitive element; contains OFR11 OFR repetitive element;
5543	14797	24133	3.24	2.0E-14	U01317.1	NT	Human beta globin region on chromosome 11
6292	15473	24914	20.64	2.0E-14	BE158781.1	EST_HUMAN	IL2-HT0397-071299-024-D04 HT0397 Homo sapiens cDNA
6292	15473	24915	20.64	2.0E-14	BE158781.1	EST_HUMAN	IL2-HT0397-071299-024-D04 HT0397 Homo sapiens cDNA
7361	16577	26088	5.36	2.0E-14	AW139800.1	EST_HUMAN	UI-H-B1-adv-a-10-0-UI.s1 NCI_CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2718234 3'
8033	14767	24133	1.87	2.0E-14	U01317.1	NT	Human beta globin region on chromosome 11
1074	10299	19449	1.33	1.0E-14	AL163246.2	NT	Homo sapiens chromosome 21 segment HS21C046
1410	10823	19787	5.94	1.0E-14	AL163268.2	NT	Homo sapiens chromosome 21 segment HS21C068
1410	10823	19788	5.94	1.0E-14	AL163268.2	NT	Homo sapiens chromosome 21 segment HS21C068
1970	11174	20380	12.87	1.0E-14	L44140.1	NT	Homo sapiens chromosome X region from filamin (FLN) gene to glucose-6-phosphate dehydrogenase (G6PD) gene, complete cds's
2151	11349	20565	5.32	1.0E-14	AL163303.2	NT	Homo sapiens chromosome 21 segment HS21C103
2372	11585	20786	32.19	1.0E-14	AF001689.1	NT	Homo sapiens ribosomal protein L23A (RPL23A) gene, complete cds
2895	12133	21269	1.12	1.0E-14	P05227	SWISSPROT	HISTIDINE-RICH PROTEIN PRECURSOR (CLONE PFHRP-II)
3132	12367	21497	5.58	1.0E-14	BF335227.1	EST_HUMAN	RC2-CT0432-310700-013-e09_1 CT0432 Homo sapiens cDNA
3132	12367	21498	5.56	1.0E-14	BF335227.1	EST_HUMAN	RC2-CT0432-310700-013-e09_1 CT0432 Homo sapiens cDNA
3865	13081	22197	2.03	1.0E-14	AA682894.1	EST_HUMAN	ae89c12.s1 Stralagene schizo brain S11 Homo sapiens cDNA clone IMAGE:871350 3'
4469	13667	22758	2.01	1.0E-14	AW275852.1	EST_HUMAN	xq39h10.x1 NCI_CGAP_Lu28 Homo sapiens cDNA clone IMAGE:2753059 3'

Page 152 of 382  
Table 4  
Single Exon Probes Expressed in HELA Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6578	14800	24173	2.32	1.0E-14	AF128145.1	NT	Bos taurus xenobiotic/medium-chain fatty acid:CoA ligase form XL-III mRNA, nuclear mRNA encoding mitochondrial protein, complete cds
5959	18067	24591	10.71	1.0E-14	11437150	NT	Homo sapiens promitin (mouse)-like 1 (PROML1), mRNA
5959	18067	24592	10.71	1.0E-14	11437150	NT	Homo sapiens promitin (mouse)-like 1 (PROML1), mRNA
1555	10769	19941	1.52	9.0E-15	7427522	NT	Homo sapiens transcription factor IGHM enhancer 3, JM11 protein, JM4 protein, JM5 protein, TS4 protein, JM10 protein, A4 differentiation-dependent protein, triple LIM domain protein 6, and synaptophysin genes, complete cds; and L-type calcium channel $\alpha$
2139	11337		1.35	9.0E-15	AF198779.1	NT	RC2-CT0432-310700-013-409_1 CT0432 Homo sapiens cDNA
5002	14189	23279	1.12	9.0E-15	BF335227.1	EST_HUMAN	GAG POLYPROTEIN[CONTAINS: CORE PROTEINS P15, P12, P30, P10]
6289	15470	24911	3.85	9.0E-15	P21416	SWISSPROT	601149632F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3164023 5'
2763	9739		0.96	8.0E-15	BE281492.1	EST_HUMAN	3x77d02.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2700483 3' similar to contains THR.12 THR repetitive element
7180	16367		3.7	7.0E-15	AW241958.1	EST_HUMAN	Homo sapiens Xq pseudautosomal region, segment 2/2
1001	10232	16387	8.38	6.0E-15	AJ271738.1	NT	QV1-LT0038-150200-070-c10 LT0038 Homo sapiens cDNA
7650	18391		1.99	6.0E-15	AW836843.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C103
416	9669	18809	8.63	5.0E-15	AL163208.2	NT	Homo sapiens mRNA for transcription factor
						NT	Homo sapiens mRNA for transcription factor
						NT	LY1142F Human fetal heart, Lambda ZAP Express Homo sapiens cDNA clone LY1142 5' similar to ANF(CARDIODILATIN)
2718	11895	21112	2.62	5.0E-15	U61328.1	NT	Human hereditary haemochromatosis region, histone 2A-like protein gene, hereditary haemochromatosis (HLA-H) gene, RoRet gene, and sodium phosphate transporter (NPT3) gene, complete cds
3445	12870		1.05	5.0E-15	AW298817.1	EST_HUMAN	U1H-BWG-ajb-g-10-0-U1.s1 NCI_CGAP_Sub6 Homo sapiens cDNA clone IMAGE:2731219 3'
7267	16486		1.87	5.0E-15	AV730036.1	EST_HUMAN	AV730056 HTF Homo sapiens cDNA clone HTFAVE06 5'
433	9298	18400	3.42	4.0E-15	AL163303.2	NT	Homo sapiens chromosome 21 segment HS21C103
7628	15592	25053	2.78	4.0E-15	AJ130894.1	NT	Homo sapiens mRNA for transcription factor
7628	15592	25054	2.78	4.0E-15	AJ130894.1	NT	Homo sapiens mRNA for transcription factor
4200	13404		7.67	3.0E-15	N89452.1	EST_HUMAN	LY1142F Human fetal heart, Lambda ZAP Express Homo sapiens cDNA clone LY1142 5' similar to ANF(CARDIODILATIN)
4948	14135		5.47	3.0E-15	P82485	SWISSPROT	NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 5
5054	14236	23323	4.65	3.0E-15	AA078097.1	EST_HUMAN	7P01F03 Chromosome 7 Placental cDNA Library Homo sapiens cDNA clone 7P01F03
5054	14236	23324	4.65	3.0E-15	AA078097.1	EST_HUMAN	7P01F03 Chromosome 7 Placental cDNA Library Homo sapiens cDNA clone 7P01F03
6189	15380	24820	3.53	3.0E-15	M27685.1	NT	Mus musculus ultra high sulfur keratin gene, complete cds
6199	15380	24821	3.53	3.0E-15	M27685.1	NT	Mus musculus ultra high sulfur keratin gene, complete cds
						NT	cc36a07.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1351764 3' similar to contains MER19.11
7046	16223		2.34	3.0E-15	AA807128.1	EST_HUMAN	MER19 repetitive element

Table 4

## Single Exon Probes Expressed in HELA Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7374	16580	26079	3.8	3.0E-15	AB026898.1	NT	Homo sapiens DNA, DLEC1 to ORCTL4 gene region, section 1/2 (DLEC1, ORCTL3, ORCTL4 genes, complete cds)
8746	18275		1.51	3.0E-15	AJ271735.1	NT	Homo sapiens Xq pseudautosomal region; segment 1/2
254	9530	18661	5.23	2.0E-15	AF223391.1	NT	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced
373	9639	18772	4.08	2.0E-15	AF223391.1	NT	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced
373	9639	18773	4.08	2.0E-15	AF223391.1	NT	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced
1515	10729		1.55	2.0E-15	8923201	NT	Homo sapiens hypothetical protein FLJ20212 (FLJ20212), mRNA
3483	12707	21843	0.82	2.0E-15	AF223391.1	NT	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced
3483	12707	21844	0.82	2.0E-15	AF223391.1	NT	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced
4925	13819		2.81	2.0E-15	AI806335.1	EST_HUMAN	W07706.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2349823 3' similar to TR:Q61043
6197	15378	24819	2.21	2.0E-15	AA704195.1	EST_HUMAN	Q61043 NINEIN ;
6253	15434	24873	4.9	2.0E-15	W05084.1	EST_HUMAN	z77603.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:460924 3'
6747	15942	25402	3.39	2.0E-15	D14547.1	NT	WP:F44F4.8 CE02227 TRANSPOSASE ;
7415	16627		3.67	2.0E-15	AJ271735.1	NT	Human DNA, SINE repetitive element
8109	12707	21843	2.56	2.0E-15	AF223391.1	NT	Homo sapiens Xq pseudautosomal region; segment 1/2
9109	12707	21844	2.56	2.0E-15	AF223391.1	NT	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced
2730	11809		4.02	1.0E-15	AI889984.1	EST_HUMAN	bc28105.x1 NC1_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:2270745 3' similar to TR:Q13539 Q13539
2974	12211	21348	1.56	1.0E-15	BE043584.1	EST_HUMAN	MARINER TRANSPOSASE ;
3107	12342	21470	1.11	1.0E-15	P08547	SWISSPROT	hk40e02.y1 NC1_CGAP_OV44 Homo sapiens cDNA clone IMAGE:2869162 5'
4353	13555	22651	0.89	1.0E-15	BE182696.1	EST_HUMAN	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG
5822	15039	24441	1.78	1.0E-15	T95763.1	EST_HUMAN	RC3-HT0649-100500-022-b05 HT0649 Homo sapiens cDNA
6091	15292		1.87	1.0E-15	BE074217.1	EST_HUMAN	ye40e10.s1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:120234 3' similar to contains MER8 repetitive element ;
6607	15803	25258	3.75	1.0E-15	AI200976.1	EST_HUMAN	QV3-BT0569-270100-074-g05 BT0569 Homo sapiens cDNA

Page 154 of 382  
Table 4  
Single Exon Probes Expressed in HELA Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6607	15803	25259	3.75	1.0E-15	AI200976.1	EST_HUMAN	qf88h08.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1755227 3'
6778	15974	25431	2.94	1.0E-15	4507208	NT	Homo sapiens spermidine synthase (SRM) mRNA
7395	16609	26100	6.95	1.0E-15	AF044083.1	NT	Homo sapiens major histocompatibility locus class III region
9182	18089	23806	5.74	1.0E-15	AI783944.1	EST_HUMAN	tr31c05.x1 NCI_CGAP_Ov23 Homo sapiens cDNA clone IMAGE:2218912 3' similar to contains Alu repetitive element
4507	13703	22787	1.15	9.0E-16	4503188	NT	Homo sapiens cut (Drosophila)-like 1 (CCAAT displacement protein) (CUTL1) mRNA
7565	16770	26281	2.85	9.0E-16	F08888.1	EST_HUMAN	HSC23F051 normalized infant brain cDNA Homo sapiens cDNA clone c-2305
9130	18186		9.02	7.0E-16	T94149.1	EST_HUMAN	ye28c12.11 Straglene lung (#837210) Homo sapiens cDNA clone IMAGE:119062 5'
2109	11308		7.46	6.0E-16	AW97261.1	EST_HUMAN	EST384702 IMAGE resequences, MAGL Homo sapiens cDNA
1484	10697	19872	0.96	5.0E-16	AJ251154.1	NT	Mus musculus olfactory receptor cluster, OR37A, OR37B, OR37C, OR37E genes and OR37D pseudogene
2640	11823	21038	2.42	5.0E-16	AA992176.1	EST_HUMAN	qf80c04.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1623078 3' similar to contains element L1 repetitive element
8052	17188	26728	3.64	5.0E-16	BF217388.1	EST_HUMAN	601885734F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4104128 5'
8225	18003		12.84	5.0E-16	11418127	NT	Homo sapiens GTP binding protein 1 (GTPBP1), mRNA
2348	11539	20762	0.96	4.0E-16	AW797168.1	EST_HUMAN	QV1-UM0038-200300-115-g02 UM0038 Homo sapiens cDNA
2348	11539	20763	0.96	4.0E-16	AW797168.1	EST_HUMAN	QV1-UM0036-200300-115-g02 UM0036 Homo sapiens cDNA
3434	12659	21790	5.03	4.0E-16	Q16653	SWISSPROT	MYELIN-OLIGODENDROCYTE GLYCOPROTEIN PRECURSOR
4124	13330	22428	5.95	4.0E-16	BE083875.1	EST_HUMAN	PM4-BT0650-010400-002-g09 BT0650 Homo sapiens cDNA
4124	13330	22429	5.95	4.0E-16	BE083875.1	EST_HUMAN	PM4-BT0650-010400-002-g09 BT0650 Homo sapiens cDNA
6380	15560	25016	35.48	4.0E-16	AL163284.2	NT	Homo sapiens chromosome 21 segment HS21C084
7772	16967	26480	1.68	4.0E-16	AV730030.1	EST_HUMAN	AV730030 HTF Homo sapiens cDNA clone HTFAWA03 5'
8421	17493		1.39	4.0E-16	P08548	SWISSPROT	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG
8514	17548		0.28	4.0E-16	C05947	EST_HUMAN	C05947 Human pancreatic islet Homo sapiens cDNA clone hbc5355
8525	17555	23988	2.97	4.0E-16	6912459	NT	Homo sapiens Grb2-associated binder 2 (KIAA0571), mRNA
8808	17728		1.45	4.0E-16	R18591.1	EST_HUMAN	y96b11.11 Soares infant brain 1N1B Homo sapiens cDNA clone IMAGE:30489 5'
130	9413	18548	1.45	3.0E-16	AW022862.1	EST_HUMAN	df45c01.y1 Morton Fetal Cochlea Homo sapiens cDNA clone IMAGE:2486376 5'
130	9413	18549	1.45	3.0E-16	AW022862.1	EST_HUMAN	df45c01.y1 Morton Fetal Cochlea Homo sapiens cDNA clone IMAGE:2486376 5'
472	9725		2.3	3.0E-16	AL046445.1	EST_HUMAN	DKFZp434P037.1 434 (synonym: hies3) Homo sapiens cDNA clone DKFZp434P037 5'
482	9734		1.72	3.0E-16	AF135446.1	NT	Homo sapiens TSX (TSX) pseudogene, exon 5
1453	10666	18840	1.97	3.0E-16	Q28983	SWISSPROT	ZONADHESIN PRECURSOR
2630	12168	21300	4.26	3.0E-16	P03200	SWISSPROT	ENVELOPE GLYCOPROTEIN GP340 (MEMBRANE ANTIGEN) (MA) [CONTAINS: GLYCOPROTEIN GP220]
3907	13123	22241	0.76	3.0E-16	T08169.1	EST_HUMAN	EST06060 Infant Brain, Benito Soares Homo sapiens cDNA clone HIBBA13 5' end

Page 155 of 382  
Table 4  
Single Exon Probes Expressed in HELA Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4961	14148	23240	1.01	3.0E-16	AV661393.1	EST_HUMAN	AV661393 GLC Homo sapiens cDNA clone GLCGSA01 3'
6971	15866	25326	3.01	3.0E-16	AI002636.1	EST_HUMAN	am88h05.s1 Stralagene schizo brain S11 Homo sapiens cDNA clone IMAGE:1684185 3' similar to contains THR.b2 THR repetitive element ;
7118	16295	25777	6.55	3.0E-16	L78810.1	NT	Homo sapiens ADP/ATP carrier protein (ANT-2) gene, complete cds
978	10211		1.32	2.0E-16	AL163279.2	NT	Homo sapiens chromosome 21 segment HS21C079
2650	11833		1.1	2.0E-16	J03061.1	NT	Human SSAV-related endogenous retroviral LTR-like element
4159	13363	22463	1.66	2.0E-16	X89211.1	NT	H.sapiens DNA for endogenous retroviral like element
8450	15947	25115	2.24	2.0E-16	AI732637.1	EST_HUMAN	nz47706.x5 NCL_CGAP_P12 Homo sapiens cDNA clone IMAGE:1280947 similar to TR:O54849 O54849 HYPOTHETICAL 42.9 KD PROTEIN. [2] TR:O08905, contains MER7.11 MER7 repetitive element ;
7502	16709	26196	3.45	2.0E-16	5902145	NT	Homo sapiens ubiquitin carrier protein E2-C (UBCH10), mRNA
189	9468	18597	2.2	1.0E-16	AF200719.1	NT	Homo sapiens pituitary tumor transforming gene protein (PTTG) gene, complete cds
387	9681		32.18	1.0E-16	AA628592.1	EST_HUMAN	af39g11.s1 Soares_fetal_fetus Nb2HF8 9w Homo sapiens cDNA clone IMAGE:1034084 3' similar to contains OFR.12 OFR repetitive element ;
1941	11145	20344	2.99	1.0E-16	BF327942.1	EST_HUMAN	QV0-BN0149-070700-293-at10 BN0148 Homo sapiens cDNA
5844	15061		25.98	1.0E-16	U45983.1	NT	Homo sapiens CCR8 chemokine receptor (CMKBR8) gene, complete cds
5913	15130	24539	3.2	1.0E-16	Q02779	SWISSPROT	MITOGEN-ACTIVATED PROTEIN KINASE KINASE 10 (MIXED LINEAGE KINASE 2) (PROTEIN KINASE MST)
6314	15061		7.17	1.0E-16	U45983.1	NT	Homo sapiens CCR8 chemokine receptor (CMKBR8) gene, complete cds
3719	12939	22056	2.63	9.0E-17	AW900048.1	EST_HUMAN	CM1-NN1003-200300-153-e01 NN1003 Homo sapiens cDNA
5974	15188		1.99	9.0E-17	AI392984.1	EST_HUMAN	tg22c11.x1 NCL_CGAP_CLL1 Homo sapiens cDNA clone IMAGE:2109524 3' similar to contains MER28.12 MER28 repetitive element ;
6496	15693		3.16	9.0E-17	AW150257.1	EST_HUMAN	xg48g12.x1 NCL_CGAP_U11 Homo sapiens cDNA clone IMAGE:2630950 3' similar to contains OFR.12 OFR repetitive element ;
7142	16319		2.25	9.0E-17	AF200719.1	NT	Homo sapiens pituitary tumor transforming gene protein (PTTG) gene, complete cds
1025	10251		1.34	8.0E-17	AW880701.1	EST_HUMAN	QV0-OT0032-080300-155-d01 OT0032 Homo sapiens cDNA
3870	13086		1.01	8.0E-17	AL163280.2	NT	Homo sapiens chromosome 21 segment HS21C080
5482	18056	24084	3.83	8.0E-17	BE172081.1	EST_HUMAN	MR0-HT0559-060300-003-e04 HT0559 Homo sapiens cDNA
6198	15379		1.82	8.0E-17	AV730759.1	EST_HUMAN	AV730759 HTF Homo sapiens cDNA clone HTFACB07 5'
1457	10670		4.26	7.0E-17	6753097	NT	Mus musculus apolipoprotein B editing complex 2 (ApoBec2), mRNA
5347	14577		3.44	7.0E-17	AF216650.1	NT	Homo sapiens putative MTAP (MTAP) mRNA, partial cds, alternatively spliced
5960	15175	24593	7.8	7.0E-17	AF228843.1	NT	Mus musculus WNT-2 gene, partial cds; putative ankyrin-related protein and cystic fibrosis transmembrane conductance regulator (CFTR) genes, section 1 of 2 of the complete cds; and unknown gene



Table 4  
Single Exon Probes Expressed in HELA Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
208	9488	18622	8.24	6.0E-17	AW983880.1	EST_HUMAN	RC1-HN0003-220300-021-004 HN0003 Homo sapiens cDNA hi81d04.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2878895 3' similar to contains L1.12 L1 repetitive element;
5784	15011	24415	1.71	6.0E-17	AW662772.1	EST_HUMAN	
427	9282	18394	4.13	5.0E-17	T64110.1	EST_HUMAN	yc05h08.r1 Strategene lung (#337210) Homo sapiens cDNA clone IMAGE:79839 5'
6328	15509	24955	1.75	5.0E-17	T81043.1	EST_HUMAN	yd2b04.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:109327 5'
3614	12835	21955	0.65	4.0E-17	AA643697.1	EST_HUMAN	hi86d05.s1 NCI_CGAP_Cot0 Homo sapiens cDNA clone IMAGE:1058528 3'
8028	17163	28700	2.43	4.0E-17	AL163247.2	NT	Homo sapiens chromosome 21 segment HS21C047
8435	17601		2.34	4.0E-17	A1073546.1	EST_HUMAN	ov45d04.x1 Soares testis_NHT Homo sapiens cDNA clone IMAGE:1840288 3' similar to TR:Q18530
2088	11288	20482	1.45	3.0E-17	AW119123.1	EST_HUMAN	Q16530 PMS3 MRNA ;contains MER10.12 MER10 repetitive element ;
3157	12392		1.06	3.0E-17	P35410	SWISSPROT	xd89d09.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2804784 3'
3621	12842	21981	1.18	3.0E-17	BE326522.1	EST_HUMAN	MAS-RELATED G PROTEIN-COUPLED RECEPTOR MRG
3621	12842	21982	1.16	3.0E-17	BE326522.1	EST_HUMAN	hw05b04.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3181989 3'
							hw05b04.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3181989 3'
6992	16170	25642	5.16	3.0E-17	AB026898.1	NT	Homo sapiens DNA, DLEC1 to ORCTL4 gene region, section 1/2 (DLEC1, ORCTL3, ORCTL4 genes, complete cds)
8398	17476		3.23	3.0E-17	11417986	NT	Homo sapiens SEC14 (S. cerevisiae)-like 2 (SEC14L2), mRNA
358	9826	18756	4.54	2.0E-17	A1270080.1	EST_HUMAN	qt63a06.x1 NCI_CGAP_Eso2 Homo sapiens cDNA clone IMAGE:1058922 3' similar to contains Alu repetitive element;
359	9826	18756	2.24	2.0E-17	A1270080.1	EST_HUMAN	qt63a06.x1 NCI_CGAP_Eso2 Homo sapiens cDNA clone IMAGE:1058922 3' similar to contains Alu repetitive element;
995	10227		1.92	2.0E-17	AA722832.1	EST_HUMAN	zq81d04.s1 Soares fetal heart NBH19W Homo sapiens cDNA clone IMAGE:399761 3'
2410	11602	20822	2.54	2.0E-17	Q28983	SWISSPROT	ZONADHESIN PRECURSOR
2410	11602	20823	2.54	2.0E-17	Q28983	SWISSPROT	ZONADHESIN PRECURSOR
2880	12118	21249	6.89	2.0E-17	P12036	SWISSPROT	NEUROFILAMENT TRIPLET H PROTEIN (200 KDA NEUROFILAMENT PROTEIN) (NEUROFILAMENT HEAVY POLYPEPTIDE) (NF-H)
5378	14607	23717	1.9	2.0E-17	M27685.1	NT	Mus musculus ultra high sulfur keratin gene, complete cds
5378	14607	23718	1.9	2.0E-17	M27685.1	NT	Mus musculus ultra high sulfur keratin gene, complete cds
5774	14982		1.81	2.0E-17	AF055066.1	NT	Homo sapiens MHC class 1 region
7029	16206	25683	2.43	2.0E-17	BE298988.1	EST_HUMAN	600944690F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:2860615 5'
7042	16218	25684	3.53	2.0E-17	AL163247.2	NT	Homo sapiens chromosome 21 segment HS21C047
7042	16218	25685	3.53	2.0E-17	AL163247.2	NT	Homo sapiens chromosome 21 segment HS21C047
7154	16331	25814	6.53	2.0E-17	D13391.1	NT	Human CYP19 gene for aromatase cytochrome P-450, promoter region (containing two cis-acting transcriptional regulatory elements)
758	8959	19146	3.33	1.0E-17	P08183	SWISSPROT	MULTIDRUG RESISTANCE PROTEIN 1 (P-GLYCOPROTEIN 1)

Table 4

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1683	10895		1.36	1.0E-17	AJ271736.1	NT	Homo sapiens Xq pseudautosomal region, segment 2/2
1738	10950	20133	5.60	1.0E-17	AL163207.2	NT	Homo sapiens chromosome 21 segment HS21C007
2086	11266	20499	1.89	1.0E-17	P02461	SWISSPROT	COLLAGEN ALPHA 1(III) CHAIN PRECURSOR
2304	11498	20718	3.54	1.0E-17	U79410.1	NT	Homo sapiens thrombospondin 2 (THBS2) gene, promoter region and exons 1A and 1B
3543	12766		0.83	1.0E-17	AF224669.1	NT	Homo sapiens mannosidase, beta A, lysosomal (MANBA) gene, and ubiquitin-conjugating enzyme E2D 3
4119	13325		8.44	1.0E-17	R09942.1	EST_HUMAN	(UBE2D3) genes, complete cds
7955	17094	26825	1.98	1.0E-17	Q28824	SWISSPROT	MYOSIN LIGHT CHAIN KINASE, SMOOTH MUSCLE (MLCK) [CONTAINS: TELOKIN]
2434	11625	20847	1.78	9.0E-18	AA174078.1	EST_HUMAN	4p18g12.x1 Straglene fetal retina 937202 Homo sapiens cDNA clone IMAGE:609862 3'
3769	12987	22103	1.31	8.0E-18	4758977	NT	Homo sapiens protein tyrosine phosphatase, non-receptor type substrate 1 (PTPNS1) mRNA
354	9622	18750	49.6	7.0E-18	AW316976.1	EST_HUMAN	xx10b04.x1 NCI CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2837071 3' similar to gb:L20868 60S
354	9622	18751	49.6	7.0E-18	AW316976.1	EST_HUMAN	RIBOSOMAL PROTEIN L4 (HUMAN);
8936	9622	18750	4.04	7.0E-18	AW316976.1	EST_HUMAN	xx10b04.x1 NCI CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2837071 3' similar to gb:L20868 60S
8936	9622	18751	4.04	7.0E-18	AW316976.1	EST_HUMAN	RIBOSOMAL PROTEIN L4 (HUMAN);
3264	12497	21627	1.38	6.0E-18	X71791.2	NT	xx10b04.x1 NCI CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2837071 3' similar to gb:L20868 60S
4759	13950		3.42	6.0E-18	P52181	SWISSPROT	RIBOSOMAL PROTEIN L4 (HUMAN);
6542	15738		3.47	6.0E-18	11428155	NT	Rattus norvegicus partial Gdn/Pn-1 gene for glia-derived neurotrophin, enhancer region
7694	16933	26402	2.2	6.0E-18	AL163246.2	NT	PROTEIN-GLUTAMINE GAMMA-GLUTAMYL TRANSFERASE (TISSUE TRANSGLUTAMINASE) (TGase C) (TGC)
7873	17082	26588	1.96	6.0E-18	X87344.1	NT	Homo sapiens similar to high-mobility group (nonhistone chromosomal) protein 4 (H. sapiens) (LOC63446), mRNA
8231	17350		2.73	6.0E-18	11428885	NT	Homo sapiens chromosome 21 segment HS21C046
8671	17648	23977	1.73	6.0E-18	U87929.1	NT	H. sapiens DMA, DMB, HLA-Z1, IPP2, LMP2, TAP1, LMP7, TAP2, DOB, DOB2 and RING8, 9, 13 and 14 genes
1158	10378	19530	17.47	5.0E-18	A1280214.1	EST_HUMAN	Homo sapiens similar to ribosomal protein L12 (H. sapiens) (LOC63081), mRNA
4303	13504	22601	1.26	5.0E-18	10946865	NT	Human aconitase hydratase (ACO2) gene, exon 4
5311	14542	23611	1.95	5.0E-18	AF087913.1	NT	qim5g11.x1 Soares_placenta_8w0weeks_2NHP8to9W Homo sapiens cDNA clone IMAGE:1893668 3' similar to contains Alu repetitive element
7551	16756	26249	4.21	5.0E-18	10242378	NT	Mus musculus gasdermin (Gsdm), mRNA
7551	16756	26250	4.21	5.0E-18	10242378	NT	Human endogenous retrovirus HERV-P-147D
							Homo sapiens lymphocyte activation-associated protein (LOC51088), mRNA
							Homo sapiens lymphocyte activation-associated protein (LOC51088), mRNA

Table 4

### Single Exon Probes Expressed in HELA Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8800	17725		5.65	5.0E-18	AW887182.1	EST_HUMAN	MR1-SN0035-060400-001-g11 SN0035 Homo sapiens cDNA
9151	17854		14.87	5.0E-18	AV650547.1	EST_HUMAN	AV650547 GLC Homo sapiens cDNA clone GLCGA02 3'
123	9408	18541	1.78	4.0E-18	BE044076.1	EST_HUMAN	ho36h04.x1 NCI_CGAP_U11 Homo sapiens cDNA clone IMAGE:3039511 3' similar to contains MER29.b3 MER29 repetitive element;
123	9408	18542	1.78	4.0E-18	BE044076.1	EST_HUMAN	ho36h04.x1 NCI_CGAP_U11 Homo sapiens cDNA clone IMAGE:3039511 3' similar to contains MER29.b3 MER29 repetitive element;
1691	10903	20090	18.8	4.0E-18	AA621814.1	EST_HUMAN	nq24f11.s1 NCI_CGAP_Cot10 Homo sapiens cDNA clone IMAGE:1144845 3' similar to gb:M26328 KERATIN, TYPE I, CYTOSKELETAL 18 (HUMAN);
1854	11061		1.02	4.0E-18	A1738592.1	EST_HUMAN	wi33h08.x1 NCI_CGAP_Cot16 Homo sapiens cDNA clone IMAGE:2392095 3'
2167	11365	20584	1.64	4.0E-18	Q06430	SWISSPROT	N-ACETYLGLUCOSAMINIDE BETA-1,6-N-ACETYLGLUCOSAMINYLTRANSFERASE (N- ACETYLGLUCOSAMINYLTRANSFERASE) (L-BRANCHING ENZYME) (IGNT)
2167	11365	20585	1.64	4.0E-18	Q06430	SWISSPROT	N-ACETYLGLUCOSAMINIDE BETA-1,6-N-ACETYLGLUCOSAMINYLTRANSFERASE (N- ACETYLGLUCOSAMINYLTRANSFERASE) (L-BRANCHING ENZYME) (IGNT)
3774	12692	22107	0.61	4.0E-18	A1581586.1	EST_HUMAN	ar83b06.x1 Barslead colon HPLRB7 Homo sapiens cDNA clone IMAGE:2173138 3' similar to contains Alu repetitive element;
5376	14605	23714	2.33	4.0E-18	A1017565.1	EST_HUMAN	cu23a06.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1627138 3'
5376	14605	23715	2.33	4.0E-18	A1017565.1	EST_HUMAN	cu23a06.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1627138 3'
7575	16780	26275	7.21	4.0E-18	AA371807.1	EST_HUMAN	EST83653 Pituitary gland, subtracted (prolactin/growth hormone) II Homo sapiens cDNA 5' end similar to EST containing O family repeat
859	10085	19258	6.09	3.0E-18	AA814198.1	EST_HUMAN	ab23h11.s1 NCI_CGAP_Kid5 Homo sapiens cDNA clone IMAGE:1324581 3' similar to SW:RS5_HUMAN
938	10171	19327	3.12	3.0E-18	BE088634.1	EST_HUMAN	P46782 40S RIBOSOMAL PROTEIN S6. ;
3927	13143	22260	1.29	3.0E-18	AL163247.2	NT	CMD-BT0690-210300-298-g07 BT0690 Homo sapiens cDNA Homo sapiens chromosome 21 segment HS21C047
6009	13259	24983	5.16	3.0E-18	BE001671.1	EST_HUMAN	PMO-BN0081-100300-001-b08 BN0081 Homo sapiens cDNA
8941	17819		5.72	3.0E-18	AW022015.1	EST_HUMAN	df31h12.y1 Morton Fetal Cochlea Homo sapiens cDNA clone IMAGE:2485126 5'
255	9531	18682	3.74	2.0E-18	AW838820.1	EST_HUMAN	QV1-LT0036-150200-070-e07 LT0036 Homo sapiens cDNA
1161	10383		130.1	2.0E-18	BE256097.1	EST_HUMAN	6011-L14352F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3355044 5'
3087	12323	21445	0.97	2.0E-18	Q39875	SWISSPROT	DYNEIN GAMMA CHAIN, FLAGELLAR OUTER ARM
5400	14628		2.82	2.0E-18	AA868610.1	EST_HUMAN	ak53a07.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1408652 3' similar to TR:O14577
5442	14668	23824	3.16	2.0E-18	D14547.1	NT	O14577 BAC CLONE RG114A08 FROM TQ31, COMPLETE SEQUENCE. ;
5442	14668	23825	3.16	2.0E-18	D14547.1	NT	Human DNA, SINE repetitive element Human DNA, SINE repetitive element
5788	15013	24417	3.75	2.0E-18	AW665853.1	EST_HUMAN	hi94g01.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2979894 3' similar to contains MER19.12 MER19 repetitive element ;

Page 159 of 382  
Table 4  
Single Exon Probes Expressed in HELA Cells

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7546	16751	26245	5.35	2.0E-18	AW470791.1	EST_HUMAN	ha33406.x1 NCI_CGAP_Kid12 Homo sapiens cDNA clone IMAGE:2875499 3' similar to contains THIR.b3 THIR repetitive element;
8223	17353	26880	6.03	2.0E-18	AW151299.1	EST_HUMAN	X947e09.x1 NCI_CGAP_U11 Homo sapiens cDNA clone IMAGE:2630728 3' similar to contains MER8.b2 MER8 repetitive element;
8800	10383		6.58	2.0E-18	BE256097.1	EST_HUMAN	601114352F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3355044 5'
4409	13809		0.91	1.0E-18	T95406.1	EST_HUMAN	ye43g05.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:120536 5' similar to contains L1 repetitive element;
4614	13808		0.94	1.0E-18	Y10198.1	NT	Homo sapiens PHEX gene
5369	14599	23677	2.61	1.0E-18	AV653405.1	EST_HUMAN	AV653405 GLC Homo sapiens cDNA clone GLCCKE11 3'
5475	14702	24057	3.08	1.0E-18	D00099.1	NT	Homo sapiens mRNA for Na,K-ATPase alpha-subunit, complete cds
5475	14702	24058	3.08	1.0E-18	D00099.1	NT	Homo sapiens mRNA for Na,K-ATPase alpha-subunit, complete cds
7040	16217	25692	6.86	1.0E-18	U91328.1	NT	Human hereditary haemochromatosis region, histone 2A-like protein gene, hereditary haemochromatosis (H1A-H) gene, RoRet gene, and sodium phosphate transporter (NP73) gene, complete cds
8548	17572	23993	2.92	1.0E-18	AF003528.1	NT	Homo sapiens glycican 3 (GPC3) gene, partial cds and flanking repeat regions
552	9803	18930	5.11	9.0E-19	AA281861.1	EST_HUMAN	zt11d06.r1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:712811 5' similar to contains MER19.12 MER19 repetitive element;
553	9803	18930	4	9.0E-19	AA281861.1	EST_HUMAN	zt11d06.r1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:712811 5' similar to contains MER19.12 MER19 repetitive element;
6412	15609		3.42	9.0E-19	F08688.1	EST_HUMAN	HSC23F051 normalized infant brain cDNA Homo sapiens cDNA clone c-23105
6676	15871	25330	3.24	9.0E-19	AL163203.2	NT	Homo sapiens chromosome 21 segment HS21C003
6676	15871	25331	3.24	9.0E-19	AL163203.2	NT	Homo sapiens chromosome 21 segment HS21C003
7687	16888	26394	4.7	9.0E-19	AB032868.1	NT	Homo sapiens mRNA for KIAA1143 protein, partial cds
8303	9803	18930	10.58	9.0E-19	AA281861.1	EST_HUMAN	zt11d06.r1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:712811 5' similar to contains MER19.12 MER19 repetitive element;
1055	10281		1.04	8.0E-19	AW974902.1	EST_HUMAN	EST387007 MAGI resequences, MAGN Homo sapiens cDNA
2210	11407	20631	1.9	7.0E-19	4758139	NT	Homo sapiens DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 6 (RNA helicase, S4kD) (DDX6) mRNA
5851	15069	24478	2.02	7.0E-19	AF092090.1	NT	Rattus norvegicus cp151 mRNA, partial cds
8443	18362		2.65	7.0E-19	AA705694.1	EST_HUMAN	z60b01.s1 Soares fetal liver spleen 1NFLS_S1 Homo sapiens cDNA clone IMAGE:435145 3'
3761	12880		1.41	6.0E-19	AW852930.1	EST_HUMAN	PMO-CT0248-131099-001-g01 CT0248 Homo sapiens cDNA
4458	13856	22750	1.47	6.0E-19	P34986	SWISSPROT	OLFACTORY RECEPTOR 6 (M50)
4458	13856	22751	1.47	6.0E-19	P34986	SWISSPROT	OLFACTORY RECEPTOR 6 (M50)
4813	14002		1.34	6.0E-19	AJ271735.1	NT	Homo sapiens Xq pseudautosomal region, segment 1/2

Table 4

## Single Exon Probes Expressed In HELA Cells

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5050	14232	23317	1.01	6.0E-19	AL120817.1	EST_HUMAN	DKFZp762F192.1 762 (synonym: hmel2) Homo sapiens cDNA clone DKFZp762F192.5'
5594	14818	24194	5.29	5.0E-19	Q00183	SWISSPROT	ZONA PELLUCIDA SPERM-BINDING PROTEIN B PRECURSOR (ZONA PELLUCIDA GLYCOPROTEIN ZP-X) (RC55)
8070	17205	26739	7.83	5.0E-19	AW183725.1	EST_HUMAN	x87b02.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2664171 3' similar to contains element MSR1 repetitive element;
561	9811	18934	1.19	4.0E-19	AB007970.1	NT	Homo sapiens mRNA, chromosome 1 specific transcript KIAA0501
2642	11825	21040	1.28	4.0E-19	BF697382.1	EST_HUMAN	602130910F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:4287674 5'
3836	13053	22165	1	3.0E-19	Q28997	SWISSPROT	BETA-2 ADRENERGIC RECEPTOR
3836	13053	22166	1	3.0E-19	Q28997	SWISSPROT	BETA-2 ADRENERGIC RECEPTOR
4271	13474	22570	0.6	3.0E-19	O43900	SWISSPROT	LIM-ONLY PROTEIN 6 (TRIPLE LIM DOMAIN PROTEIN 6)
4271	13474	22571	0.6	3.0E-19	O43900	SWISSPROT	LIM-ONLY PROTEIN 6 (TRIPLE LIM DOMAIN PROTEIN 6)
4441	13641	22732	1.37	3.0E-19	AV708136.1	EST_HUMAN	AV708136 ADC Homo sapiens cDNA clone ADCAMAT1 5'
6249	15430		2.23	3.0E-19	11432214	NT	Homo sapiens similar to aldo-keto reductase family 1, member B11 (aldose reductase-like) (H. sapiens) (LOC83222), mRNA
8697	17665		14.35	3.0E-19	AF165520.1	NT	Homo sapiens phorbol-in protein (PBI) mRNA, complete cds
2528	11714	20831	42.82	2.0E-19	AL183201.2	NT	Homo sapiens chromosome 21 segment HS21C001
4439	13639		1.65	2.0E-19	AB11763.1	EST_HUMAN	q991e02.x1 NCL_CGAP_Kid5 Homo sapiens cDNA clone IMAGE:1915898 3' similar to TR:Q69388 Q69388 POLJENV GENE:
6572	15768	25231	5.48	2.0E-19	AA012854.1	EST_HUMAN	z834c08.r1 Soares retina N2b4HR Homo sapiens cDNA clone IMAGE:360880 5'
8260	17387	26919	1.88	2.0E-19	BF330867.1	EST_HUMAN	RC3-BT0333-250800-114-604 BT0333 Homo sapiens cDNA
8260	17387	26920	1.88	2.0E-19	BF330867.1	EST_HUMAN	RC3-BT0333-250800-114-604 BT0333 Homo sapiens cDNA
498	8741		1.85	1.0E-19	BE408611.1	EST_HUMAN	601304125F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3638310 5'
2130	11329	20548	1.23	1.0E-19	H30795.1	EST_HUMAN	y979g07.r1 Soares adult brain N2b4HB55Y Homo sapiens cDNA clone IMAGE:184188 5' similar to contains MER10 repetitive element;
2677	11859		1.79	1.0E-19	D38044.1	NT	Human gene for Ah-receptor, exon 7-9
2800	12040		6.21	1.0E-19	4758977	NT	Homo sapiens protein tyrosine phosphatase, non-receptor type substrate 1 (PTPNS1) mRNA
3379	12806	21740	1.3	1.0E-19	AA834967.1	EST_HUMAN	aj49b12.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1393631 3' similar to contains MER37.12 MER37 repetitive element;
5700	14819	24313	2.41	1.0E-19	U12186.1	NT	Oryctolagus cuniculus sodium/dicarboxylate cotransporter mRNA, partial cds
6598	15891		3.46	1.0E-19	T69920.1	EST_HUMAN	y972b02.r1 Soares fetal liver spleen INFILS Homo sapiens cDNA clone IMAGE:123243 5' similar to contains OIR repetitive element;
7129	16308	25786	49.35	1.0E-19	AW812259.1	EST_HUMAN	RC0-ST0174-191099-031-605 ST0174 Homo sapiens cDNA
7133	16310	25792	2.88	1.0E-19	N44631.1	EST_HUMAN	y931e08.r1 Soares melanocyte 2NbHM Homo sapiens cDNA clone IMAGE:272872 5'

Page 161 of 382  
Table 4  
Single Exon Probes Expressed in HELA Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8233	17362	26900	1.92	1.0E-19	U93163.1	NT	Homo sapiens IMAGE-B2 (IMAGE-B2), IMAGE-B3 (IMAGE-B3), IMAGE-B4 (IMAGE-B4), and IMAGE-B1 (IMAGE-B1) genes, complete cds
5954	15170	24584	2.54	8.0E-20	7657286	NT	Mus musculus keratin-associated protein 9-1 (Krtap9-1), mRNA
5954	15170	24585	2.54	8.0E-20	7657286	NT	Mus musculus keratin-associated protein 9-1 (Krtap9-1), mRNA
3243	12476	21609	0.6	7.0E-20	BF326455.1	EST_HUMAN	PMA-AN0098-05090-003-a04 AN0096 Homo sapiens cDNA
6086	14532	23556	6.05	7.0E-20	AL138120.1	EST_HUMAN	DKFZ547D092_1 347 (synonym: hfr1) Homo sapiens cDNA clone DKFZ547D092 5'
6624	15820	25279	10.96	7.0E-20	AA557657.1	EST_HUMAN	h46c04.s1 NCL_CGAP_P4 Homo sapiens cDNA clone IMAGE:1043718 similar to contains MER29.b2 MER29 repetitive element ;
6624	15820	25280	10.96	7.0E-20	AA557657.1	EST_HUMAN	h46c04.s1 NCL_CGAP_P4 Homo sapiens cDNA clone IMAGE:1043718 similar to contains MER29.b2 MER29 repetitive element ;
8205	17336		9.91	7.0E-20	6912633	NT	Homo sapiens ribosomal protein L13a (RPL13A), mRNA
3530	12753	21886	3.7	6.0E-20	P39188	SWISSPROT	ALU SUBFAMILY J SEQUENCE CONTAMINATION WARNING ENTRY
4258	13461	22553	3.37	6.0E-20	BE622434.1	EST_HUMAN	601441231F1.NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3916231 5'
4595	13789		1.15	5.0E-20	AV725123.1	EST_HUMAN	AV725123 HTC Homo sapiens cDNA clone HTC8TA01 5'
6440	15637	25103	5.79	5.0E-20	W90525.1	EST_HUMAN	zh78d08.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:418191 3' similar to contains MER30.11 MER30 repetitive element ;
6440	15637	25104	5.79	5.0E-20	W90525.1	EST_HUMAN	zh78d08.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:418191 3' similar to contains MER30.11 MER30 repetitive element ;
1597	10811	19689	1.55	4.0E-20	AL163247.2	NT	Homo sapiens chromosome 21 segment HS21C047
6435	15632		6.61	4.0E-20	AI874352.1	EST_HUMAN	tz94g03.x1 NCL_CGAP_Ov35 Homo sapiens cDNA clone IMAGE:2293396 3'
2108	11307	20521	0.91	3.0E-20	U03868.1	NT	Human BXP21 gene
4192	13396	22496	1.29	3.0E-20	P23273	SWISSPROT	OLFACTORY RECEPTOR-LIKE PROTEIN 114
4627	13821	22910	0.81	3.0E-20	AA037616.1	EST_HUMAN	zk36b12.s1 Soares_pregnant_uterus_NbHPU Homo sapiens cDNA clone IMAGE:484895 3' similar to contains L1.13 L1 repetitive element ;
6753	15948		3.21	3.0E-20	D14547.1	NT	Human DNA, SINE repetitive element
7256	16476		2.1	3.0E-20	P11369	SWISSPROT	RETROVIRUS-RELATED POLYPROTEIN [CONTAINS: REVERSE TRANSCRIPTASE ; ENDONUCLEASE]
8459	17515	24021	17.57	3.0E-20	BE888422.1	EST_HUMAN	601514180F1.NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3915522 5'
840	10077		13.56	2.0E-20	AW303668.1	EST_HUMAN	xz24e10.x1 NCL_CGAP_U4 Homo sapiens cDNA clone IMAGE:2761068 3' similar to SW:RS5_MOUSE P97461 40S RIBOSOMAL PROTEIN S6 ;
1119	10343	19403	3.84	2.0E-20	AA516335.1	EST_HUMAN	ng69h09.s1 NCL_CGAP_Lip2 Homo sapiens cDNA clone IMAGE:940087 similar to TR:G1224066 G1224066 ORF2: FUNCTION UNKNOWN ;
1119	10343	19494	3.84	2.0E-20	AA516335.1	EST_HUMAN	ng69h09.s1 NCL_CGAP_Lip2 Homo sapiens cDNA clone IMAGE:940087 similar to TR:G1224066 G1224066 ORF2: FUNCTION UNKNOWN ;

Page 162 of 382  
Table 4  
Single Exon Probes Expressed in HELA Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2769	10077		10.39	2.0E-20	AW303888.1	EST_HUMAN	x24e10.x1 NCI_CGAP_U14 Homo sapiens cDNA clone IMAGE:2761098 3' similar to SW:R55_MOUSE
4865	14152	23243	4.5	2.0E-20	Q28983	SWISSPROT	P97461 40S RIBOSOMAL PROTEIN S5.
4865	14152	23244	4.5	2.0E-20	Q28983	SWISSPROT	ZONADHESIN PRECURSOR
5176	14354		2.31	2.0E-20	5174538	NT	Homo sapiens malate dehydrogenase 1, NAD (soluble) (MDH1) mRNA
6826	16020	25485	8.64	2.0E-20	D10083.1	NT	Homo sapiens RGH1 gene, retrovirus-like element
6826	16020	25486	8.64	2.0E-20	D10083.1	NT	Homo sapiens RGH1 gene, retrovirus-like element
8862	18088	23802	2.03	2.0E-20	H55371.1	EST_HUMAN	CHIR220310 Chromosome 22 exon Homo sapiens cDNA clone G22_391 5'
1881	11949	20393	4.81	1.0E-20	AA281061.1	EST_HUMAN	z11d08.r1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:712811 5' similar to contains MER19.12
4431	13631	22728	1.25	1.0E-20	BF115158.1	EST_HUMAN	MER19 repetitive element
6820	16014	25479	2.76	1.0E-20	11418491	NT	h184b06.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:3135155 3' similar to contains L1.12 L1
8086	17221	26757	3.06	1.0E-20	AF223391.1	NT	Homo sapiens Autosomal Highly Conserved Protein (AHCP), mRNA
8596	17603		2.02	1.0E-20	AA420453.1	EST_HUMAN	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-48, and partial cds, alternatively spliced
8306	17412		2.65	9.0E-21	AW898189.1	EST_HUMAN	nc60g08.r1 NCI_CGAP_P11 Homo sapiens cDNA clone IMAGE:7456894 similar to contains L1.13 L1
8071	17206	26739	4.47	8.0E-21	AA808411.1	EST_HUMAN	RC3-NN00688-090500-021-b03 NN00688 Homo sapiens cDNA
8473	17526		2.75	8.0E-21	O21330	SWISSPROT	cb71f08.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1336835 3'
2036	11237	20444	2.12	7.0E-21	P15800	SWISSPROT	ATP SYNTHASE A CHAIN (PROTEIN 6)
2036	11237	20445	2.12	7.0E-21	P15800	SWISSPROT	LAMININ BETA-2 CHAIN PRECURSOR (S-LAMININ) (LAMININ CHAIN B3)
4242	13445		6.6	7.0E-21	AA048502.1	EST_HUMAN	LAMININ BETA-2 CHAIN PRECURSOR (S-LAMININ) (LAMININ CHAIN B3)
6874	15869	25328	7.23	7.0E-21	D14718.1	NT	z687a06.r1 Soares_pregnant_uterus_NbHPU Homo sapiens cDNA clone IMAGE:487858 5'
							Human chromosomal protein HMG1 related gene
7286	16505	25996	3.34	7.0E-21	AA723404.1	EST_HUMAN	zq73d03.s1 Soares_fetal_heart_NbHH19W Homo sapiens cDNA clone IMAGE:398981 3' similar to
7817	17010	26523	2.14	7.0E-21	7706668	NT	gb:M14338 VITAMIN K-DEPENDENT PROTEIN S PRECURSOR (HUMAN);contains THR.13 OFR
4081	13291	22390	0.95	6.0E-21	BE408811.1	EST_HUMAN	Homo sapiens PTD013 protein (PTD013), mRNA
933	10166	19323	0.75	5.0E-21	5802031	NT	601304125F1 NIH_MGC 21 Homo sapiens cDNA clone IMAGE:3638310 5'
4357	13559	22854	3.53	5.0E-21	BE686839.1	EST_HUMAN	Homo sapiens protein tyrosine phosphatase, non-receptor type 21 (PTPN21), mRNA
4815	14004	23106	7.11	5.0E-21	4885474	NT	601849871F1 NIH_MGC 74 Homo sapiens cDNA clone IMAGE:3933880 5'
8389	17470		1.84	5.0E-21	AA393574.1	EST_HUMAN	Homo sapiens melanoma antigen, family C, 1 (MAGEC1), mRNA
							z172c04.r1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:727878 5'

Table 4

## Single Exon Probes Expressed in HELA Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1707	10919	20104	1.53	4.0E-21	AA970713.1	EST_HUMAN	008608.s1 NCL CGAP_Kid5 Homo sapiens cDNA clone IMAGE:1573084 3' similar to TR:Q16530 Q16530 PMS3 MRNA ; contains ORF:11 ORF repetitive element ;
6027	15235	24658	3.09	4.0E-21	AB019576.1	NT	Rattus norvegicus mRNA for rTIM, complete cds
1805	11014	20207	4.17	3.0E-21	AA218891.1	EST_HUMAN	2415d06.s1 Stratiotes fetal retina 937202 Homo sapiens cDNA clone IMAGE:629771 3'
2239	11434	20658	1.89	3.0E-21	AL163201.2	NT	Homo sapiens chromosome 21 segment HS21C001
3045	12281	21408	3.89	3.0E-21	AJ007873.1	NT	Homo sapiens LGMD2B gene
5744	14963		2.05	3.0E-21	BF184739.1	EST_HUMAN	601844465F1 NIH_MGC_54 Homo sapiens cDNA clone IMAGE:4064945 5'
6113	15207	24628	6.92	3.0E-21	BF361083.1	EST_HUMAN	RC1-OT0083-100800-019-g08 OT0083 Homo sapiens cDNA
6889	16167	25639	14.95	3.0E-21	AW687760.1	EST_HUMAN	CM1-NN0063-280400-203-h08 NN0063 Homo sapiens cDNA
8981	18262	23698	5.77	3.0E-21	AL163213.2	NT	Homo sapiens chromosome 21 segment HS21C013
148	9430		16.59	2.0E-21	BE163247.1	EST_HUMAN	QV3-HT0458-170200-090-g12 HT0458 Homo sapiens cDNA
943	10176	19328	0.75	2.0E-21	AB007857.2	NT	Homo sapiens mRNA for KIAA0397 protein, partial cds
943	10176	19330	0.75	2.0E-21	AB007857.2	NT	Homo sapiens mRNA for KIAA0397 protein, partial cds
1222	10440		2.48	2.0E-21	BE064410.1	EST_HUMAN	RC4-BT0311-141199-011-h08 BT0311 Homo sapiens cDNA
2602	11786	21006	2.67	2.0E-21	Q28983	SWISSPROT	ZONADHESIN PRECURSOR
2602	11786	21007	2.67	2.0E-21	Q28983	SWISSPROT	ZONADHESIN PRECURSOR
4888	14076		0.95	2.0E-21	AW151673.1	EST_HUMAN	x67610.x1 NCL CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2623146 3' similar to contains MER10.12
6583	15779	25239	2.42	2.0E-21	BE141785.1	EST_HUMAN	MER10 repetitive element ;
6726	15921	25380	4.85	2.0E-21	AU136779.1	EST_HUMAN	QV0-HT0103-091199-050-g11 HT0103 Homo sapiens cDNA
7625	16827		2.09	2.0E-21	BE350127.1	EST_HUMAN	AU136779 PLACE1 Homo sapiens cDNA clone IMAGE:1005052 5'
7666	17056	26576	2.39	2.0E-21	BE973826.1	EST_HUMAN	h109g01.x1 NCL CGAP_Kid13 Homo sapiens cDNA clone IMAGE:3146256 3' similar to contains MER28.b3
7866	17056	26577	2.39	2.0E-21	BE973826.1	EST_HUMAN	MER28 repetitive element ;
8706	17669		9.43	2.0E-21	AF176815.1	NT	601680636F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:3951008 5'
1262	10477	19639	1.38	1.0E-21	AA557657.1	EST_HUMAN	601680636F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:3951008 5'
1406	10819		2.37	1.0E-21	AF601264.1	EST_HUMAN	Homo sapiens putative 8-hydroxyguanine DNA glycosylase gene, complete cds
5969	15087		2.67	1.0E-21	AL079752.1	EST_HUMAN	h148c04.s1 NCL CGAP_P14 Homo sapiens cDNA clone IMAGE:1043718 similar to contains MER29.b2
6162	15345	24782	4.61	1.0E-21	AI223104.1	EST_HUMAN	MER29 repetitive element ;
9107	17927		1.29	1.0E-21	AF048133.1	NT	ar88d12.x1 Barstead colt1 HPLRB7 Homo sapiens cDNA clone IMAGE:2152343 3'
9281	18042	23826	2.86	1.0E-21	11435947	NT	DKFZp4340830_r1 434 (synonym: hbs3) Homo sapiens cDNA clone IMAGE:2152343 3'
							qg47405.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1838336 3' similar to gb:M64241 QIM PROTEIN (HUMAN);
							Homo sapiens chromosome Xp22 410-8
							Homo sapiens chromosome 12 open reading frame 3 (C12ORF3), mRNA



Page 164 of 382  
Table 4  
Single Exon Probes Expressed in HELA Cells

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4404	13604	22704	6.07	9.0E-22	AI702438.1	EST_HUMAN	tz94a03.x1 NCL_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2296204 3' similar to TR:Q15408 Q15408
7372	16588	26077	5.14	9.0E-22	AV761874.1	EST_HUMAN	NEUTRAL PROTEASE LARGE SUBUNIT.
8198	17330	26872	3.42	9.0E-22	AU140358.1	EST_HUMAN	AV761874 MDS Homo sapiens cDNA clone MDSCG05 5'
956	10189		3.77	8.0E-22	BE144748.1	EST_HUMAN	AU140358 PLACE2 Homo sapiens cDNA clone PLACE2000394 5'
671	9916	19045	7.04	7.0E-22	AL163246.2	NT	CM0-HT0179-281099-076-h05 HT0179 Homo sapiens cDNA
4288	13471	22564	2.26	7.0E-22	Q81838	SWISSPROT	Homo sapiens chromosome 21 segment HS21C048
5063	14243	23330	1	7.0E-22	AB008681.1	NT	ALPHA-2-MACROGLOBULIN PRECURSOR (ALPHA2M)
6728	15824	25383	5.03	7.0E-22	M78590.1	EST_HUMAN	Homo sapiens gene for activin receptor type IIB, complete cds
6963	16141	25610	3.07	7.0E-22	AF009650.1	NT	EST00738 Fetal brain, Stratagene (cat#838206) Homo sapiens cDNA clone HFBFCF07
6539	16735		2.7	6.0E-22	AW029123.1	EST_HUMAN	Homo sapiens T cell receptor beta locus, TCRBV7S3A2 to TCRBV12S2 region
5884	15101	24512	3.17	5.0E-22	AL163303.2	NT	wx05g07.x1 NCL_CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2542812 3'
7173	16350	25828	5.76	5.0E-22	U60822.1	NT	Homo sapiens chromosome 21 segment HS21C103
8942	17820		2.41	5.0E-22	BF476511.1	EST_HUMAN	Human dystrophin (DMD) gene, exons 7, 8 and 9, and partial cds
3615	12836		0.97	4.0E-22	AJ271735.1	NT	neaz7b06.x1 NCL_CGAP_P28 Homo sapiens cDNA clone IMAGE:3255888 3' similar to contains Alu repetitive element
7310	16528	26019	2.62	4.0E-22	BF218030.1	EST_HUMAN	Homo sapiens Xq pseudautosomal region; segment 1/2
9113	17831		1.68	4.0E-22	AL163208.2	NT	601882813F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4095434 5'
966	10199		1	3.0E-22	AI499678.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C009
2534	11722	20839	3.24	3.0E-22	AI859038.1	EST_HUMAN	hm14h10.x1 NCL_CGAP_Co14 Homo sapiens cDNA clone IMAGE:2156611 3' similar to gbl.19593 HIGH AFFINITY INTERLEUKIN-8 RECEPTOR B (HUMAN); contains L1.L1 repetitive element;
3653	12874		1.38	3.0E-22	D14718.1	NT	w68b04.x1 NCL_CGAP_Bm25 Homo sapiens cDNA clone IMAGE:2428839 3' similar to SW:RL21_HUMAN
4814	14003	23105	2.9	3.0E-22	AI090125.1	EST_HUMAN	P46778 80S RIBOSOMAL PROTEIN L21;
1923	11127		3.44	2.0E-22	N24942.1	EST_HUMAN	Human chromosomal protein HMG1 related gene
2489	11679	20806	1.17	2.0E-22	P24916	SWISSPROT	qb28c07.x1 Soares_pregnant_uterus_NbhPU Homo sapiens cDNA clone IMAGE:1697580 3' similar to contains MER12.12 MER12 repetitive element;
3398	12625	21756	3.95	2.0E-22	8394043	NT	YK73005.s1 Soares_melanocyte_2NbhHM Homo sapiens cDNA clone IMAGE:267369 3'
4211	13414	22509	1.48	2.0E-22	AW817794.1	EST_HUMAN	IMMEDIATE EARLY GENE 13 PROTEIN PRECURSOR
5742	14661	24361	3.5	2.0E-22	BF092116.1	EST_HUMAN	Homo sapiens protein kinase, AMP-activated, gamma 3 non-catalytic subunit (PRKAG3), mRNA
6893	16171	25643	2.51	2.0E-22	AJ276522.1	EST_HUMAN	PM1-ST0262-261199-001-c12 ST0262 Homo sapiens cDNA
8234	17363	26801	2.32	2.0E-22	AW418960.1	EST_HUMAN	RC0-TN0079-150900-025-h12 TN0079 Homo sapiens cDNA
8271	17919	23872	1.45	2.0E-22	AL163280.2	NT	q76h06.x1 Soares_NHMPu_S1 Homo sapiens cDNA clone IMAGE:1878289 3' similar to contains MER28.13 MER28 repetitive element;
							ha24f04.x1 NCL_CGAP_Kid12 Homo sapiens cDNA clone IMAGE:2874655 3'
							Homo sapiens chromosome 21 segment HS21C080

Page 165 of 382  
Table 4  
Single Exon Probes Expressed in HELA Cells

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1844	11052	20243	1.57	1.0E-22	AW85517.1	EST_HUMAN	PMA-SN0020-010400-009-H02 SN0020 Homo sapiens cDNA
2548	11734	20951	1.88	1.0E-22	U50871.1	NT	Human familial Alzheimer's disease (STM2) gene, complete cds
3388	12615	21748	1.63	1.0E-22	D14547.1	NT	Human DNA, SINE repetitive element
9182	17061		6.27	9.0E-23	AW802801.1	EST_HUMAN	IL2JUM0076-070400-061-F11 UM0078 Homo sapiens cDNA
3548	12769	21897	0.65	8.0E-23	AF198349.1	NT	Gallus gallus Dach2 protein (Dach2) mRNA, complete cds
3282	12513		2.13	7.0E-23	AV647248.1	EST_HUMAN	AV647248 GLC Homo sapiens cDNA clone GLCAW C07 3'
7609	16812	26308	4.68	7.0E-23	5031952	NT	Homo sapiens Nct56 (D. melanogaster)-like protein (NOT56L) mRNA
3412	12638		1.55	6.0E-23	AF198333.1	NT	Rattus norvegicus RIM1B (Rim1B) mRNA, complete cds
4254	13457	22549	1.11	6.0E-23	AL163249.2	NT	Homo sapiens chromosome 21 segment HS21C049
8412	17488	24008	2.85	6.0E-23	AF224689.1	NT	Homo sapiens mannosidase, beta A, lysosomal (MANBA) gene, and ubiquitin-conjugating enzyme E2D 3
8412	17486	24009	2.85	6.0E-23	AF224689.1	NT	(UBE2D3) genes, complete cds
8617	17614	23967	4.22	6.0E-23	AI208130.1	EST_HUMAN	Homo sapiens mannosidase, beta A, lysosomal (MANBA) gene, and ubiquitin-conjugating enzyme E2D 3
							q959c03.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1839460 3' similar to SW:MOV10_MOUSE P23249 PROTEIN MOV-10.;
5414	14642	23774	4.25	5.0E-23	U82871.2	NT	Homo sapiens chromosome Xq28 melanoma antigen family A2a (MAGEA2A), melanoma antigen family A12 (MAGEA12), melanoma antigen family A2b (MAGEA2B), melanoma antigen family A3 (MAGEA3), cathectin (CALT), NAD(P)H dehydrogenase-like protein (NSDHL), and LI+
5769	18064	24388	4.03	5.0E-23	AF179818.1	NT	Pongo pygmaeus olfactory receptor (PPY116) gene, partial cds
6267	18064	24388	3.15	5.0E-23	AF179818.1	NT	Pongo pygmaeus olfactory receptor (PPY116) gene, partial cds
6410	15607	25073	3.27	3.0E-23	AA130168.1	EST_HUMAN	z35g09.r1 Soares_pregnant_uterus_NbHPU Homo sapiens cDNA clone IMAGE:503968 5' similar to contains MER29.12 MER29 repetitive element.;
6839	16044	25508	4.41	3.0E-23	Z70694.1	NT	Human endogenous retroviral element HC2
6839	16044	25509	4.41	3.0E-23	Z70694.1	NT	Human endogenous retroviral element HC2
7172	16349		2.65	3.0E-23	AW897927.1	EST_HUMAN	RC3-NN0066-270400-011-H01 NN0066 Homo sapiens cDNA
672	9917	19048	6.01	2.0E-23	AJ289880.1	NT	Homo sapiens KIAA0851 gene (partial), X13 gene and LZTFL1 gene
1151	11944		2.89	2.0E-23	M55270.1	NT	Human matrix Gla protein (MGP) gene, complete cds
2748	11927	21141	1.08	2.0E-23	P22105	SWISSPROT	TENASCIN-X PRECURSOR (TN-X) (HEXABRACHION-LIKE)
2748	11927	21142	1.08	2.0E-23	P22105	SWISSPROT	TENASCIN-X PRECURSOR (TN-X) (HEXABRACHION-LIKE)
3350	12578		1.34	2.0E-23	AI201458.1	EST_HUMAN	q973f11.x1 NC1 CGAP_P128 Homo sapiens cDNA clone IMAGE:1843757 3' similar to TR:Q13537 Q13537
3697	12817		4.49	2.0E-23	BE165980.1	EST_HUMAN	MER37 TRANSPOSABLE ELEMENT, COMPLETE CONSENSUS SEQUENCE.;
3954	13189	22283	3.05	2.0E-23	H59931.1	EST_HUMAN	MR3-HT0487-150200-113-g01 HT0487 Homo sapiens cDNA
3954	13189	22284	3.05	2.0E-23	H59931.1	EST_HUMAN	yt16a02.r1 Soares fetal liver spleen TNFSL Homo sapiens cDNA clone IMAGE:205418 5'

Page 166 of 382  
Table 4  
Single Exon Probes Expressed in HELA Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6418	15615		8.05	2.0E-23	AF280107.1	NT	Homo sapiens cytochrome P450 polypeptide 43 (CYP3A43) gene, partial cds; cytochrome P450 polypeptide 4 (CYP3A4) and cytochrome P450 polypeptide 7 (CYP3A7) genes, complete cds; and cytochrome P450 polypeptide 5 (CYP3A5) gene, partial cds
8395	17474		4.45	2.0E-23	M32858.1	NT	Human alcohol dehydrogenase gamma subunit (ADH3) gene, exon 1
8951	17825		1.87	2.0E-23	AF009680.1	NT	Homo sapiens T cell receptor beta locus, TCRBV7S3A2 to TCRBV12S2 region
9079	18295		1.78	2.0E-23	AU133931.1	EST_HUMAN	AU133931 OVARC1 Homo sapiens cDNA clone OVARC1000946 5'
4527	13723	22819	1.69	1.0E-23	AL163252.2	NT	Homo sapiens chromosome 21 segment HS21C052
4777	13968		4.93	1.0E-23	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C010
5973	15187		2.6	1.0E-23	BE378471.1	EST_HUMAN	601238455F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3608653 5'
6582	15778	25238	2.4	1.0E-23	AA448097.1	EST_HUMAN	zw8206.f1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:782698 5' similar to contains PTR5.12 PTR5 repetitive element
559	9809		1.82	9.0E-24	AA663213.1	EST_HUMAN	ab75a08.s1 Stratiogene fetal retina 937202 Homo sapiens cDNA clone IMAGE:852758 3' similar to TRE19822 E19822 CA PROTEIN
4649	13843	22833	1.06	8.0E-24	P23269	SWISSPROT	OLFACTORY RECEPTOR-LIKE PROTEIN I3
4649	13843	22834	1.06	8.0E-24	P23269	SWISSPROT	OLFACTORY RECEPTOR-LIKE PROTEIN I3
3853	13089		1.26	7.0E-24	AW837954.1	EST_HUMAN	QV0-DT0047-170200-122-a08 DT0047 Homo sapiens cDNA
7234	18455		2.37	7.0E-24	AW303317.1	EST_HUMAN	xy17603.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2813405 3' similar to contains Alu repetitive element; contains MER19.12 MER19 repetitive element
713	9655		2.33	6.0E-24	AB001421.1	NT	Macaca fuscata mRNA for Testis-Specific Protein Y (TSPY), complete cds
848	10085	19244	16.07	8.0E-24	AL163249.2	NT	Homo sapiens chromosome 21 segment HS21C049
3847	13163	22278	8.91	5.0E-24	AJ226043.1	NT	Homo sapiens 959 kb contig between AML1 and CBR1 on chromosome 21q22, segment 3/3
5828	14852	24235	3.4	4.0E-24	AA594178.1	EST_HUMAN	nm31h05.e1 NCI_CGAP_Gast1 Homo sapiens cDNA clone IMAGE:1085529 3' similar to SW.POL_MLVRK P31795 POL POLYPROTEIN
7735	16832	26440	2.1	4.0E-24	BE544822.1	EST_HUMAN	601078812F1 NIH_MGC_12 Homo sapiens cDNA clone IMAGE:3464498 5'
8794	17721	23962	2.81	4.0E-24	AB029018.1	NT	Homo sapiens mRNA for KIAA1083 protein, partial cds
9053	17924	23875	1.67	4.0E-24	11418318	NT	Homo sapiens G-2 and S-phase expressed 1 (GTSE1), mRNA
6901	16058	25526	2.35	3.0E-24	AL163252.2	NT	Homo sapiens chromosome 21 segment HS21C052
8876	17773	23942	2.46	3.0E-24	BF127762.1	EST_HUMAN	601810449F1 NIH_MGC_46 Homo sapiens cDNA clone IMAGE:4053396 5'
2315	11509	20730	2.19	2.0E-24	AA167539.1	EST_HUMAN	zp111608.r1 Stratiogene fetal retina 937202 Homo sapiens cDNA clone IMAGE:609161 5'
3781	12959		0.88	2.0E-24	AW888189.1	EST_HUMAN	RC3-NH0068-090500-021-b03 NH0068 Homo sapiens cDNA
8714	18339		9.69	2.0E-24	M28877.1	NT	Human O family dispersed repeat element
1671	10884	20068	2.13	1.0E-24	7706340	NT	Homo sapiens CGI-127 protein (LOC51846), mRNA
2633	11816		1.53	1.0E-24	AW820194.1	EST_HUMAN	QV0-ST0294-100400-185-c10 ST0294 Homo sapiens cDNA
2985	12222	21355	1.19	1.0E-24	D86423.1	NT	Mus musculus mRNA for HGT keratin, partial cds

Table 4

## Single Exon Probes Expressed in HELA Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4256	13459		2.16	1.0E-24	AF143313.1	NT	Homo sapiens PTEN (PTEN) gene, exon 2
6312	15493	24939	3.94	1.0E-24	AL163303.2	NT	Homo sapiens chromosome 21 segment HS21C103
6439	15636	25102	3.19	1.0E-24	AW901184.1	EST_HUMAN	Clon-NN1010-130300-281-c07 NN1010 Homo sapiens cDNA
9288	18048		1.24	1.0E-24	BE877411.1	EST_HUMAN	7d83h03.x1 Lupski_dorsal_root_ganglion Homo sapiens cDNA clone IMAGE:3279605 3' similar to contains MER10.13 MER10 repetitive element ;
8194	17326	26668	1.83	9.0E-25	7708707	NT	Homo sapiens putative secreted protein (SIG11), mRNA
5020	14207	23262	3.45	7.0E-25	AA483944.1	EST_HUMAN	ne92e10.s1 NCL_CGAP_Kid1 Homo sapiens cDNA clone IMAGE:911754 similar to contains MER1.b2 MER1 repetitive element ;
6535	15731	25195	4.4	7.0E-25	AA488646.1	EST_HUMAN	ne08a09.s1 NCL_CGAP_Co3 Homo sapiens cDNA clone IMAGE:880408 3' similar to contains THR.b2 THR repetitive element ;
8195	17327	26889	10.9	7.0E-25	AA583540.1	EST_HUMAN	nf25h06.s1 NCL_CGAP_P11 Homo sapiens cDNA clone IMAGE:914843 similar to SW.R14A_YEAST P36105 PROBABLE 60S RIBOSOMAL PROTEIN L14EA. ;
6085	14531		4.79	6.0E-25	W87623.1	EST_HUMAN	zh85f07.r1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:416889 5'
6384	15564	25021	10.69	6.0E-25	7305360	NT	Mus musculus obaglin (Obag), mRNA
7863	17053	26574	4.51	5.0E-25	AW970107.1	EST_HUMAN	EST391217 MAGE resequences, MAGP Homo sapiens cDNA
1448	10661	19836	3.01	4.0E-25	T98107.1	EST_HUMAN	ye58h04.r1 Soares_fetal_liver_spleen_1NFLS_Homo sapiens cDNA clone IMAGE:121783 5'
3380	12607		2.94	4.0E-25	AW887871.1	EST_HUMAN	PM3-OT0093-280200-001-g07 OT0093 Homo sapiens cDNA
4307	13508		3.15	4.0E-25	BE170957.1	EST_HUMAN	QV3-HT0543-140400-149-e11 HT0543 Homo sapiens cDNA
3292	12523	21654	3.43	3.0E-25	8923321	NT	Homo sapiens hypothetical protein FLJ20344 (FLJ20344), mRNA
3292	12523	21655	3.43	3.0E-25	8923321	NT	Homo sapiens hypothetical protein FLJ20344 (FLJ20344), mRNA
4616	14104	23197	0.71	3.0E-25	P28622	SWISSPROT	KALLISTATIN PRECURSOR (KALLIKREIN INHIBITOR) (PROTEASE INHIBITOR 4)
5255	14428	23504	0.97	3.0E-25	H52187.1	EST_HUMAN	ye60b11.r1 Soares_fetal_liver_spleen_1NFLS_Homo sapiens cDNA clone IMAGE:209661 5' similar to contains MER8 repetitive element ;
6577	15773	25234	4.44	3.0E-25	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C010
7601	16804	26299	2.11	3.0E-25	AA579013.1	EST_HUMAN	nf30h10.s1 NCL_CGAP_P11 Homo sapiens cDNA clone IMAGE:915331 similar to contains L.11 L1 repetitive element ;
1355	10570	19735	3.88	2.0E-25	5032158	NT	Homo sapiens transducin (beta)-like 1 (TBL1) mRNA
2274	11469	20690	8.59	2.0E-25	BE88016.1	EST_HUMAN	601511530F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3913087 5'
2784	11696	20914	6.4	2.0E-25	P17008	SWISSPROT	40S RIBOSOMAL PROTEIN S16
4172	13376	22475	1.92	2.0E-25	P17008	SWISSPROT	40S RIBOSOMAL PROTEIN S16
4172	13376	22476	1.92	2.0E-25	P17008	SWISSPROT	40S RIBOSOMAL PROTEIN S16
7006	16184	25656	3.35	2.0E-25	AL449573.1	EST_HUMAN	AL449573 Homo sapiens Testis (Stavrides GS) Homo sapiens cDNA
369	9635	18768	1.02	1.0E-25	AL040228.1	EST_HUMAN	DKFZp434h0313_r1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434h0313 5'
1255	10471		3.27	1.0E-25	9835487	NT	Human endogenous retrovirus, complete genome

Page 168 of 382  
Table 4  
Single Exon Probes Expressed in HELA Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2398	11591	20809	2.1	1.0E-25	Q06055	SWISSPROT	ATP SYNTHASE LIPID-BINDING PROTEIN P2 PRECURSOR (ATPASE PROTEIN 9) (SUBUNIT C)
4875	14063	23158	3.1	1.0E-25	BE182737.1	EST_HUMAN	PM1-HT0454-080100-002-H09 HT0454 Homo sapiens cDNA
5996	18070	24709	2.98	1.0E-25	AA582690.1	EST_HUMAN	nm54h11.s1 NCI_CGAP_Kid6 Homo sapiens cDNA clone IMAGE:1087749 3'
6428	15828	25091	5.51	1.0E-25	AA709079.1	EST_HUMAN	z95g04.s1 Soares_fetal_heart_NbHH19W Homo sapiens cDNA clone IMAGE:384822 3' similar to contains PTR5.13 PTR5 repetitive element 1
7541	16748	26240	3.92	1.0E-25	U93163.1	NT	Homo sapiens MAGE-B2 (MAGE-B2), MAGE-B3 (MAGE-B3), MAGE-B4 (MAGE-B4), and MAGE-B1 (MAGE-B1) genes, complete cds
8408	17484	26597	1.54	1.0E-25	D14547.1	NT	Human DNA, SINE repetitive element
8409	17484	26598	1.54	1.0E-25	D14547.1	NT	Human DNA, SINE repetitive element
9234	18008		1.31	1.0E-25	X51755.1	NT	Human lambda-immunoglobulin constant region complex (germline)
2445	11638	20857	1.4	9.0E-26	AL183218.2	NT	Homo sapiens chromosome 21 segment HS21C018
8272	18107		2.48	9.0E-26	AL183285.2	NT	Homo sapiens chromosome 21 segment HS21C085
5532	14756		1.92	8.0E-26	D14547.1	NT	Human DNA, SINE repetitive element
1556	10770	19942	2.5	7.0E-26	AF003528.1	NT	Homo sapiens X-linked anhidrotic ectodermal dysplasia protein gene (EDA), exon 2 and flanking repeat regions
3958	13173	22288	1.42	7.0E-26	X89211.1	NT	H. sapiens DNA for endogenous retroviral like element
4141	13347	22446	2.19	7.0E-26	AW340153.1	EST_HUMAN	hd02a12.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2808368 3'
8172	17304		9.62	7.0E-26	AA115895.1	EST_HUMAN	zn30d08.r1 Stratagene neuroepithelium NT2RAMI 937234 Homo sapiens cDNA clone IMAGE:548943 5' similar to gb:M14338 VITAMIN K-DEPENDENT PROTEIN S PRECURSOR (HUMAN);
8999	17659		1.79	7.0E-26	AW954559.1	EST_HUMAN	EST366628 MAGE resequences, MAGC Homo sapiens cDNA
2192	11389	20812	2.57	6.0E-26	AF028308.1	NT	Homo sapiens chromosome 9 duplication of the T cell receptor beta locus and trypsinogen gene families
3320	12549	21683	1.57	6.0E-26	AA206131.1	EST_HUMAN	zq52h04.r1 Stratagene neuroepithelium (#937231) Homo sapiens cDNA clone IMAGE:945271 5'
8180	17312	26854	6.07	6.0E-26	AL183210.2	NT	Homo sapiens chromosome 21 segment HS21C010
1185	10408	19560	3.11	5.0E-26	AI708235.1	EST_HUMAN	as38h08.x1 Barstead aorta HPLRB6 Homo sapiens cDNA clone IMAGE:2319519 3' similar to WP:F49C12.11 CE03371
1185	10406	19561	3.11	5.0E-26	AI708235.1	EST_HUMAN	as38h08.x1 Barstead aorta HPLRB6 Homo sapiens cDNA clone IMAGE:2319519 3' similar to WP:F49C12.11 CE03371
6883	18074		3.97	4.0E-26	7657670	NT	Homo sapiens upstream binding transcription factor, RNA polymerase I (UBTF), mRNA
7253	18473	25065	4.16	4.0E-26	BE266187.1	EST_HUMAN	601191345F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3535210 5'
7869	17059	26580	1.85	4.0E-26	AL183246.2	NT	Homo sapiens chromosome 21 segment HS21C048
1730	10942	20124	1.37	3.0E-26	D14547.1	NT	Human DNA, SINE repetitive element
1972	11176	20382	1.31	3.0E-26	AL045865.2	EST_HUMAN	DKFZp4341066_r1 434 (synonym: hies3) Homo sapiens cDNA clone DKFZp4341066 5'

Table 4

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2000	11203		3.1	3.0E-26	AA115895.1	EST_HUMAN	zr30d08.r1 Stratagene neuroepithelium NT2RAMI 937234 Homo sapiens cDNA clone IMAGE:548943 5' similar to gb:M14338 VITAMIN K-DEPENDENT PROTEIN S PRECURSOR (HUMAN);
3760	12979	22094	1.44	3.0E-26	AA152484.1	EST_HUMAN	zr30f10.r1 Stratagene colon (#937204) Homo sapiens cDNA clone IMAGE:588427 5' similar to TR:G695374
3760	12979	22095	1.44	3.0E-26	AA152484.1	EST_HUMAN	G695374 THYROID RECEPTOR INTERACTOR ;
6048	15218	24636	9.41	3.0E-26	BF245458.1	EST_HUMAN	zr30f10.r1 Stratagene colon (#937204) Homo sapiens cDNA clone IMAGE:588427 5' similar to TR:G695374
7313	16531		1.99	3.0E-26	AF036405.1	NT	zr30f10.r1 Stratagene colon (#937204) Homo sapiens cDNA clone IMAGE:588427 5' similar to TR:G695374
8102	17236	26772	2.54	3.0E-26	AW875651.1	EST_HUMAN	G695374 THYROID RECEPTOR INTERACTOR ;
8102	17236	26773	2.54	3.0E-26	AW875651.1	EST_HUMAN	zr30f10.r1 Stratagene colon (#937204) Homo sapiens cDNA clone IMAGE:588427 5' similar to TR:G695374
8128	17263	26807	10.41	3.0E-26	AA583173.1	EST_HUMAN	G695374 THYROID RECEPTOR INTERACTOR ;
9183	17974		1.58	3.0E-26	AW073434.1	EST_HUMAN	zr30f10.r1 Stratagene colon (#937204) Homo sapiens cDNA clone IMAGE:588427 5' similar to TR:G695374
688	9931	19062	6.9	2.0E-26	AL163282.2	NT	zr30f10.r1 Stratagene colon (#937204) Homo sapiens cDNA clone IMAGE:588427 5' similar to TR:G695374
1834	11042		3.51	2.0E-26	AL038099.2	EST_HUMAN	G695374 THYROID RECEPTOR INTERACTOR ;
3197	12432	21568	4.94	2.0E-26	X86894.1	NT	zr30f10.r1 Stratagene colon (#937204) Homo sapiens cDNA clone IMAGE:588427 5' similar to TR:G695374
7338	16554		3.33	2.0E-26	D87875.1	NT	zr30f10.r1 Stratagene colon (#937204) Homo sapiens cDNA clone IMAGE:588427 5' similar to TR:G695374
7771	16966	26479	4.24	2.0E-26	AB01412.1	EST_HUMAN	G695374 THYROID RECEPTOR INTERACTOR ;
7956	17095		2.02	2.0E-26	AF055063.1	NT	zr30f10.r1 Stratagene colon (#937204) Homo sapiens cDNA clone IMAGE:588427 5' similar to TR:G695374
8522	17553		2.64	2.0E-26	AB037859.1	NT	G695374 THYROID RECEPTOR INTERACTOR ;
8733	18284	23683	1.44	2.0E-26	BE170371.1	EST_HUMAN	zr30f10.r1 Stratagene colon (#937204) Homo sapiens cDNA clone IMAGE:588427 5' similar to TR:G695374
134	9417	18551	11.48	1.0E-26	BE170371.1	EST_HUMAN	G695374 THYROID RECEPTOR INTERACTOR ;
2014	11218	20426	1.53	1.0E-26	AL039363.2	EST_HUMAN	zr30f10.r1 Stratagene colon (#937204) Homo sapiens cDNA clone IMAGE:588427 5' similar to TR:G695374
2528	11717	20834	1.71	1.0E-26	BE814995.1	EST_HUMAN	G695374 THYROID RECEPTOR INTERACTOR ;
2647	11830		22.1	1.0E-26	AF261085.1	NT	zr30f10.r1 Stratagene colon (#937204) Homo sapiens cDNA clone IMAGE:588427 5' similar to TR:G695374
6014	15264		2.88	1.0E-26	BE165980.1	EST_HUMAN	G695374 THYROID RECEPTOR INTERACTOR ;
7469	16677		3.11	1.0E-26	AL038487.1	EST_HUMAN	zr30f10.r1 Stratagene colon (#937204) Homo sapiens cDNA clone IMAGE:588427 5' similar to TR:G695374
8780	18357		2.07	1.0E-26	H55093.1	EST_HUMAN	G695374 THYROID RECEPTOR INTERACTOR ;
6855	16107		3.98	9.0E-27	U93163.1	NT	zr30f10.r1 Stratagene colon (#937204) Homo sapiens cDNA clone IMAGE:588427 5' similar to TR:G695374
8275	17396		5.28	9.0E-27	BF445556.1	EST_HUMAN	G695374 THYROID RECEPTOR INTERACTOR ;

Page 170 of 382  
Table 4  
Single Exon Probes Expressed in HELA Cells

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10	8308	18408	2.21	8.0E-27	AI831462.1	EST_HUMAN	wj48c04.x1 NCL_CGAP_Lu18 Homo sapiens cDNA clone IMAGE:2408150 3' similar to contains THR.b2 THR repetitive element ;
584	9814		5.13	8.0E-27	AL163227.2	NT	Homo sapiens chromosome 21 segment HS21C027
1420	10633	19801	56.1	8.0E-27	AW162737.1	EST_HUMAN	au87h08.x1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2783295 3' similar to gb:K00558 TUBULIN ALPHA-1 CHAIN (HUMAN);
1420	10633	19802	56.1	8.0E-27	AW162737.1	EST_HUMAN	au87h08.x1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2783295 3' similar to gb:K00558 TUBULIN ALPHA-1 CHAIN (HUMAN);
2133	11331	20551	1.68	8.0E-27	AW864776.1	EST_HUMAN	PM2-SN0018-220300-002-007 SN0018 Homo sapiens cDNA
3148	12383	21518	3.14	8.0E-27	P12236	SWISSPROT	ADP,ATP CARRIER PROTEIN, LIVER ISOFORM T2 (ADP/ATP TRANSLOCASE 3) (ADENINE NUCLEOTIDE TRANSLOCATOR 3) (ANT 3)
3327	12556	21693	0.68	8.0E-27	AF181897.1	NT	Homo sapiens WRN (WRN) gene, complete cds
6077	14523		6.24	8.0E-27	BE929560.1	EST_HUMAN	MR4-BT0398-250800-204-005 BT0398 Homo sapiens cDNA
6104	15198	24618	2.63	8.0E-27	N84970.1	EST_HUMAN	J1751F Human fetal heart, Lambda ZAP Express Homo sapiens cDNA clone J1751 5' similar to REPETITIVE ELEMENT L1
690	9833		1.34	7.0E-27	Z70694.1	NT	Human endogenous retroviral element HC2
5122	14301		2.35	7.0E-27	AW628172.1	EST_HUMAN	h151h12.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2975879 3' similar to TR:O76040 O76040 ORF2: FUNCTION UNKNOWN. ;
7335	18551		4.9	7.0E-27	AJ271735.1	NT	Homo sapiens Xq pseudautosomal region; segment 1/2
8926	17809		1.82	7.0E-27	AV723365.1	EST_HUMAN	AV723365 HTB Homo sapiens cDNA clone HTBAHE02 5'
7314	16532	26021	25.43	6.0E-27	M26897.1	NT	Human nuclear protein (B23) mRNA, complete cds
7145	16322	25803	3.44	5.0E-27	BF66614.1	EST_HUMAN	602121491F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4278527 5'
7145	16322	25804	3.44	5.0E-27	BF66614.1	EST_HUMAN	602121491F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4278527 5'
8130	17284	26808	2.76	4.0E-27	X89211.1	NT	H. sapiens DNA for endogenous retroviral like element
2008	11211	20421	7.24	3.0E-27	X60658.1	NT	R. rattus RYA3 mRNA for a potential ligand-binding protein
4257	13480	22552	1.33	3.0E-27	BE071924.1	EST_HUMAN	PM0-BT0527-090100-001-011 BT0527 Homo sapiens cDNA
5392	14592	23689	6.3	3.0E-27	AA077705.1	EST_HUMAN	7B44C08 Chromosome 7 Fetal Brain cDNA Library Homo sapiens cDNA clone 7B44C08
6856	16108	25574	3.1	3.0E-27	BF033327.1	EST_HUMAN	601458531F1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3862086 5'
9287	18045		1.79	3.0E-27	AW502868.1	EST_HUMAN	U1-HF-BN0-akq-e-12-0-U1.r NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3077879 5'
43	9339	18446	20.19	2.0E-27	AF054187.1	NT	Homo sapiens alpha NAC mRNA, complete cds
1860	11087		35.81	2.0E-27	AA565345.1	EST_HUMAN	nk01b10.s1 NCL_CGAP_Pt11 Homo sapiens cDNA clone IMAGE:1000699 similar to gb:M17888 50S ACIDIC RIBOSOMAL PROTEIN P1 (HUMAN);
3073	12309		12.63	2.0E-27	AW628172.1	EST_HUMAN	h151h12.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2975879 3' similar to TR:O76040 O76040 ORF2: FUNCTION UNKNOWN. ;

Page 171 of 382  
Table 4  
Single Exon Probes Expressed in HELA Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3190	12425	21558	1.36	2.0E-27	AF111187.2	NT	Homo sapiens jun dimerization protein gene, partial cds; cfos gene, complete cds; and unknown gene
3190	12425	21558	1.36	2.0E-27	AF111187.2	NT	Homo sapiens jun dimerization protein gene, partial cds; cfos gene, complete cds; and unknown gene
6844	16033		2.26	2.0E-27	AA551527.1	EST_HUMAN	h08h05.s1 NCI_CGAP_Thy1 Homo sapiens cDNA clone IMAGE:943737 similar to contains L1 L3 L1 repetitive element ;
7528	16733	26223	3.41	2.0E-27	AU121685.1	EST_HUMAN	AU121685 MAMMA1 Homo sapiens cDNA clone MAMMA1000748 5'
8021	11087		18.89	2.0E-27	AA565345.1	EST_HUMAN	h01b10.s1 NCI_CGAP_Pt11 Homo sapiens cDNA clone IMAGE:1000689 similar to gb:M17886 60S
442	9698		2.08	1.0E-27	AL163246.2	NT	ACIDIC RIBOSOMAL PROTEIN P1 (HUMAN); Homo sapiens chromosome 21 segment HS21CD46
1004	10235	19388	1.34	1.0E-27	AB026898.1	NT	Homo sapiens DNA, DLEC1 to ORCTL4 gene region, section 1/2 (DLEC1, ORCTL3, ORCTL4 genes, complete cds)
4057	13267		1.07	1.0E-27	BE350127.1	EST_HUMAN	h09g01.x1 NCI_CGAP_Kid13 Homo sapiens cDNA clone IMAGE:3146256 3' similar to contains MER29.b3
5900	15117	24529	5.8	1.0E-27	6005855	NT	MER29 repetitive element ; Homo sapiens Retine-derived POU-domain factor-1 (RPF-1), mRNA
6026	15234	24656	1.89	1.0E-27	F30158.1	EST_HUMAN	HSPD20461 HM3 Homo sapiens cDNA clone s4000095C10
6026	15234	24657	1.89	1.0E-27	F30158.1	EST_HUMAN	HSPD20461 HM3 Homo sapiens cDNA clone s4000095C10
6760	15955		2.91	1.0E-27	BE079780.1	EST_HUMAN	RC6-BT0627-140200-011-E06 BT0627 Homo sapiens cDNA
6989	16177	25848	3.53	1.0E-27	D87449.1	NT	Human mRNA for KIAA0260 gene, partial cds
8196	17328	26870	3.61	1.0E-27	AF111093.1	NT	Bos taurus latrophilin 3 splice variant bbah mRNA, complete cds
139	9420		1.89	9.0E-28	BE348399.1	EST_HUMAN	hw17e11.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3183188 3' similar to TR:Q07314 Q07314
316	9587	18718	2.2	9.0E-28	AU126260.1	EST_HUMAN	SECRETED NEUREXIN III-ALPHA-C PRECURSOR, [3] TR:Q07280 TR:Q07313 ;
8355	17448		6.41	9.0E-28	BF377859.1	EST_HUMAN	AU126260 NT2RP1 Homo sapiens cDNA clone NT2RP1000443 5'
8699	18204		2.25	8.0E-28	AW157571.1	EST_HUMAN	OM2-TN0140-070900-372-g01 TN0140 Homo sapiens cDNA
1189	10410	19564	20.71	7.0E-28	AU142750.1	EST_HUMAN	au83h08.x1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2782811 3' similar to
7742	16938	26447	10.67	7.0E-28	11417866	NT	TR:O60302 O60302 KIAA0555 PROTEIN, contains element MER22 repetitive element ; AU142750 Y78AA1 Homo sapiens cDNA clone Y78AA1000824 5'
8314	17418		2.77	7.0E-28	AV735348.1	EST_HUMAN	Homo sapiens gamma-glutamyltransferase-like activity 1 (GGT1A1), mRNA
8971	17841		3.8	6.0E-28	AA504582.1	EST_HUMAN	AV735348 CB Homo sapiens cDNA clone CBFAKA12 5'
323	9594		2.63	5.0E-28	A1921003.1	EST_HUMAN	aa60a03.r1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:825340 5' similar to contains Alu
3985	13199	22307	1.47	5.0E-28	R79762.1	EST_HUMAN	repetitive element; contains element PTR5 repetitive element ; w018c07.x1 NCI_CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2455692 3' similar to contains THR.b1
							THR repetitive element ;
							y88f10.r1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:146443 5'



Table 4

## Single Exon Probes Expressed in HELA Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2588	11774	20994	2.43	4.0E-28	AW195068.1	EST_HUMAN	xt33c09.x1 NCL_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2695504 3' similar to SW:GG95_HUMAN
2803	12171	21304	1.12	4.0E-28	4505316	NT	Q08379 GOLGIN-85 ;
3072	12308	21430	4.2	4.0E-28	BE409100.1	EST_HUMAN	Homo sapiens myosin phosphatase, target subunit 1 (MYPT1), mRNA
5271	14444	23515	12.18	4.0E-28	AF219927.1	NT	601300703F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3635305 5'
6222	15403	24844	2.04	4.0E-28	AI188941.1	EST_HUMAN	Homo sapiens diacylglycerol kinase iso1a (DGK1) gene, exon 23
7441	16849		4.32	4.0E-28	AF028308.1	NT	qf69f10.x1 Soares, testis, NIH Homo sapiens cDNA clone IMAGE:1755019 3' similar to gb:M19503 LINE-1
7578	16781		24.75	4.0E-28	AB038241.1	NT	REVERSE TRANSCRIPTASE HOMOLOG (HUMAN);
7594	15403	24844	3.74	4.0E-28	AI188941.1	EST_HUMAN	Homo sapiens chromosome 9 duplication of the T cell receptor beta locus and tyrosinogen gene families
1290	10505		1.95	3.0E-28	AF155382.1	NT	Felis catus GAPDH mRNA for glyceraldehyde-3-phosphate dehydrogenase, complete cds
6727	15922	25381	2.47	3.0E-28	BF354030.1	EST_HUMAN	qf69f10.x1 Soares, testis, NIH Homo sapiens cDNA clone IMAGE:1755019 3' similar to gb:M19503 LINE-1
7609	16714	26202	1.85	3.0E-28	U53588.1	NT	REVERSE TRANSCRIPTASE HOMOLOG (HUMAN);
8776	17708		2.07	3.0E-28	AI831991.1	EST_HUMAN	Homo sapiens metalloproteinase-like, disintegrin-like, cysteine-rich protein 2 epsilon (ADAM22) mRNA, complete cds
8970	17840	23912	1.53	3.0E-28	11430460	NT	MR3-HT0713-280500-013-f09 HT0713 Homo sapiens cDNA
8970	17840	23913	1.53	3.0E-28	11430460	NT	Homo sapiens MHC class 1 region
88	9381	18511	7.51	2.0E-28	BE062167.1	EST_HUMAN	wj98f07.x1 NCL_CGAP_Lym12 Homo sapiens cDNA clone IMAGE:2410885 3' similar to contains Alu repetitive element; contains element HGR repetitive element ;
1173	10394	19546	10.56	2.0E-28	Y11107.3	NT	Homo sapiens low density lipoprotein-related protein 2 (LRP2), mRNA
2439	11630	20851	1.92	2.0E-28	AI348634.1	EST_HUMAN	Homo sapiens low density lipoprotein-related protein 2 (LRP2), mRNA
5802	15019		6.05	2.0E-28	BF212805.1	EST_HUMAN	RC1-BT0254-220300-019-c05 BT0254 Homo sapiens cDNA
6953	16131		4.38	2.0E-28	AW972305.1	EST_HUMAN	Homo sapiens ITGB4 gene for integrin beta 4 subunit, exons 3-41
8137	17270	26815	2.58	2.0E-28	AF224689.1	NT	q035b06.x1 NCL_CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1810483 3' similar to contains L1 b2 L1 repetitive element ;
8756	17697		1.37	2.0E-28	H06376.1	EST_HUMAN	601814196F1 NIH_MGC_54 Homo sapiens cDNA clone IMAGE:4048751 5'
1472	10885	19860	2.38	1.0E-28	D38044.1	EST_HUMAN	EST384394 MAGE resequences, MAGL Homo sapiens cDNA
2188	11383	20607	5.07	1.0E-28	BF333236.1	EST_HUMAN	Homo sapiens mannosidase, beta A, lysosomal (MANBA) gene, and ubiquitin-conjugating enzyme E2D 3 (UBE2D3) genes, complete cds
4586	13760		2.28	1.0E-28	U09410.1	NT	yf76c09.r1 Soares infant brain 1N1B Homo sapiens cDNA clone IMAGE:44300 5'
6414	15811		6.26	1.0E-28	11428895	NT	Human gene for Ah-receptor, exon 7-9
6489	15686		3.16	1.0E-28	8922793	NT	Human zinc finger protein ZNF131 mRNA, partial cds
							Homo sapiens similar to ribosomal protein L12 (H. sapiens) (LOC63091), mRNA
							Homo sapiens hypothetical protein FLJ10968 (FLJ10968), mRNA

Table 4

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6848	16037	25501	4.97	1.0E-28	AA308744.1	EST_HUMAN	EST179815 HCC cell line (metastasis to liver in mouse)    Homo sapiens cDNA 5' end similar to similar to retroviral LTR
7030	16207	25684	3.28	1.0E-28	4758431	NT	Homo sapiens gamma-glutamyltransferase-like activity 1 (GGTLA1), mRNA
7030	16207	25685	3.28	1.0E-28	4758431	NT	Homo sapiens gamma-glutamyltransferase-like activity 1 (GGTLA1), mRNA
8319	17422		3.88	1.0E-28	AA054182.1	EST_HUMAN	zf51cd01.r1 Soares retina N2b4HR Homo sapiens cDNA clone IMAGE:380448 5'
9106	18091		1.83	1.0E-28	AL163247.2	NT	Homo sapiens chromosome 21 segment HS21C047
9211	18313	23593	3.18	9.0E-29	AW663987.1	EST_HUMAN	h176g06.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2978286 3'
8873	17770		3.8	8.0E-29	Q00130	SWISSPROT	HYPOTHETICAL GENE 50 PROTEIN
1582	10795	18972	1.91	7.0E-29	AW968447.1	EST_HUMAN	EST378521 MAG2 resequences, MAG1 Homo sapiens cDNA
9264	18030		6.86	7.0E-29	AJ132352.1	NT	Rattus norvegicus mRNA for 45 kDa secretory protein, partial
602	9849	18968	15.71	6.0E-29	A1936748.1	EST_HUMAN	wp69b01.x1 NCI_CGAP_Bm25 Homo sapiens cDNA clone IMAGE:2466985 3' similar to TR:O15475
8628	17621		5.29	6.0E-29	BE940436.1	EST_HUMAN	O15475 UNNAMED HERV-H PROTEIN ; contains LTR7.b1 LTR7 repetitive element ;
8719	17673		1.47	6.0E-29	BF568097.1	EST_HUMAN	RC3-UT0062-210800-021-c05 UT0062 Homo sapiens cDNA
5022	14209		1.78	5.0E-29	AL163203.2	NT	602184092F1 NIH_MGC_42 Homo sapiens cDNA clone IMAGE:4300079 5'
6690	15885		9.84	5.0E-29	AW887541.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C003
3188	12433		2.82	4.0E-29	A1752367.1	EST_HUMAN	RC3-OT0091-170300-011-c12 OT0091 Homo sapiens cDNA
5659	14892		7.39	4.0E-29	BE184930.1	EST_HUMAN	cn15c02.x1 Normal Human Trabecular Bone Cells Homo sapiens cDNA clone NHTBC_cn15c02 random
6696	15894	25355	5.52	4.0E-29	J04888.1	NT	QV1-HT0471-280300-121-a05 HT0471 Homo sapiens cDNA
4408	13608	22706	1.67	3.0E-28	AB042297.1	NT	Human 90 kD heat shock protein gene, complete cds
4744	13935	23039	1.07	3.0E-28	BF333238.1	EST_HUMAN	Homo sapiens PTS gene for 6-pyruvoyltetrahydropterin synthase, complete cds
6854	16042	25506	2.62	3.0E-28	AW303317.1	EST_HUMAN	QV1-BT0821-120900-360-b03 BT0821 Homo sapiens cDNA
6928	16121		2.61	3.0E-28	AL163246.2	NT	xv17b03.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2813405 3' similar to contains Alu repetitive element; contains MER19.2 MER19 repetitive element ;
7818	17011	28524	2.7	3.0E-28	AA403053.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C046
8518	17550		1.56	3.0E-29	D63882.1	NT	Human HsLM15 mRNA for HsLM15, complete cds
489	8751	18878	1.54	2.0E-28	AF084869.1	NT	Q1335769 GAG-POL POLYPYRROLINE ;
489	8751	18879	1.54	2.0E-28	AF084869.1	NT	Human HsLM15 mRNA for HsLM15, complete cds
1519	10733	19803	6.77	2.0E-28	A1963604.1	EST_HUMAN	Homo sapiens envelope protein RIC-6 (env) gene, complete cds
1519	10733	19804	6.77	2.0E-28	A1963604.1	EST_HUMAN	Homo sapiens envelope protein RIC-6 (env) gene, complete cds
							wr65d10.x1 NCI_CGAP_U1 Homo sapiens cDNA clone IMAGE:2492563 3' similar to TR:O15548 O15548
							HERV-E ENVELOPE GLYCOPROTEIN ;
							wr65d10.x1 NCI_CGAP_U1 Homo sapiens cDNA clone IMAGE:2492563 3' similar to TR:O15548 O15548
							HERV-E ENVELOPE GLYCOPROTEIN ;

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4284	13487	22558	1.91	2.0E-29	AL163268.2	NT	Homo sapiens chromosome 21 segment HS21C068
6914	16102	25568	4.35	2.0E-29	AL163248.2	NT	Homo sapiens chromosome 21 segment HS21C048
6914	16102	25569	4.35	2.0E-29	AL163248.2	NT	Homo sapiens chromosome 21 segment HS21C048
7147	16324	25806	4.53	2.0E-29	AL163248.2	NT	Homo sapiens chromosome 21 segment HS21C048
7147	16324	25807	4.53	2.0E-29	AL163248.2	NT	Homo sapiens chromosome 21 segment HS21C048
8012	17152		1.9	2.0E-29	11425108	NT	Homo sapiens splicing factor similar to dnalJ (SPF31), mRNA
8047	17183		2.01	2.0E-29	AW880701.1	EST_HUMAN	QV0-OT0032-080300-155-d01 OT0032 Homo sapiens cDNA
8284	17391		1.8	2.0E-29	AL163227.2	NT	Homo sapiens chromosome 21 segment HS21C027
6714	15909	25368	11.36	1.0E-29	AW983890.1	EST_HUMAN	RC1-HN0003-220300-021-b04 HN0003 Homo sapiens cDNA hz20c07.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1288332 3' similar to contains MER4.b1
5920	16137	24548	3.11	9.0E-30	AA761215.1	EST_HUMAN	MER4 repetitive element;
8398	17475		4.04	9.0E-30	11422745	NT	Homo sapiens zinc/ferritin regulated transporter-like (ZIRT1), mRNA
5797	15014		9.51	8.0E-30	F08688.1	EST_HUMAN	HSC23F051 normalized infant brain cDNA Homo sapiens cDNA clone c-23105
6550	15746	25208	3.85	8.0E-30	AA383873.1	EST_HUMAN	EST197317 Thymus 1 Homo sapiens cDNA 5' end similar to EST containing O family repeat
1504	10717		1.52	7.0E-30	BE091133.1	EST_HUMAN	PM4-BT0724-150400-004-d11 BT0724 Homo sapiens cDNA
1743	10955	20138	1.39	6.0E-30	D25303.1	NT	Human mRNA for integrin alpha subunit, complete cds
3153	12388	21520	2.68	6.0E-30	BE008076.1	EST_HUMAN	QV0-BN0147-290400-214-f12 BN0147 Homo sapiens cDNA
9235	14488		2.32	6.0E-30	X51755.1	NT	Human lambda-immunoglobulin constant region complex (germline)
3989	13203	22311	40.02	5.0E-30	A1369992.1	EST_HUMAN	Ig92g03.x1 NCI_CGAP_CLL1 Homo sapiens cDNA clone IMAGE:2116276 3' similar to contains Alu repetitive element;
5285	18132		5.38	5.0E-30	U87631.1	NT	Human acetylcholinesterase (AChE) gene, exon 7
7464	18672		3.56	5.0E-30	AL163278.2	NT	Homo sapiens chromosome 21 segment HS21C078
7714	16913	26421	7.8	5.0E-30	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C010
7714	16913	26422	7.8	5.0E-30	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C010
2111	11310	20523	2.02	4.0E-30	AW937471.1	EST_HUMAN	QV3-DT0043-090200-080-c08 DT0043 Homo sapiens cDNA
2111	11310	20524	2.02	4.0E-30	AW937471.1	EST_HUMAN	QV3-DT0043-090200-080-c08 DT0043 Homo sapiens cDNA
6746	15941	26401	4.27	4.0E-30	AW812488.1	EST_HUMAN	CM1-ST0181-091189-035-f08 ST0181 Homo sapiens cDNA qq93c05.x1 Soares_tetral_fetus_Nb2-IF8_9w Homo sapiens cDNA clone IMAGE:1938920 3' similar to contains MER28 b2 MER28 repetitive element;
1180	10382		1.64	3.0E-30	A1338551.1	EST_HUMAN	contains MER28 b2 MER28 repetitive element;
3740	12860	22075	0.64	3.0E-30	AF128863.1	NT	Homo sapiens telomerase reverse transcriptase (TERT) gene, exons 1-8
7759	16955	26463	2.59	3.0E-30	P34056	SWISSPROT	TRANSCRIPTION FACTOR AP-2
681	9924	19055	0.91	2.0E-30	AW857315.1	EST_HUMAN	CM0-CT0307-310100-158-h03 CT0307 Homo sapiens cDNA
1092	10316		2.41	2.0E-30	F08688.1	EST_HUMAN	HSC23F051 normalized infant brain cDNA Homo sapiens cDNA clone c-23105
1473	10686	19861	4.84	2.0E-30	BE175877.1	EST_HUMAN	RC5-HT0582-110400-013-H08 HT0582 Homo sapiens cDNA

Page 175 of 382  
Table 4  
Single Exon Probes Expressed in HELA Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2675	11857	21072	8.46	2.0E-30	BE785232.1	EST_HUMAN	IL2-NT0101-280700-116-E04 NT0101 Homo sapiens cDNA
2870	12108	21237	8.13	2.0E-30	AF114158.1	NT	Homo sapiens Y-linked zinc finger protein (ZFY) gene, complete cds
3771	12989	22105	1.85	2.0E-30	AW20581.1	EST_HUMAN	U1H-B11-efo-c-12-0-U1.s1 NCI_CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2722558 3'
4787	13978	23078	1.85	2.0E-30	BE288945.1	EST_HUMAN	601118860F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3029438 5'
4787	13978	23080	1.85	2.0E-30	BE288945.1	EST_HUMAN	601118860F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3029438 5'
6633	15829	25291	6.69	2.0E-30	C18939.1	EST_HUMAN	C18939 Human placenta cDNA (TFujwara) Homo sapiens cDNA clone GEN-570C01 5'
6685	15860	25318	2.21	2.0E-30	BE670817.1	EST_HUMAN	7e37c12.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3284682 3' similar to SW:DHSA_HUMAN P31040 SUCCINATE DEHYDROGENASE [UBIQUINONE] FLAVOPROTEIN SUBUNIT PRECURSOR ;
6885	15860	25319	2.21	2.0E-30	BE670817.1	EST_HUMAN	7e37c12.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3284682 3' similar to SW:DHSA_HUMAN P31040 SUCCINATE DEHYDROGENASE [UBIQUINONE] FLAVOPROTEIN SUBUNIT PRECURSOR ;
7072	16249	25722	2.78	2.0E-30	AW971588.1	EST_HUMAN	EST3383657 MAGE resequencing, MAGL Homo sapiens cDNA
7102	16279	25759	5.6	2.0E-30	AW470791.1	EST_HUMAN	ha33c06.x1 NCI_CGAP_Kid12 Homo sapiens cDNA clone IMAGE:2875499 3' similar to contains THR.b3 THR repetitive element ;
291	9565	18698	16.27	1.0E-30	C18939.1	EST_HUMAN	C18939 Human placenta cDNA (TFujwara) Homo sapiens cDNA clone GEN-570C01 5'
544	9795	18919	3.42	1.0E-30	AW468897.1	EST_HUMAN	ha33c06.x1 NCI_CGAP_Kid12 Homo sapiens cDNA clone IMAGE:2875499 3' similar to contains THR.b3 THR repetitive element ;
723	9885	19103	2.56	1.0E-30	AL163203.2	NT	Homo sapiens chromosome 21 segment HS21C003
2179	11376	20598	19.88	1.0E-30	AA664377.1	EST_HUMAN	ac77b08.s1 Stragene lung (#837210) Homo sapiens cDNA clone IMAGE:868599 3'
2425	11616	20838	2.33	1.0E-30	BF347728.1	EST_HUMAN	602022560F1 NCI_CGAP_Brm67 Homo sapiens cDNA clone IMAGE:4157891 5'
2882	12200	21334	1.51	1.0E-30	5803091	NT	Homo sapiens methionine aminopeptidase; eIF-2-associated p67 (MNPEP), mRNA
3019	12255	21384	0.91	1.0E-30	AA315045.1	EST_HUMAN	EST188988 HCC cell line (matelastis to liver in mouse) II Homo sapiens cDNA 5' end
6386	15566	25073	2.19	1.0E-30	BF183230.1	EST_HUMAN	601809932F1 NIH_MGC_18 Homo sapiens cDNA clone IMAGE:4040694 5'
9037	18228	22082	0.91	1.0E-30	H55593.1	EST_HUMAN	CHR220532 Chromosome 22 exon Homo sapiens cDNA clone C22_728 5'
3748	12988	22082	0.91	9.0E-31	T73025.1	EST_HUMAN	yc65e08.r1 Stragene liver (#837224) Homo sapiens cDNA clone IMAGE:85570 5'
3748	12988	22083	0.91	9.0E-31	T73025.1	EST_HUMAN	yc65e08.r1 Stragene liver (#837224) Homo sapiens cDNA clone IMAGE:85570 5'
1084	10308	19461	2.7	8.0E-31	8923389	NT	Homo sapiens hypothetical protein FLJ20420 (FLJ20420), mRNA
2376	11569		13.17	8.0E-31	AL163208.2	NT	Homo sapiens chromosome 21 segment HS21C008
718	9890		1.45	7.0E-31	AA372637.1	EST_HUMAN	EST84555 Colon adenocarcinoma IV Homo sapiens cDNA 5' end
2628	11811	21028	2.27	7.0E-31	BE328517.1	EST_HUMAN	hw05a11.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3182012 3'
2628	11811	21029	2.27	7.0E-31	BE328517.1	EST_HUMAN	hw05a11.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3182012 3'
8871	17769	23940	2.52	7.0E-31	X51755.1	NT	Human lambda-immunoglobulin constant region complex (germline)

Page 176 of 382  
Table 4  
Single Exon Probes Expressed in HELA Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3658	12879		2.63	6.0E-31	AF223391.1	NT	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced
6509	15705		6.07	6.0E-31	AF055086.1	NT	Homo sapiens MHC class 1 region
7324	16540	26029	2.02	6.0E-31	AU119105.1	EST_HUMAN	AU119105 HEMBA1 Homo sapiens cDNA clone HEMBA1005050 5'
8455	17512	24020	1.83	6.0E-31	AW312868.1	EST_HUMAN	RCS-BT0377-091299-031-D12 BT0377 Homo sapiens cDNA
8594	18152		2.61	6.0E-31	BE864488.1	EST_HUMAN	601433087F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3918524 5'
197	9477	18609	1.74	5.0E-31	M60694.1	NT	Homo sapiens type I DNA topoisomerase gene, exon 8
197	9477	18610	1.74	5.0E-31	M60694.1	NT	Homo sapiens type I DNA topoisomerase gene, exon 8
6812	15808		9.55	5.0E-31	BF056540.1	EST_HUMAN	7068704.x1 NCI_CGAP_GC6 Homo sapiens cDNA clone IMAGE:3443479 3' similar to TR:Q13537 Q13537 SIMILAR TO POGO ELEMENT. ; contains L1.11 L1 repetitive element ;
603	9850		4.69	4.0E-31	AJ271735.1	NT	Homo sapiens Xq pseudautosomal region; segment 1/2
1590	10803	19878	0.95	4.0E-31	Q10473	SWISSPROT	POLYPEPTIDE N-ACETYL GALACTOSAMINYL TRANSFERASE (PROTEIN-UDP ACETYL GALACTOSAMINYL TRANSFERASE) (UDP-GALNAc:POLYPEPTIDE, N-ACETYL GALACTOSAMINYL TRANSFERASE) (GALNAc-T1)
1787	10997		2.49	4.0E-31	AL163280.2	NT	Homo sapiens chromosome 21 segment HS21C080
2742	11921		1.88	4.0E-31	5730038	NT	Homo sapiens SET domain and minner transposase fusion gene (SETMAR) mRNA
8634	17624		1.25	4.0E-31	AJ230125.1	NT	Homo sapiens GGT1 gene, exon 1
9010	17871		1.44	4.0E-31	AB008881.1	NT	Homo sapiens gene for activin receptor type IIB, complete cds
2555	11742	20960	5.53	3.0E-31	6005871	NT	Homo sapiens SEC63, endoplasmic reticulum translocon component (S. cerevisiae) like (SEC63L), mRNA
8226	15407	24849	7.95	3.0E-31	4826853	NT	Homo sapiens NADH dehydrogenase (ubiquinone) 1 beta subcomplex 8 (19kD, ASH) (NDUFB8) mRNA
6512	15709		2.89	3.0E-31	AL163208.2	NT	Homo sapiens chromosome 21 segment HS21C006
6951	16129	25597	3.74	3.0E-31	D14523.1	NT	Horse mRNA for ferritin L-chain, complete cds
7226	16447	25637	2.86	3.0E-31	P11174	SWISSPROT	40S RIBOSOMAL PROTEIN S15 (RIG PROTEIN)
7712	16911		7.41	3.0E-31	BF035327.1	EST_HUMAN	601459531F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3862086 5'
1883	11090	20281	1.64	2.0E-31	AW838171.1	EST_HUMAN	QV2-L T0051-260300-111-033 LT0051 Homo sapiens cDNA
2308	11502	20724	2.54	2.0E-31	AL119245.1	EST_HUMAN	DKFZp781G1513 t1 761 (synonym: hamy2) Homo sapiens cDNA clone IMAGE:838413 3' similar to contains aa8811.1.1 Strategene fetal retina 937202 Homo sapiens cDNA clone IMAGE:3148256 3' similar to contains THR 12 THR repetitive element ;
2404	11596	20818	4.8	2.0E-31	AA458824.1	EST_HUMAN	h08g01.x1 NCI_CGAP_Kid13 Homo sapiens cDNA clone IMAGE:3148256 3' similar to contains MER29 b3
5542	14786	24132	2.77	2.0E-31	BE350127.1	EST_HUMAN	MER29 repetitive element ;
8795	15990		2.34	2.0E-31	AA87764.1	EST_HUMAN	in06104.31 NCI_CGAP_Co10 Homo sapiens cDNA clone IMAGE:1161055 3' similar to TR:Q13537 Q13537 MER37 TRANSPOSABLE ELEMENT, COMPLETE CONSENSUS SEQUENCE. ;

Table 4

## Single Exon Probes Expressed in HELA Cells

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6830	16024	25489	4.65	2.0E-31	7681635	NT	Homo sapiens B9 protein (B9), mRNA
7098	16275	25754	3	2.0E-31	BE408611.1	EST_HUMAN	601304125F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3638310 5'
7098	16275	25755	3	2.0E-31	BE408611.1	EST_HUMAN	601304125F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3638310 5'
8585	17585		2.14	2.0E-31	AF148512.1	NT	Homo sapiens headkinase II gene, promoter region
8712	18380		2.48	2.0E-31	AI114527.1	EST_HUMAN	HA1110 Human fetal liver cDNA library Homo sapiens cDNA
16	9312	18415	7.1	1.0E-31	U93163.1	NT	Homo sapiens IMAGE-B2 (IMAGE-B2), IMAGE-B3 (IMAGE-B3), IMAGE-B4 (IMAGE-B4), and IMAGE-B1 (IMAGE-B1) genes, complete cds
1638	10852	20030	6.59	1.0E-31	O65371	SWISSPROT	OLFACTORY RECEPTOR 2C1
1638	10852	20031	6.59	1.0E-31	O95371	SWISSPROT	OLFACTORY RECEPTOR 2C1
1638	10852	20032	6.59	1.0E-31	O95371	SWISSPROT	OLFACTORY RECEPTOR 2C1
4637	13831	22818	1.87	1.0E-31	AL134376.1	EST_HUMAN	DKFZp47B235.1 547 (synonym: hibr1) Homo sapiens cDNA clone DKFZp47B235 5'
4637	13831	22819	1.87	1.0E-31	AL134376.1	EST_HUMAN	DKFZp47B235.1 547 (synonym: hibr1) Homo sapiens cDNA clone DKFZp47B235 5'
5322	14554	23624	3.51	1.0E-31	AW391678.1	EST_HUMAN	MR3-ST0220-151299-028-a08_1 ST0220 Homo sapiens cDNA
5726	14944	24340	2.11	1.0E-31	AF048727.1	NT	Homo sapiens minisatellite ceb1 repeat region
7490	16697	26182	2.54	1.0E-31	AI086434.1	EST_HUMAN	qT21h03.x1 NCJ_CGAP_Bm25 Homo sapiens cDNA clone IMAGE:1750708 3' similar to TR:Q16595 Q16595 FRATAXIN.
8257	17384	26917	6.47	1.0E-31	AW303317.1	EST_HUMAN	xv1703.x1 Soares_NFL_I_GBC_S1 Homo sapiens cDNA clone IMAGE:2813405 3' similar to contains Alu repetitive element; contains MER19.12 MER19 repetitive element;
5950	15166	24579	2.53	9.0E-32	AV723978.1	EST_HUMAN	AV723978 HTB Homo sapiens cDNA clone HTBAAG01 5'
2045	11246	20456	7.85	8.0E-32	AI056770.1	EST_HUMAN	ort15a09.x1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:1675384 3'
4876	14084	23159	0.96	7.0E-32	P52591	SWISSPROT	NUCLEAR ENVELOPE PORE MEMBRANE PROTEIN POM 121 (PORE MEMBRANE PROTEIN OF 121 KD) (P145)
8538	17563		3.22	7.0E-32	X17283.1	NT	Human chromosome 22 Immunoglobulin V(K) gene, part with 5' breakpoint between orphon and neighbouring non-amplified region
1041	10287	19418	48.91	5.0E-32	AF118627.1	NT	Homo sapiens PRO1181 mRNA, complete cds
939	10172		2.6	4.0E-32	AL163246.2	NT	Homo sapiens chromosome 21 segment HS21C048
6336	15516	24962	3.11	4.0E-32	11432574	NT	Homo sapiens AT-binding transcription factor 1 (ATBF1), mRNA
6336	15516	24963	3.11	4.0E-32	11432574	NT	Homo sapiens AT-binding transcription factor 1 (ATBF1), mRNA
462	9715	18550	3.57	3.0E-32	Y17283.1	NT	Homo sapiens FLI-1 gene, partial
1454	10667	19841	10.88	3.0E-32	AV731500.1	EST_HUMAN	AV731500 HTF Homo sapiens cDNA clone HTFAK007 5'
6875	16066	25534	6.4	3.0E-32	AV758634.1	EST_HUMAN	AV758634 BM Homo sapiens cDNA clone BMFBH12 5'
6875	16066	25535	6.4	3.0E-32	AV758634.1	EST_HUMAN	AV758634 BM Homo sapiens cDNA clone BMFBH12 5'
7489	16706	26182	9.12	3.0E-32	AA777621.1	EST_HUMAN	z95a07.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:448500 3' similar to contains THR.13 THR repetitive element;

Table 4

## Single Exon Probes Expressed in HELA Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8568	17587		5.38	3.0E-32	BE279086.1	EST_HUMAN	601156285F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3139701 5'
8950	14491	23579	3.58	3.0E-32	5174574	NT	Homo sapiens myeloid/lymphoid or mixed-lineage leukemia (trithorax (Drosophila) homolog), translocated to, 4 (MLLT4) mRNA
8950	14491	23580	3.58	3.0E-32	5174574	NT	Homo sapiens myeloid/lymphoid or mixed-lineage leukemia (trithorax (Drosophila) homolog), translocated to, 4 (MLLT4) mRNA
9112	17630		2.82	3.0E-32	BE279086.1	EST_HUMAN	601156285F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3139701 5'
5863	15081	24493	5.72	2.0E-32	Z38133.1	NT	H. sapiens mRNA for myosin
5863	15081	24494	5.72	2.0E-32	Z38133.1	NT	H. sapiens mRNA for myosin
9228	18006	23847	1.47	2.0E-32	AV738449.1	EST_HUMAN	AV738449 CB Homo sapiens cDNA clone CBFBI A08 5'
9228	18006	23848	1.47	2.0E-32	AV738449.1	EST_HUMAN	AV738449 CB Homo sapiens cDNA clone CBFBI A08 5'
2636	11819		1.51	1.0E-32	D84430.1	NT	Homo sapiens mRNA for phenylalanyl tRNA synthetase, complete cds
3059	12295		1.32	1.0E-32	BE743299.1	EST_HUMAN	601573207F1 NIH_MGC_8 Homo sapiens cDNA clone IMAGE:3834433 5'
6106	15200	24618	6.26	1.0E-32	11439789	NT	Homo sapiens chromosome 11 open reading frame 9 (C11ORF9), mRNA
6853	15848	25307	7.33	1.0E-32	AA720574.1	EST_HUMAN	hw21g02.s1 NCJ_CGAP_GC80 Homo sapiens cDNA clone IMAGE:1241138 3' similar to contains THR.13 THR repetitive element;
3456	12681		5.61	9.0E-33	BE327112.1	EST_HUMAN	hw07c05.x1 NCJ_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3182216 3' similar to TR:O86539 O86539 WW DOMAIN BINDING PROTEIN 11.1;
5837	15054		3.19	9.0E-33	AF223391.1	NT	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced
6712	15807	25366	2.29	9.0E-33	BF347228.1	EST_HUMAN	602021164F1 NCJ_CGAP_Brn67 Homo sapiens cDNA clone IMAGE:4156670 5'
7378	16594		7.28	9.0E-33	AL163280.2	NT	Homo sapiens chromosome 21 segment HS21C080
63	9359	18480	4.34	7.0E-33	5031736	NT	Homo sapiens short-chain alcohol dehydrogenase family member (HEP27) mRNA
63	9359	18481	4.34	7.0E-33	5031736	NT	Homo sapiens short-chain alcohol dehydrogenase family member (HEP27) mRNA
2127	11326	20544	2.68	7.0E-33	AI590115.1	EST_HUMAN	hw12b09.x1 NCJ_CGAP_U12 Homo sapiens cDNA clone IMAGE:2178609 3' similar to contains OFR.11 OFR repetitive element;
2811	11795		9	7.0E-33	AV730058.1	EST_HUMAN	AV730058 HTF Homo sapiens cDNA clone HTFAVE08 5'
3208	12442		18.26	7.0E-33	AW971307.1	EST_HUMAN	EST383398 IMAGE resequences, MAGL Homo sapiens cDNA
4472	13670	22761	0.96	7.0E-33	AA157467.1	EST_HUMAN	z55060.1.11 Stratagene endothelial cell B37223 Homo sapiens cDNA clone IMAGE:590328 5'
7405	16617	26107	4.91	7.0E-33	BF347229.1	EST_HUMAN	602021164F1 NCJ_CGAP_Brn67 Homo sapiens cDNA clone IMAGE:4156670 5'
7800	16993	26506	2.26	7.0E-33	AW971568.1	EST_HUMAN	EST383657 IMAGE resequences, MAGL Homo sapiens cDNA
8545	17570	23991	5.15	7.0E-33	AA601416.1	EST_HUMAN	hw16h01.s1 NCJ_CGAP_Phe1 Homo sapiens cDNA clone IMAGE:1100881 3' similar to contains L1.1 L1 repetitive element;
3717	12937		1.15	6.0E-33	AL163285.2	NT	Homo sapiens chromosome 21 segment HS21C085
6647	15842	25303	4.52	6.0E-33	J04038.1	NT	Human glyceraldehyde-3-phosphate dehydrogenase (GAPDH) gene, complete cds

Page 179 of 382  
Table 4  
Single Exon Probes Expressed in HELA Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6681	15876	25335	3.6	6.0E-33	11429198	NT	Homo sapiens similar to RAD23 (S. cerevisiae) homolog B (H. sapiens) (LOC63277), mRNA
1747	10959		1.81	5.0E-33	BF373515.1	EST_HUMAN	QV1-F10169-100700-271-e02 F10169 Homo sapiens cDNA
1846	11054		1.22	5.0E-33	11141884	NT	Homo sapiens solute carrier family 5 (choline transporter), member 7 (SLC5A7), mRNA
1863	11070	20280	4	5.0E-33	4507208	NT	Homo sapiens spermidine synthase (SRM) mRNA
1863	11070	20261	4	5.0E-33	4507208	NT	Homo sapiens spermidine synthase (SRM) mRNA
2237	11432		3.28	5.0E-33	AL163285.2	NT	Homo sapiens chromosome 21 segment HS21C085
4035	13245	22348	0.68	5.0E-33	AB014599.1	NT	Homo sapiens mRNA for KIAA0699 protein, partial cds
8343	17440		1.31	5.0E-33	11433063	NT	Homo sapiens ubiquitin protein ligase E3A (human papilloma virus E6-associated protein, Angelman syndrome) (UBE3A), mRNA
1136	10359		1.64	4.0E-33	AL163207.2	NT	Homo sapiens chromosome 21 segment HS21C007
2095	11295	20507	2.46	4.0E-33	4759987	NT	Homo sapiens RAB1, member RAS oncogene family (RAB1) mRNA
2384	11577		2.74	4.0E-33	AA626621.1	EST_HUMAN	ab51b11.1 Stratagene lung carcinoma 937218 Homo sapiens cDNA clone IMAGE:844317 5' similar to contains Alu repetitive element; contains MER28 b2 MER28 repetitive element ;
2510	11899	20918	16.8	4.0E-33	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C010
4480	13678	22768	1.55	4.0E-33	AW293349.1	EST_HUMAN	UI-H-B12-abl-c-03-Q-U1.s1 NC1 CGAP_Sub4 Homo sapiens cDNA clone IMAGE:2727149 3'
5397	14626	23739	24.3	4.0E-33	AA053053.1	EST_HUMAN	Z71a09.r1 Stratagene colon (#937204) Homo sapiens cDNA clone IMAGE:510038 5' similar to gb:X12871_ma1 HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN A1 (HUMAN);
1097	10321		6.43	3.0E-33	BE350127.1	EST_HUMAN	h09g01.x1 NC1 CGAP_Kid13 Homo sapiens cDNA clone IMAGE:3146256 3' similar to contains MER29 b3 MER29 repetitive element ;
1098	10321		3.04	3.0E-33	BE350127.1	EST_HUMAN	h09g01.x1 NC1 CGAP_Kid13 Homo sapiens cDNA clone IMAGE:3146256 3' similar to contains MER29 b3 MER29 repetitive element ;
2413	12016		2.64	3.0E-33	AV647851.1	EST_HUMAN	AV647851 GLC Homo sapiens cDNA clone GLC8CF09 3'
17	9313		0.77	2.0E-33	AI160189.1	EST_HUMAN	qb67g03.x1 Soares_fetal_heart_NbH19W Homo sapiens cDNA clone IMAGE:1705204 3' similar to contains OFR.11 OFR repetitive element ;
104	9313		2.62	2.0E-33	AI160189.1	EST_HUMAN	qb67g03.x1 Soares_fetal_heart_NbH19W Homo sapiens cDNA clone IMAGE:1705204 3' similar to contains OFR.11 OFR repetitive element ;
4411	13611		4.41	2.0E-33	BE159039.1	EST_HUMAN	MRO-HT0405-160300-202-d08 HT0405 Homo sapiens cDNA
5006	14163	23282	25.82	2.0E-33	AA626683.1	EST_HUMAN	ab51g11.1 Stratagene lung carcinoma 937218 Homo sapiens cDNA clone IMAGE:844388 5' similar to gb:X00734_cds1 TUBULIN BETA-5 CHAIN (HUMAN);
5125	14304	23393	1.41	2.0E-33	11421332	NT	Homo sapiens hypothetical protein SIRP-b2 (SIRP-b2), mRNA
5125	14304	23394	1.41	2.0E-33	11421332	NT	Homo sapiens hypothetical protein SIRP-b2 (SIRP-b2), mRNA
5638	15055	24462	1.83	2.0E-33	A1277492.1	EST_HUMAN	qb66d01.1 Soares_NbHMPu_S1 Homo sapiens cDNA clone IMAGE:1680181 3'
8	9304		1.97	1.0E-33	AF003528.1	NT	Homo sapiens X-linked anhidrotic ectodermal dysplasia protein gene (EDA), exon 2 and flanking repeat regions



Table 4

## Single Exon Probes Expressed in HELA Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7867	17057	26578	2	1.0E-33	AW956818.1	EST_HUMAN	QV3-BN0047-230200-102-b03 BN0047 Homo sapiens cDNA
8187	17299	26842	5.98	1.0E-33	U60822.1	NT	Human dystrophin (DMD) gene, exons 7, 8 and 9, and partial cds
8841	17750		2	1.0E-33	A1927191.1	EST_HUMAN	wo88c06.x1 NCI_CGAP_Kd11 Homo sapiens cDNA clone IMAGE:2482410 3'
9024	9304		5.11	1.0E-33	AF003528.1	NT	Homo sapiens X-linked arylidrotic ectodermal dysplasia protein gene (EDA), exon 2 and flanking repeat regions
9059	17890	23898	1.63	1.0E-33	AV727809.1	EST_HUMAN	AV727809 HTC Homo sapiens cDNA clone HTCCNC12 5'
9246	18017		2.54	9.0E-34	AJ271735.1	NT	Homo sapiens Xq pseudautosomal region; segment 1/2
2137	11335	20553	1.18	8.0E-34	892275.1	NT	Homo sapiens hypothetical protein FLJ10900 (FLJ10900), mRNA
1446	10659	19834	2.78	7.0E-34	T70845.1	EST_HUMAN	yd15605.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:108320 5'
8816	17813		2.89	7.0E-34	H12868.1	EST_HUMAN	y14c10.r1 Soares placenta Np2HP Homo sapiens cDNA clone IMAGE:148722 5'
477	9729	18862	1.31	6.0E-34	U10891.1	NT	Human G2 protein mRNA, partial cds
477	9729	18863	1.31	6.0E-34	U10891.1	NT	Human G2 protein mRNA, partial cds
8418	17490	24010	1.7	8.0E-34	U03698.1	NT	Mus musculus DAB2J hair-specific (hach-1) gene
1845	11053		3.27	5.0E-34	7708500	NT	Homo sapiens Npw38-binding protein NpwBP (LOC51729), mRNA
5094	14274	23357	4.37	5.0E-34	U30883.1	NT	Homo splicing factor SRP55-1 (SRP55) mRNA, complete cds
6736	15931	25391	2.28	5.0E-34	AF078779.1	NT	Rattus norvegicus putative four repeat ion channel mRNA, complete cds
7247	16487	25958	2.25	5.0E-34	AB037856.1	NT	Homo sapiens mRNA for KIAA1435 protein, partial cds
7806	18989		1.91	5.0E-34	AL163209.2	NT	Homo sapiens chromosome 21 segment HS21C009
1987	11171	20377	2.12	4.0E-34	AI804687.1	EST_HUMAN	t894c06.x1 NCI_CGAP_P728 Homo sapiens cDNA clone IMAGE:2249184 3'
2679	11861	21075	0.94	4.0E-34	8922807	NT	Homo sapiens hypothetical protein FLJ10989 (FLJ10989), mRNA
3137	12372	21503	1.09	4.0E-34	5903186	NT	Homo sapiens splicing factor 3a, subunit 3, 60kD (SF3A3), mRNA
7711	16910		5.66	3.0E-34	BF035327.1	EST_HUMAN	601458531F1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3862086 5'
1495	10708	19881	11.67	1.0E-34	P12236	SWISSPROT	ADP-ATP CARRIER PROTEIN, LIVER ISOFORM T2 (ADP/ATP TRANSLOCASE 3) (ADENINE NUCLEOTIDE TRANSLOCATOR 3) (ANT 3)
3654	12875	21993	1.4	1.0E-34	AF003528.1	NT	Homo sapiens X-linked arylidrotic ectodermal dysplasia protein gene (EDA), exon 2 and flanking repeat regions
4047	13257	22358	0.98	1.0E-34	AY009397.1	NT	Homo sapiens WNT3 precursor (WNT3) mRNA, complete cds
4047	13257	22359	0.98	1.0E-34	AY009397.1	NT	Homo sapiens WNT3 precursor (WNT3) mRNA, complete cds
4476	13674		5.59	1.0E-34	BE071414.1	EST_HUMAN	RC2-BT0506-240400-018-h08 BT0506 Homo sapiens cDNA
5728	14947	24344	2.28	1.0E-34	BE874052.1	EST_HUMAN	601484430F1 NIH_MGC_69 Homo sapiens cDNA clone IMAGE:3862086 5'
5728	14947	24345	2.28	1.0E-34	BE874052.1	EST_HUMAN	601484430F1 NIH_MGC_69 Homo sapiens cDNA clone IMAGE:3862086 5'
6891	16169	25641	10.13	1.0E-34	AL036635.1	EST_HUMAN	DKFZp584A1563_r1 584 (synonym: hfr2) Homo sapiens cDNA clone DKFZp584A1563 5'
8804	18316		2.28	1.0E-34	AA807087.1	EST_HUMAN	cc31c11.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1351316 3' similar to gb:X68203 TYROSINE-PROTEIN KINASE RECEPTOR FLT4 PRECURSOR (HUMAN);

Table 4

## Single Exon Probes Expressed in HELA Cells

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9050	17922		4.53	1.0E-34	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C010
3624	12845	21984	1.17	9.0E-35	AW663302.1	EST_HUMAN	h777008.y1 NCI_CGAP_GU1 Homo sapiens cDNA clone IMAGE:2968787 5'
230	9508		17.95	8.0E-35	6031180	NT	Homo sapiens prohibitin (PHB) mRNA
1709	10921	20106	3.14	8.0E-35	BF589037.1	EST_HUMAN	nae33a08.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:3258134 3' similar to TR:O75912
1709	10921	20107	3.14	8.0E-35	BF589037.1	EST_HUMAN	nae33a08.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:3258134 3' similar to TR:O75912
4883	14071	23168	4.02	8.0E-35	BF183185.1	EST_HUMAN	O75912 DIACYLGLYCEROL KINASE IOTA. ;
7281	16500	25983	2.31	8.0E-35	BE378480.1	EST_HUMAN	601806588F1 NIH_MGC_18 Homo sapiens cDNA clone IMAGE:4040324 5'
8535	17560		3.51	8.0E-35	BF569282.1	EST_HUMAN	601230488F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3608513 5'
5867	15085	24469	1.62	7.0E-35	11425417	NT	602184624T1 NIH_MGC_42 Homo sapiens cDNA clone IMAGE:4300660 3'
1417	10630	19798	1.02	8.0E-35	AA757115.1	EST_HUMAN	Homo sapiens phosphatidylinositol glycan, class L (PIGL), mRNA
1937	11141	20337	1.3	8.0E-35	6005975	NT	ah53h03.s1 Soares_testis_NHT Homo sapiens cDNA clone 1309397 3'
4030	13240	22344	0.89	8.0E-35	AW297191.1	EST_HUMAN	Homo sapiens zinc finger protein 208 (ZNF208), mRNA
6427	15624	25089	5.25	8.0E-35	6005921	NT	U1-H-BWO-ajd-4-09-0-J1.s1 NCI_CGAP_Sub6 Homo sapiens cDNA clone IMAGE:2731433 3'
143	9425	18559	70.69	5.0E-35	AF154830.1	NT	Homo sapiens triple functional domain (PTPRF interacting) (TRIO), mRNA
1684	10898	20083	1.66	5.0E-35	X63392.1	NT	Homo sapiens carboxyl phosphatase synthetase 1 mRNA, complete cds
2738	11917	21131	2.17	5.0E-35	AB007866.2	NT	H. sapiens immunoglobulin kappa light chain variable region L14
2970	12208	21344	1.15	5.0E-35	6912639	NT	Homo sapiens mRNA for KIAA0408 protein, partial cds
							Homo sapiens Ring1 and YY1 binding protein (RYBP), mRNA
							Homo sapiens cdk2 kinase (CLK2), propin1, cdk1, glucocorticoidase (GBA), and metaxin genes, complete cds; metaxin pseudogene and glucocorticoidase pseudogene; and thrombospondin3 (THBS3) gene, partial cds
4403	13603	22703	1.74	5.0E-35	AF023268.1	NT	601431984F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3917229 5'
6523	15719		3.88	5.0E-35	BE800992.1	EST_HUMAN	zh84f12.r1 Soares_fetal_liver_spleen_1NLS_S1 Homo sapiens cDNA clone IMAGE:428015 5'
7733	16930		3.48	5.0E-35	AA001786.1	EST_HUMAN	601103719F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3350405 5'
1438	10650	19824	34.03	4.0E-35	BE267907.1	EST_HUMAN	y198a07.r1 Soares_fetal_liver_spleen_1NLS Homo sapiens cDNA clone IMAGE:241236 5' similar to contains PTR5 repetitive element;
1788	10998	20193	8.81	4.0E-35	H91193.1	EST_HUMAN	Homo sapiens X-linked anhidrotic ectodermal dysplasia protein gene (EDA), exon 2 and flanking repeat regions
4819	14008		0.63	4.0E-35	AF003528.1	NT	601300705F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3635401 5'
5138	14314		0.99	4.0E-35	BE409102.1	EST_HUMAN	h08g01.x1 NCI_CGAP_Kid13 Homo sapiens cDNA clone IMAGE:3146256 3' similar to contains MER28 b3
6169	15351		1.9	4.0E-35	BE350127.1	EST_HUMAN	MER29 repetitive element;
8628	15824	25286	7.14	4.0E-35	AL046596.1	EST_HUMAN	DKFZp434L148_r1 434 (synonym: hies3) Homo sapiens cDNA clone DKFZp434L148 5'
1558	10772	19945	49.16	3.0E-35	BE288182.1	EST_HUMAN	601125260F1 NIH_MGC_8 Homo sapiens cDNA clone IMAGE:3345083 5'

Table 4

## Single Exon Probes Expressed in HELA Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2299	11494		3.28	3.0E-35	AF224492.1	NT	Homo sapiens phospholipid scramblase 1 gene, complete cds
5359	14589	23665	24.64	3.0E-35	BF433100.1	EST_HUMAN	7n25a09.x1 NCL_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3565381 3' similar to TR:Q8QZH7
5359	14589	23666	24.64	3.0E-35	BF433100.1	EST_HUMAN	Q8QZH7 F-BOX PROTEIN FBL2 ;
108	11959	18528	1.05	2.0E-35	N88965.1	EST_HUMAN	7n25a09.x1 NCL_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3565381 3' similar to TR:Q8QZH7
1106	10416	16570	0.8	2.0E-35	T11909.1	EST_HUMAN	Q8QZH7 F-BOX PROTEIN FBL2 ;
2184	11381	20805	6.37	2.0E-35	AB018413.1	NT	K6932F Human fetal heart, Lambda ZAP Express Homo sapiens cDNA clone K6932 5' similar to REPETITIVE ELEMENT
2644	11827	21042	1.22	2.0E-35	AW665005.1	EST_HUMAN	REPETITIVE ELEMENT
3283	12514	21644	1.02	2.0E-35	6912459	NT	A871F Heart Homo sapiens cDNA clone A871
3283	12514	21645	1.02	2.0E-35	6912459	NT	Homo sapiens mRNA for Gab2, complete cds
3532	12755		1.11	2.0E-35	AB020702.1	NT	H86a12.x1 Scores_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2979166 3' similar to SW:TR12_HUMAN Q14689 THYROID RECEPTOR INTERACTING PROTEIN 12 ;
3988	13104	22221	0.69	2.0E-35	BE247575.1	EST_HUMAN	Homo sapiens Grb2-associated binder 2 (KIAA0571), mRNA
3988	13104	22222	0.69	2.0E-35	BE247575.1	EST_HUMAN	Homo sapiens Grb2-associated binder 2 (KIAA0571), mRNA
4673	13967		2.75	2.0E-35	H49239.1	EST_HUMAN	Homo sapiens mRNA for KIAA0895 protein, partial cds
5481	14708	24063	2	2.0E-35	BF332417.1	EST_HUMAN	TCBAP2E4328 Pediatric pre-B cell acute lymphoblastic leukemia Baylor-HGSC project=TCBA Homo sapiens cDNA clone TCBAP4328
7376	16592	26080	5.53	2.0E-35	X59417.1	NT	TCBAP2E4328 Pediatric pre-B cell acute lymphoblastic leukemia Baylor-HGSC project=TCBA Homo sapiens cDNA clone TCBAP4328
8289	12514	21644	1.22	2.0E-35	6912459	NT	TCBAP2E4328 Pediatric pre-B cell acute lymphoblastic leukemia Baylor-HGSC project=TCBA Homo sapiens cDNA clone TCBAP4328
8289	12514	21645	1.22	2.0E-35	6912459	NT	TCBAP2E4328 Pediatric pre-B cell acute lymphoblastic leukemia Baylor-HGSC project=TCBA Homo sapiens cDNA clone TCBAP4328
8470	17523	24023	1.28	2.0E-35	BE904978.1	EST_HUMAN	TCBAP2E4328 Pediatric pre-B cell acute lymphoblastic leukemia Baylor-HGSC project=TCBA Homo sapiens cDNA clone TCBAP4328
8470	17523	24024	1.28	2.0E-35	BE904978.1	EST_HUMAN	TCBAP2E4328 Pediatric pre-B cell acute lymphoblastic leukemia Baylor-HGSC project=TCBA Homo sapiens cDNA clone TCBAP4328
9026	17678		8.59	2.0E-35	AL163210.2	NT	TCBAP2E4328 Pediatric pre-B cell acute lymphoblastic leukemia Baylor-HGSC project=TCBA Homo sapiens cDNA clone TCBAP4328
9144	11959	18528	2	2.0E-35	N88965.1	EST_HUMAN	TCBAP2E4328 Pediatric pre-B cell acute lymphoblastic leukemia Baylor-HGSC project=TCBA Homo sapiens cDNA clone TCBAP4328
48	9345	18455	4.75	1.0E-35	AA631949.1	EST_HUMAN	TCBAP2E4328 Pediatric pre-B cell acute lymphoblastic leukemia Baylor-HGSC project=TCBA Homo sapiens cDNA clone TCBAP4328
48	9345	18456	4.75	1.0E-35	AA631949.1	EST_HUMAN	TCBAP2E4328 Pediatric pre-B cell acute lymphoblastic leukemia Baylor-HGSC project=TCBA Homo sapiens cDNA clone TCBAP4328
760	10001	19147	72.69	1.0E-35	AW389473.1	EST_HUMAN	TCBAP2E4328 Pediatric pre-B cell acute lymphoblastic leukemia Baylor-HGSC project=TCBA Homo sapiens cDNA clone TCBAP4328
760	10001	19148	72.69	1.0E-35	AW389473.1	EST_HUMAN	TCBAP2E4328 Pediatric pre-B cell acute lymphoblastic leukemia Baylor-HGSC project=TCBA Homo sapiens cDNA clone TCBAP4328
919	10154		2.05	1.0E-35	T87947.1	EST_HUMAN	TCBAP2E4328 Pediatric pre-B cell acute lymphoblastic leukemia Baylor-HGSC project=TCBA Homo sapiens cDNA clone TCBAP4328

Page 183 of 382  
Table 4  
Single Exon Probes Expressed in HELA Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2507	11695	20913	1.56	1.0E-35	7705994	NT	Homo sapiens hypothetical protein (LOC51233), mRNA
2723	11802	21118	1.21	1.0E-35	BE350127.1	EST_HUMAN	h09g01.x1 NCL_CGAP_Kid13 Homo sapiens cDNA clone IMAGE:3146256 3' similar to contains MER29.b3 MER29 repetitive element:
2723	11902	21119	1.21	1.0E-35	BE350127.1	EST_HUMAN	h09g01.x1 NCL_CGAP_Kid13 Homo sapiens cDNA clone IMAGE:3146256 3' similar to contains MER29.b3 MER29 repetitive element:
3108	12343	21471	1.33	1.0E-35	6006030	NT	Homo sapiens transcription elongation factor B (SII), polypeptide 1-like (TCEB1L), mRNA
3127	12362	21491	1.95	1.0E-35	AV650422.1	EST_HUMAN	AV650422 GLC Homo sapiens cDNA clone GLCCEFO8 3'
3127	12362	21492	1.95	1.0E-35	AV650422.1	EST_HUMAN	AV650422 GLC Homo sapiens cDNA clone GLCCEFO8 3'
4414	13614	22709	4.94	1.0E-35	7656805	NT	Mus musculus activin receptor interacting protein 1 (Arip1-pending), mRNA
4414	13614	22710	4.84	1.0E-35	7656805	NT	Mus musculus activin receptor interacting protein 1 (Arip1-pending), mRNA
6933	18076	25592	3.9	1.0E-35	AU158595.1	EST_HUMAN	AU158595 PLACE3 Homo sapiens cDNA clone PLACE3000382 3'
6933	18076	25593	3.9	1.0E-35	AU158595.1	EST_HUMAN	AU158595 PLACE3 Homo sapiens cDNA clone PLACE3000382 3'
8237	17368		4.28	1.0E-35	AI525119.1	EST_HUMAN	promin-7.D01.r bvtumor Homo sapiens cDNA 5'
8321	18273		2.31	1.0E-35	11418274	NT	Homo sapiens fibulin 1 (FBLN1), mRNA
8537	17562		2.05	1.0E-35	11418110	NT	Homo sapiens casein kinase 1, epsilon (CSNK1E), mRNA
8915	17803		2.34	1.0E-35	BE782832.1	EST_HUMAN	601584833F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3938985 5'
2881	12119	21250	1.79	7.0E-36	AW857579.1	EST_HUMAN	CM1-CT0315-091299-063-d07 CT0315 Homo sapiens cDNA
3082	12318		5.8	7.0E-36	4557498	NT	Homo sapiens C-terminal binding protein 2 (CTBP2), mRNA
6360	15540	24994	5.98	7.0E-36	U06872.1	NT	Human carcinoembryonic antigen gene family member 12 (CGM12), gene, exons L and LUN
6360	15540	24995	5.98	7.0E-36	U06872.1	NT	Human carcinoembryonic antigen gene family member 12 (CGM12), gene, exons L and LUN
8704	17668	23948	2.64	7.0E-36	AF052051.1	NT	Homo sapiens glutathione transferase A4 gene, exon 1
1973	11177	20383	1.77	6.0E-36	7706822	NT	Homo sapiens nihurin 2 (NINJ2), mRNA
2382	11575		5.88	6.0E-36	AB035346.1	NT	Homo sapiens TCE6 gene, exon 12
3618	12839	21958	0.86	6.0E-36	BF515101.1	EST_HUMAN	UJH-BW1-anv-c-12-0-UI.s1 NCL_CGAP_Sub7 Homo sapiens cDNA clone IMAGE:3083542 3'
5353	14583	23659	6.31	6.0E-36	AK435169.1	EST_HUMAN	h03005.x1 Soares_NSF_F8_gw_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:2126195 3' similar to gbM111949 PANCREATIC SECRETORY TRYPSIN INHIBITOR PRECURSOR (HUMAN);
6125	15309	24742	3.34	6.0E-36	AW780143.1	EST_HUMAN	h006h02.x1 NCL_CGAP_Cot14 Homo sapiens cDNA clone IMAGE:3036627 3' similar to SW:IMA2_HUMAN P52282 IMPORTIN ALPHA-2 SUBUNIT;
8081	17216	28750	2.26	6.0E-36	A1380499.1	EST_HUMAN	h05c09.x1 NCL_CGAP_CLL1 Homo sapiens cDNA clone IMAGE:2107024 3' similar to contains MER9.b2 MER9 repetitive element;
135	9418	18552	9.86	5.0E-36	AJ271735.1	NT	Homo sapiens Xq pseudautosomal region; segment 1/2
2708	11687	21104	47.02	5.0E-36	BE388436.1	EST_HUMAN	601285567F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3607289 5'
3580	12811	21831	2.13	5.0E-36	AL163209.2	NT	Homo sapiens chromosome 21 segment HS21C009
4798	13987	23093	2.18	5.0E-36	5728728	NT	Homo sapiens API5-like 1 (API5L1), mRNA

Page 184 of 382  
Table 4  
Single Exon Probes Expressed in HELA Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4788	13987	23084	2.18	5.0E-36	5729729	NT	Homo sapiens API5-like 1 (API5L1), mRNA
8287	9418	18552	4.4	5.0E-36	AJ271735.1	NT	Homo sapiens Xq pseudautosomal region; segment 1/2
6593	17602	24008	2.39	5.0E-36	11417882	NT	Homo sapiens calcineurin binding protein 1 (KIAA0330), mRNA
1232	10450	19608	1.85	4.0E-36	BE010038.1	EST_HUMAN	PM3-BN0176-100400-001-g04 BN0176 Homo sapiens cDNA
1444	10657	19833	1.45	4.0E-36	P10268	SWISSPROT	RETROVIRUS-RELATED POLYPROTEIN [CONTAINS: REVERSE TRANSCRIPTASE ; ENDONUCLEASE]
1622	10835	20011	1.15	4.0E-36	BE382574.1	EST_HUMAN	601298574F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3628388 5'
2189	11386		5.46	4.0E-36	AW247772.1	EST_HUMAN	2820020.5prime NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2820020 5'
3328	12557	21894	0.79	4.0E-36	BE389289.1	EST_HUMAN	601282266F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3604168 5'
3328	12557	21895	0.79	4.0E-36	BE389289.1	EST_HUMAN	601282266F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3604168 5'
5161	14340	23429	0.59	4.0E-36	AA905361.1	EST_HUMAN	ak05b11.s1 Scores_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1506909 3' similar to SW:D3H1_RAT P29268 3-HYDROXYISOBUTYRATE DEHYDROGENASE PRECURSOR ;
5691	14911	24305	2.59	4.0E-36	11497041	NT	Homo sapiens a disintegrin and metalloproteinase domain 22 (ADAM22), transcript variant 3, mRNA
6359	15539	24993	1.69	4.0E-36	M33320.1	NT	Human platelet Glycoprotein IIb (GPIIb) gene, exons 2-29
7559	16764	26255	2.9	4.0E-36	AA400370.1	EST_HUMAN	zu09c10.r1 Scores_testis_NHT Homo sapiens cDNA clone IMAGE:743250 5'
8609	17607		1.56	4.0E-36	11420516	NT	Homo sapiens nuclear factor of activated T-cells, cytoplasmic 2 (NFATC2), mRNA
8657	18156		3.54	4.0E-36	AV753629.1	EST_HUMAN	AV753629 TP Homo sapiens cDNA clone TPGABH01 5'
9265	18032		1.38	4.0E-36	D25217.2	NT	Homo sapiens mRNA for KIAA0027 protein, partial cds
703	8945	18061	2.65	3.0E-36	AF099810.1	NT	Homo sapiens neuroxin III-alpha gene, partial cds
1489	10702	19876	0.96	3.0E-36	AF110239.1	NT	Homo sapiens calcium/calmodulin-stimulated cyclic nucleotide phosphodiesterase (PDE1A) gene, partial cds
1489	10702	19877	0.96	3.0E-36	AF110239.1	NT	Homo sapiens calcium/calmodulin-stimulated cyclic nucleotide phosphodiesterase (PDE1A) gene, partial cds
2262	11457	20675	3.92	3.0E-36	7602401	NT	Homo sapiens KIAA0952 protein (KIAA0952), mRNA
4505	13702	22798	8.01	3.0E-36	10181139	NT	Mus musculus junctophilin 1 (Jp1-pending), mRNA
7671	16870	26373	1.79	3.0E-36	BF035327.1	EST_HUMAN	601458531F1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3662086 5'
3134	12369	21500	6.47	2.0E-36	BE259287.1	EST_HUMAN	601106343F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3342708 5'
4978	14165	23255	23.75	2.0E-36	AW880376.1	EST_HUMAN	QV0-OT0030-240300-174-h04 OT0030 Homo sapiens cDNA
5434	14661	23801	2.36	2.0E-36	AF287747.1	NT	Mus musculus p47-phox gene, complete cds
5591	14815	24189	3.46	2.0E-36	T08758.1	EST_HUMAN	EST08848 Infant Brain, Bonto Soares Homo sapiens cDNA clone HIBBL28 5' end
5915	15132	24541	13.08	2.0E-36	T69829.1	EST_HUMAN	yc44a07.r1 Stratiogene liver (#937224) Homo sapiens cDNA clone IMAGE:83508 5'
895	10130	19292	1.73	1.0E-36	BE408310.1	EST_HUMAN	601300838F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3635480 5'
2113	11312	20527	1.28	1.0E-36	BE146523.1	EST_HUMAN	RC1-HT0217-131199-021-h07 HT0217 Homo sapiens cDNA
2113	11312	20528	1.28	1.0E-36	BE146523.1	EST_HUMAN	RC1-HT0217-131199-021-h07 HT0217 Homo sapiens cDNA

Table 4

### Single Exon Probes Expressed in HELA Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2183	11368	20586	1.21	1.0E-36	BF673761.1	EST_HUMAN	602136493F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4272888 5'
3318	12548		1.63	1.0E-36	AF156962.1	NT	Homo sapiens human endogenous retrovirus W proC8-19 protease (pro) gene, partial cds
5746	14965		5.34	1.0E-36	AI867714.1	EST_HUMAN	wb37c12.x1 NCL_CGAP_GC6 Homo sapiens cDNA clone IMAGE:2307882 3' similar to contains Alu repetitive element;
8445	15642	25108	4.87	1.0E-38	AA148034.1	EST_HUMAN	z051a12.1 Stragene endothelial cell 837223 Homo sapiens cDNA clone IMAGE:590398 5'
6445	15642	25109	4.87	1.0E-38	AA148034.1	EST_HUMAN	z051a12.1 Stragene endothelial cell 837223 Homo sapiens cDNA clone IMAGE:590398 5'
7115	16292	25773	5.47	1.0E-36	BF364169.1	EST_HUMAN	QV3-NN1023-010600-199-h01 NN1023 Homo sapiens cDNA
7521	16728	28217	3.97	1.0E-38	AW897636.1	EST_HUMAN	CM3-NN0061-140400-147-h12 NN0061 Homo sapiens cDNA
7919	17134	26664	4.03	1.0E-36	AW504143.1	EST_HUMAN	UJ-HF-BNO-ale-c-03-0-J1.1 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3078277 5'
8468	17521		4.59	1.0E-36	11418177	NT	Homo sapiens Ran GTPase activating protein 1 (RANGAP1), mRNA
8944	17821		3.71	1.0E-36	AL163213.2	NT	Homo sapiens chromosome 21 segment HS21C013
9209	17992		2.95	1.0E-36	AF202723.1	NT	Homo sapiens Sad1 unc-84 domain protein 2 (SUN2) mRNA, partial cds
6248	15429	24969	2.31	9.0E-37	AW009277.1	EST_HUMAN	ws80b07.x1 NCL_CGAP_Co3 Homo sapiens cDNA clone IMAGE:2504245 3'
6248	15429	24870	2.31	9.0E-37	AW009277.1	EST_HUMAN	ws80b07.x1 NCL_CGAP_Co3 Homo sapiens cDNA clone IMAGE:2504245 3'
8745	17690		2.13	9.0E-37	W22618.1	EST_HUMAN	73D4 Human retina cDNA Tsp5081-cleaved sublibrary Homo sapiens cDNA not directional
3330	12559	21697	0.99	8.0E-37	4757978	NT	Homo sapiens chimerin (chimaerin) 2 (CHN2) mRNA
5584	14808	24181	3.76	8.0E-37	BE350127.1	EST_HUMAN	ht09g01.x1 NCL_CGAP_Kid13 Homo sapiens cDNA clone IMAGE:3148256 3' similar to contains MER29.b3 MER29 repetitive element;
5584	14808	24182	3.76	8.0E-37	BE350127.1	EST_HUMAN	ht09g01.x1 NCL_CGAP_Kid13 Homo sapiens cDNA clone IMAGE:3148256 3' similar to contains MER29.b3 MER29 repetitive element;
5604	14828	24204	4.98	8.0E-37	AW840940.1	EST_HUMAN	RC1-CN0008-210100-012-a09_1 CN0008 Homo sapiens cDNA
6423	15620	25084	8.42	8.0E-37	X87344.1	NT	H.sapiens DMA, DMB, HLA-Z1, IPP2, LMP2, TAP1, LMP7, TAP2, DOB, DOB2 and RING8, 9, 13 and 14 genes
1281	10506		3.81	7.0E-37	AL042800.1	EST_HUMAN	DKFZp434E0422_r1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434E0422 5'
7342	16558	26046	9.31	7.0E-37	AI817700.1	EST_HUMAN	wk25b11.x1 NCL_CGAP_Bm25 Homo sapiens cDNA clone IMAGE:2413341 3' similar to contains PTR5.12 PTR5 repetitive element;
7471	16679	26161	4.11	7.0E-37	AI538702.1	EST_HUMAN	hm87g03.x1 NCL_CGAP_Bm25 Homo sapiens cDNA clone IMAGE:2165140 3' similar to contains L1.b3 L1 repetitive element;
9080	17904		3.34	6.0E-37	AF202723.1	NT	Homo sapiens Sad1 unc-84 domain protein 2 (SUN2) mRNA, partial cds
5705	14924	24317	4.29	5.0E-37	AA307123.1	EST_HUMAN	EST1178035 Colon carcinoma (HCC) cell line Homo sapiens cDNA 5' end
5705	14924	24318	4.29	5.0E-37	AA307123.1	EST_HUMAN	EST1178035 Colon carcinoma (HCC) cell line Homo sapiens cDNA 5' end
7494	18701		5.03	5.0E-37	7857117	NT	Homo sapiens glycine C-acetyltransferase (2-amino-3-ketobutyrate-CoA ligase) (GCAT), mRNA
2463	17518		6.75	5.0E-37	AF149773.1	NT	Homo sapiens NOD1 protein (NOD1) gene, exons 1, 2, and 3
2463	17518		4.76	4.0E-37	AA702794.1	EST_HUMAN	z190b04.s1 Soares fetal liver spleen .INFLS S1 Homo sapiens cDNA clone IMAGE:448015 3'

Table 4

## Single Exon Probes Expressed in HELA Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7602	16805	26300	1.77	4.0E-37	AL163204.2	NT	Homo sapiens chromosome 21 segment HS21C004
7602	16805	26301	1.77	4.0E-37	AL163204.2	NT	Homo sapiens chromosome 21 segment HS21C004
1984	11187	20397	2.81	3.0E-37	AL048956.1	EST_HUMAN	DKFZp434L2418_r1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434L2418
1984	11187	20398	2.81	3.0E-37	AL048956.1	EST_HUMAN	DKFZp434L2418_r1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434L2418
2478	11668		4.67	3.0E-37	AW961150.1	EST_HUMAN	EST373222 MAGE resequencing, MAGF Homo sapiens cDNA
2620	12158		3.85	3.0E-37	AW961150.1	EST_HUMAN	EST373222 MAGE resequencing, MAGF Homo sapiens cDNA
386	9680	18917	0.74	2.0E-37	D89780.1	NT	Homo sapiens mRNA for AML1, complete cds
386	9680	18918	0.74	2.0E-37	D89780.1	NT	Homo sapiens mRNA for AML1, complete cds
1088	10312	19465	2.82	2.0E-37	AU131202.1	EST_HUMAN	AU131202 NT2RP3 Homo sapiens cDNA clone NT2RP3002168 5'
1088	10312	19468	2.82	2.0E-37	AU131202.1	EST_HUMAN	AU131202 NT2RP3 Homo sapiens cDNA clone NT2RP3002168 5'
1933	11137	20333	4.55	2.0E-37	AL163247.2	NT	Homo sapiens chromosome 21 segment HS21C047
3871	13087	22203	6.5	2.0E-37	4503210	NT	Homo sapiens cytochrome P450, subfamily XXVIIA (steroid 27-hydroxylase, cerebrotendinous xanthomatosis), polypeptide 1 (CYP27A1b) mRNA
4231	13434	22528	1.04	2.0E-37	4826885	NT	Homo sapiens DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 1 (DDX1) mRNA
5955	15171	24568	3.38	2.0E-37	AA348720.1	EST_HUMAN	EST52831 Fetal heart II Homo sapiens cDNA 5' end
6477	15674	25145	3.78	2.0E-37	BF204032.1	EST_HUMAN	601869157F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4111408 5'
8084	17228	26768	20.18	2.0E-37	AF176013.1	NT	Homo sapiens J domain containing protein 1 isoform b (JDP1) mRNA, complete cds
8908	18021		3.26	2.0E-37	11417872	NT	Homo sapiens pescadillo (zebrafish) homolog 1, containing BRCT domain (PES1), mRNA
9252	18021		3.91	2.0E-37	11417872	NT	Homo sapiens pescadillo (zebrafish) homolog 1, containing BRCT domain (PES1), mRNA
2057	11258	20473	4.06	1.0E-37	AL163281.2	NT	Homo sapiens chromosome 21 segment HS21C081
3161	12986		1.04	1.0E-37	AW862082.1	EST_HUMAN	RC3-CT0347-210400-016-h03 CT0347 Homo sapiens cDNA
3938	13154	22271	1.05	1.0E-37	AF188011.1	NT	Homo sapiens ribonuclease III (RN3) mRNA, complete cds
4859	14146	23238	2.15	1.0E-37	BF31719.1	EST_HUMAN	QV0-FN0180-280700-318-c10 FN0180 Homo sapiens cDNA
6893	15888	25348	3.8	1.0E-37	AA171406.1	EST_HUMAN	zp21b02.r1 Stratiene neuroepithelium (#837231) Homo sapiens cDNA clone IMAGE:810059 5' similar to contains L1.12 L1 repetitive element
7288	16507	25988	6.48	1.0E-37	M22878.1	NT	Human somatic cytochrome c (HC1) processed pseudogene, complete cds
8766	17722		2.73	1.0E-37	BE771814.1	EST_HUMAN	CM3-FT0098-140700-243-d07 FT0098 Homo sapiens cDNA
5564	14788	24158	1.76	9.0E-38	10048482	NT	Rattus norvegicus multidomain presynaptic cytomatrix protein Piccolo (LOC56798), mRNA
1229	10447	18603	1.67	8.0E-38	11438955	NT	Homo sapiens Grb2-associated binder 2 (KIAA0571), mRNA
2462	11653	20875	1.26	8.0E-38	BF346221.1	EST_HUMAN	602018401F1 NCL_CGAP_Bimf7 Homo sapiens cDNA clone IMAGE:4153992 5'
2149	11347	20564	0.52	7.0E-38	AW972825.1	EST_HUMAN	EST384920 MAGE resequencing, MAGL Homo sapiens cDNA
4208	13411	22505	0.7	7.0E-38	H18062.1	EST_HUMAN	Yn51f07.r1 Soares adult brain N25HB55Y Homo sapiens cDNA clone IMAGE:171973 5'
3007	12243	21374	2.28	6.0E-38	BF033033.1	EST_HUMAN	601455722F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3859348 5'
8322	17424		7.1	6.0E-38	11435947	NT	Homo sapiens chromosome 12 open reading frame 3 (C12ORF3), mRNA

PCT/US 01/00670

Table 4

## Single Exon Probes Expressed in HELA Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8830	17742	23933	10.53	6.0E-38	AB002059.1	NT	Homo sapiens DNA for Human P2XM, complete cds
9233	18119	23811	1.25	6.0E-38	11418184	NT	Homo sapiens adenylosuccinate lyase (ADSL), mRNA
734	8875	19114	2.25	5.0E-38	AW971819.1	EST_HUMAN	EST383908 IMAGE resequences, MAGL Homo sapiens cDNA
2417	11608	20830	9.18	5.0E-38	AJ237740.1	NT	Homo sapiens RIBIR gene (partial), exon 8
3685	12808	22028	0.86	5.0E-38	7549804	NT	Homo sapiens deiodinase, iodothyronine, type II (DIO2), transcript variant 2, mRNA
3648	12808	22028	1.69	5.0E-38	7549804	NT	Homo sapiens deiodinase, iodothyronine, type II (DIO2), transcript variant 2, mRNA
6201	11608	20830	1.22	5.0E-38	AJ237740.1	NT	Homo sapiens RIBIR gene (partial), exon 8
6089	15289	24731	3.24	5.0E-38	BE871610.1	EST_HUMAN	601450148F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3854074 5'
119	9405	18536	5.47	4.0E-38	Z25466.1	NT	B.taurus mitochondrial aspartate aminotransferase mRNA, complete CDS
119	9405	18537	5.47	4.0E-38	Z25466.1	NT	B.taurus mitochondrial aspartate aminotransferase mRNA, complete CDS
1165	10387	19538	2.46	3.0E-38	11435947	NT	Homo sapiens chromosome 12 open reading frame 3 (C12ORF3), mRNA
2070	11270		4.56	3.0E-38	AF003530.1	NT	Homo sapiens homeobox protein CDX4 (CDX4) gene, complete cds and flanking repeat regions
3674	12895		1.86	3.0E-38	7549807	NT	Homo sapiens HIRA interacting protein 4 (dnal-like) (HIRIP4), mRNA
3638	13055	22169	1.6	3.0E-38	P53538	SWISSPROT	SSU72 PROTEIN
3638	13055	22170	1.6	3.0E-38	P53538	SWISSPROT	SSU72 PROTEIN
4617	13811		1.61	3.0E-38	BE279301.1	EST_HUMAN	601157633F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3504272 5'
5981	18069	24611	7.19	3.0E-38	AL163300.2	NT	Homo sapiens chromosome 21 segment HS21C100
8328	15510	24956	6.86	3.0E-38	BF373664.1	EST_HUMAN	CM3-F10181-140700-241-407 FT0181 Homo sapiens cDNA
6668	15863	25323	3.23	3.0E-38	H85494.1	EST_HUMAN	yv88b04.r1 Soares melanocyte 2N8HM Homo sapiens cDNA clone IMAGE:249775 5'
6668	15863	25324	3.23	3.0E-38	H85494.1	EST_HUMAN	yv88b04.r1 Soares melanocyte 2N8HM Homo sapiens cDNA clone IMAGE:249775 5'
7865	17055		2.14	3.0E-38	AL163248.2	NT	Homo sapiens chromosome 21 segment HS21C048
8086	10387	19538	1.84	3.0E-38	11435947	NT	Homo sapiens chromosome 12 open reading frame 3 (C12ORF3), mRNA
52	9349	18463	1.6	2.0E-38	AL163248.2	NT	Homo sapiens chromosome 21 segment HS21C048
1387	10601	19766	4.66	2.0E-38	5902067	NT	Homo sapiens SMT3 (suppressor of mit two 3, yeast) homolog 2 (SMT3H2), mRNA
1623	10836	20012	1.58	2.0E-38	AA437353.1	EST_HUMAN	zw30d01.r1 Soares ovary tumor NHOT Homo sapiens cDNA clone IMAGE:770785 5' similar to
1623	10836	20013	1.58	2.0E-38	AA437353.1	EST_HUMAN	zw30d01.r1 Soares ovary tumor NHOT Homo sapiens cDNA clone IMAGE:770785 5' similar to
4579	13773	22868	10.15	2.0E-38	4557867	NT	SW_M412_RABIT_P45701 MANNOSYL-OLIGOSACCHARIDE ALPHA-1,2-MANNOSIDASE :
5150	14328	23418	0.67	2.0E-38	BE298224.1	EST_HUMAN	zw30d01.r1 Soares ovary tumor NHOT Homo sapiens cDNA clone IMAGE:770785 5' similar to
5150	14328	23420	0.67	2.0E-38	BE298224.1	EST_HUMAN	SW_M412_RABIT_P45701 MANNOSYL-OLIGOSACCHARIDE ALPHA-1,2-MANNOSIDASE :
5173	14317	23408	0.75	2.0E-38	AA437181.1	EST_HUMAN	Homo sapiens keratin 18 (KRT18) mRNA
6622	15818		7.88	2.0E-38	BE165980.1	EST_HUMAN	60117386F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3532580 5'
							60117386F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3532580 5'
							zw61d09.r1 Soares testis NHT Homo sapiens cDNA clone IMAGE:758128 5' similar to TR:G817957
							G817957 GLYCINE RECEPTOR SUBUNIT ALPHA 4 :
							MR3-HT0487-150200-113-q01 HT0487 Homo sapiens cDNA



Table 4

## Single Exon Probes Expressed in HELA Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7787	16882	26495	2.23	2.0E-38	AA595480.1	EST_HUMAN	nc34g03.s1 NCI_CGAP_P23 Homo sapiens cDNA clone IMAGE:1102612 3' similar to TR:E212316 E212316 NADP DEPENDENT LEUKOTREINE B4 12-HYDROXYDEHYDROGENASE.;
7787	16882	26496	2.23	2.0E-38	AA595480.1	EST_HUMAN	nc34g03.s1 NCI_CGAP_P23 Homo sapiens cDNA clone IMAGE:1102612 3' similar to TR:E212316 E212316 NADP DEPENDENT LEUKOTREINE B4 12-HYDROXYDEHYDROGENASE.;
8024	17161	26698	6.35	2.0E-38	BE712790.1	EST_HUMAN	QV2-HT0698-080800-283-g05 HT0698 Homo sapiens cDNA
8153	17285	26828	3.85	2.0E-38	AF190501.1	NT	Homo sapiens leucine-rich repeat-containing G protein-coupled receptor 6 (LGR6) mRNA, partial cds
8153	17285	26829	3.85	2.0E-38	AF190501.1	NT	Homo sapiens leucine-rich repeat-containing G protein-coupled receptor 6 (LGR6) mRNA, partial cds
8375	17461		8.04	2.0E-38	AV726988.1	EST_HUMAN	AV726988 HTC Homo sapiens cDNA clone HTCAXH07 5'
8377	17462		2.07	2.0E-38	AB012723.1	NT	Homo sapiens gene for kinesin-like protein, complete cds
8881	17651		1.59	2.0E-38	M55630.1	NT	Human topoisomerase I pseudogene 2
8893	17661	23982	3.6	2.0E-38	H55641.1	EST_HUMAN	CHR220580 Chromosome 22 exon Homo sapiens cDNA clone C22_788 5'
8757	17698		1.89	2.0E-38	S74906.1	NT	E1 beta-pyruvate dehydrogenase beta (promoter) [human, placenta, Genomic, 1280 nt]
8243	18014		2.44	2.0E-38	11418248	NT	Homo sapiens sulfotransferase-related protein (SULTX3), mRNA
1101	10325		2.54	1.0E-38	AA401570.1	EST_HUMAN	zu62b02.r1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:742539 5' similar to contains element MER19 repetitive element;
1968	11172	20378	2.74	1.0E-38	4885288	NT	Homo sapiens guanine nucleotide binding protein-like 1 (GNL1), mRNA
1988	11191	20401	1.19	1.0E-38	7661869	NT	Homo sapiens KIAA0173 gene product (KIAA0173), mRNA
2458	11649	20871	4.36	1.0E-38	AF270631.1	NT	Homo sapiens cyclin K (CCNK) gene, exon 7
2576	11762	20963	1.1	1.0E-38	4758371	NT	Homo sapiens fibrinogen-like 1 (FGL1), mRNA
4137	13343	22444	0.96	1.0E-38	AB037863.1	NT	Homo sapiens mRNA for KIAA1442 protein, partial cds
4310	13511	22805	0.67	1.0E-38	4505016	NT	Homo sapiens low density lipoprotein receptor-related protein 6 (LRP6) mRNA, and translated products
4315	13516	22810	1.56	1.0E-38	AL163203.2	NT	Homo sapiens chromosome 21 segment HS21C003
4316	13516	22811	1.56	1.0E-38	AL163203.2	NT	Homo sapiens chromosome 21 segment HS21C003
4597	13791	22882	1.02	1.0E-38	8922543	NT	Homo sapiens hypothetical protein FLJ10600 (FLJ10600), mRNA
5672	14892	24284	4.04	1.0E-38	7305360	NT	Mus musculus obogelin (Obog), mRNA
5672	14892	24285	4.04	1.0E-38	7305360	NT	Mus musculus obogelin (Obog), mRNA
6254	15435	24874	2.8	1.0E-38	AB014512.1	NT	Homo sapiens mRNA for KIAA0512 protein, partial cds
6881	16072	25541	8.97	1.0E-38	BE350127.1	EST_HUMAN	ht09g01.x1 NCI_CGAP_Kid13 Homo sapiens cDNA clone IMAGE:3146256 3' similar to contains MER29.b3 MER29 repetitive element;
8122	17256	28798	1.81	1.0E-38	7682109	NT	Homo sapiens KIAA0426 gene product (KIAA0426), mRNA
8534	18087		1.97	1.0E-38	AL163284.2	NT	Homo sapiens chromosome 21 segment HS21C084

Page 189 of 382  
Table 4  
Single Exon Probes Expressed in HELA Cells

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
56	9353	18469	5.86	8.0E-39	4502312	NT	Homo sapiens ATPase, H+ transporting, lysosomal (vacuolar proton pump) 16kD (ATP8C) mRNA
1398	10612	18776	1.29	8.0E-39	4758229	NT	Homo sapiens estrogen receptor-binding fragment-associated gene B (EBAG98) mRNA
1797	11006		2.74	8.0E-39	A1823404.1	EST_HUMAN	wh53110.x1 NCI_CGAP_Kid111 Homo sapiens cDNA clone IMAGE:2384491 3' similar to TR:P87890 P87890
2063	11264	20477	5.62	7.0E-39	AL163227.2	NT	POL PROTEIN ;
7386	18600	26088	2.68	6.0E-39	BF331829.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C027
9152	17855		2.33	6.0E-39	BE670394.1	EST_HUMAN	QV1-BT0631-040900-357-02 BT0631 Homo sapiens cDNA
1015	10244	19366	3.22	5.0E-39	AF003528.1	NT	7634c03.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3284356 3' similar to WP:R151.6 CE00828 ;
							Homo sapiens X-linked anhidrotic ectodermal dysplasia protein gene (EDA), exon 2 and flanking repeat regions
2842	12180	21314	8.37	5.0E-39	A1750154.1	EST_HUMAN	at38b04.x1 Barstead colon HPLRB7 Homo sapiens cDNA clone IMAGE:2374063 3' similar to TR:Q15408
8845	17754		2.08	5.0E-39	11420289	NT	Q15408 NEUTRAL PROTEASE LARGE SUBUNIT ; contains LTR7.1 LTR7 repetitive element ;
557	9807	18932	97.11	4.0E-39	AB015610.1	NT	Homo sapiens hypothetical protein FLJ10803 (FLJ10803), mRNA
3548	12771	21899	0.94	4.0E-39	AL163210.2	NT	Chlorococcus aethiops mRNA for ribosomal protein S4X, complete cds
8863	17765		3.91	4.0E-39	11418177	NT	Homo sapiens chromosome 21 segment HS21C010
8883	17848		2.14	4.0E-39	BE836452.1	EST_HUMAN	Homo sapiens Ran GTPase activating protein 1 (RANGAP1), mRNA
49	9346	18457	19.73	3.0E-39	AA631949.1	EST_HUMAN	QV0-FN0063-280600-278-c06 FN0063 Homo sapiens cDNA
49	9346	18458	19.73	3.0E-39	AA631949.1	EST_HUMAN	fmfc16 Regional genomic DNA specific cDNA library Homo sapiens cDNA clone CR12-1
49	9346	18459	19.73	3.0E-39	AA631949.1	EST_HUMAN	fmfc16 Regional genomic DNA specific cDNA library Homo sapiens cDNA clone CR12-1
8366	17455	26583	6.17	3.0E-39	A1084557.1	EST_HUMAN	fmfc16 Regional genomic DNA specific cDNA library Homo sapiens cDNA clone CR12-1
8368	17455	26584	6.17	3.0E-39	A1084557.1	EST_HUMAN	ox63a10.s1 Soares_NhhMPu_S1 Homo sapiens cDNA clone IMAGE:1660986 3' similar to SW:GTR5_RAT
8413	17487		5.95	3.0E-39	H37803.1	EST_HUMAN	P43427 GLUCOSE TRANSPORTER TYPE 5, SMALL INTESTINE ;
907	10142		8.08	2.0E-39	BE409203.1	EST_HUMAN	P43427 GLUCOSE TRANSPORTER TYPE 5, SMALL INTESTINE ;
922	10157		13.75	2.0E-39	A1525119.1	EST_HUMAN	yp51c06.s1 Soares retina N204-HR Homo sapiens cDNA clone IMAGE:180854 3'
1039	10265		3.85	2.0E-39	AF000573.1	NT	601301607F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3636289 5'
1516	10730		99	2.0E-39	AW372318.1	EST_HUMAN	promina-7 D01.r bvtumor Homo sapiens cDNA 5'
1943	11147	20347	2.84	2.0E-39	AA720574.1	EST_HUMAN	Homo sapiens homocitrate 1,2-dioxygenase gene, complete cds
2592	11778	20997	1.47	2.0E-39	AL163248.2	NT	PM0-BT0340-211298-003-d02 BT0340 Homo sapiens cDNA
4397	13598	22699	1.65	2.0E-39	BF370207.1	EST_HUMAN	nmw21g02.s1 NCI_CGAP_GC80 Homo sapiens cDNA clone IMAGE:1241138 3' similar to contains THR.13 THR repetitive element ;
							Homo sapiens chromosome 21 segment HS21C048
							RC4-FN0037-280700-011-a10 FN0037 Homo sapiens cDNA

PCT/US01/00670

Table 4

## Single Exon Probes Expressed in HELA Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5437	14864	23817	4.28	2.0E-39	AA508880.1	EST_HUMAN	ng88703.s1 NCI_CGAP_P16 Homo sapiens cDNA clone IMAGE:941693
6242	15423	24864	2.22	2.0E-39	AA080987.1	EST_HUMAN	z06102.11 Stratagene hNT neuron (#937233) Homo sapiens cDNA clone IMAGE:546651 5'
7970	17149	26885	2.7	2.0E-39	D88964.1	NT	Human mRNA for KIAA0209 gene, partial cds
1502	10715	19887	3.01	1.0E-39	AJ006345.1	NT	Homo sapiens KVLQT1 gene
1502	10715	19888	3.01	1.0E-39	AJ006345.1	NT	Homo sapiens KVLQT1 gene
1517	10731	19800	6.07	1.0E-39	7657020	NT	Homo sapiens DKFZp434P211 protein (DKFZP434P211), mRNA
4663	13857	22955	7.37	1.0E-39	AW951895.1	EST_HUMAN	EST384065 MAGE resequences, MAGB Homo sapiens cDNA
4663	13857	22956	7.37	1.0E-39	AW951895.1	EST_HUMAN	EST384065 MAGE resequences, MAGB Homo sapiens cDNA
4713	13904	23004	11.24	1.0E-39	7657020	NT	Homo sapiens DKFZp434P211 protein (DKFZP434P211), mRNA
5519	14744	24111	4.29	1.0E-39	AJ278170.1	NT	Mus musculus mRNA for neuronal interacting factor X1 (NIX1) (Nix1 gene)
5519	14744	24112	4.29	1.0E-39	AJ278170.1	NT	Mus musculus mRNA for neuronal interacting factor X1 (NIX1) (Nix1 gene)
6008	15258		1.72	1.0E-39	11438738	NT	Homo sapiens tubby like protein 3 (TULP3), mRNA
8240	15421	24882	2.08	1.0E-39	D78132.1	NT	Homo sapiens mRNA for ras-related GTP-binding protein, complete cds
8791	17718		1.28	1.0E-39	U07000.1	NT	Human breakpoint cluster region (BCR) gene, complete cds
562	9812	18935	1.44	9.0E-40	5803210	NT	Homo sapiens UDP-glucose pyrophosphorylase 2 (UGP2), mRNA
1242	10458	19616	12.31	9.0E-40	4755145	NT	Homo sapiens AE-binding protein 1 (AEBP1) mRNA
1242	10458	19617	12.31	9.0E-40	4755145	NT	Homo sapiens AE-binding protein 1 (AEBP1) mRNA
1450	10663	19838	1.29	9.0E-40	4507512	NT	Homo sapiens tissue inhibitor of metalloproteinase 3 (Sorsby fundus dystrophy, pseudoinflammatory) (TIMP3) mRNA
3768	12886	22102	0.8	9.0E-40	4503784	NT	Homo sapiens fragile X mental retardation 1 (FMR1) mRNA
3950	14468	22279	4.18	9.0E-40	AB033070.1	NT	Homo sapiens mRNA for KIAA1244 protein, partial cds
4502	13541	22632	0.6	9.0E-40	4507948	NT	Homo sapiens ubiquitin specific protease 13 (isopeptidase T-3) (USP13) mRNA
3006	12242	21373	0.86	8.0E-40	AA078165.1	EST_HUMAN	7H15A04 Chromosome 7 HeLa cDNA Library Homo sapiens cDNA clone 7H15A04
3808	13114		7.24	8.0E-40	BE39854.1	EST_HUMAN	601288958F1 NIH_MGC_8 Homo sapiens cDNA clone IMAGE:3819166 5'
6383	15563	25019	2.32	7.0E-40	U60325.1	NT	Human DNA polymerase gamma mRNA, nuclear gene encoding mitochondrial protein, complete cds
6383	15563	25020	2.32	7.0E-40	U60325.1	NT	Human DNA polymerase gamma mRNA, nuclear gene encoding mitochondrial protein, complete cds
7473	16681	26164	2.72	7.0E-40	AL163246.2	NT	Homo sapiens chromosome 21 segment HS21C046
2686	11887	21080	5.57	6.0E-40	AA361275.1	EST_HUMAN	EST70527 T-cell lymphoma Homo sapiens cDNA 5' end similar to zinc finger protein family
2686	11887	21081	5.57	6.0E-40	AA361275.1	EST_HUMAN	EST70527 T-cell lymphoma Homo sapiens cDNA 5' end similar to zinc finger protein family
5632	14856		2.07	6.0E-40	BE504766.1	EST_HUMAN	hz40g01.x1 NCI_CGAP_GC8 Homo sapiens cDNA clone IMAGE:3210480 3'

Page 191 of 382  
Table 4  
Single Exon Probes Expressed in HELA Cells

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6057	15228	24845	4.62	6.0E-40	11439783	NT	Homo sapiens fatty acid desaturase 1 (FADS1), mRNA
6057	15228	24846	4.92	6.0E-40	11439783	NT	Homo sapiens fatty acid desaturase 1 (FADS1), mRNA
7084	16241	25715	10.56	6.0E-40	AV653028.1	EST_HUMAN	AV653028 GLC Homo sapiens cDNA clone GLCDGF04 3'
7084	16241	25718	10.56	6.0E-40	AV653028.1	EST_HUMAN	AV653028 GLC Homo sapiens cDNA clone GLCDGF04 3'
2565	11751	20871	3.15	5.0E-40	AL163285.2	NT	Homo sapiens chromosome 21 segment HS21C085
1842	11050	20241	2.09	4.0E-40	AI088005.1	EST_HUMAN	t81b01.x1 NCI_CGAP_P128 Homo sapiens cDNA clone IMAGE:2248873 3' similar to TR:O73505 O73505 POL PROTEIN. ;
2078	11278		4.83	4.0E-40	AF003528.1	NT	Homo sapiens X-linked anhidrotic ectodermal dysplasia protein gene (EDA), exon 2 and flanking repeat regions
4383	13584	22688	9.15	4.0E-40	7682117	NT	Homo sapiens KIAA0433 protein (KIAA0433), mRNA
6460	15657	25128	4.42	4.0E-40	AA742809.1	EST_HUMAN	nv34e10.1 NCI_CGAP_Br4 Homo sapiens cDNA clone IMAGE:1222122
6787	15982	25442	2.71	4.0E-40	BE009416.1	EST_HUMAN	PMO-BN0167-070500-002-h12 BN0167 Homo sapiens cDNA
6787	15982	25443	2.71	4.0E-40	BE009416.1	EST_HUMAN	PMO-BN0167-070500-002-h12 BN0167 Homo sapiens cDNA
7304	16522	26013	1.89	4.0E-40	AW841585.1	EST_HUMAN	RC1-CN0017-120200-012-e04 CN0017 Homo sapiens cDNA
4114	13321	22421	0.89	3.0E-40	AI925949.1	EST_HUMAN	wh1207.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2380548 3'
4889	14077		0.83	3.0E-40	AA055118.1	EST_HUMAN	zf16h09.e1 Soares_fetal_heart_Nb1H19W Homo sapiens cDNA clone IMAGE:377153 3'
5951	15167	24580	7.57	3.0E-40	11417342	NT	Homo sapiens sema domain, seven thrombospondin repeats (type 1 and type 1-like), transmembrane domain (TM) and short cytoplasmic domain, (semaphorin) 5A (SEMA5A), mRNA
6591	15787	25246	5.04	3.0E-40	5454167	NT	Homo sapiens HBV associated factor (XAP4) mRNA
7255	18475	25967	1.91	3.0E-40	D86864.1	NT	Human mRNA for KIAA0209 gene, partial cds
7593	18787	26291	1.91	3.0E-40	BE350127.1	EST_HUMAN	h09g01.x1 NCI_CGAP_Kid13 Homo sapiens cDNA clone IMAGE:3146256 3' similar to contains MER28 b3 MER29 repetitive element ;
7816	17009	26322	14.52	3.0E-40	6005813	NT	Homo sapiens serine threonine protein kinase (NDR), mRNA
330	9800		5.68	2.0E-40	AI223036.1	EST_HUMAN	qg52h08.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1838847 3'
804	10043		9.66	2.0E-40	AW303968.1	EST_HUMAN	xr24e10.x1 NCI_CGAP_U14 Homo sapiens cDNA clone IMAGE:2781098 3' similar to SW:RS5_MOUSE
1763	11002		1.97	2.0E-40	AV731601.1	EST_HUMAN	P67461 40S RIBOSOMAL PROTEIN S5 ;
1903	11109	20302	3.35	2.0E-40	4506188	NT	AV731601 HTF Homo sapiens cDNA clone HTFAZE05 5'
1903	11109	20303	3.35	2.0E-40	4506188	NT	Homo sapiens proteasome (prosome, macropain) subunit, alpha type, 7 (PSMA7) mRNA, and translated products
2038	11240	20448	1.44	2.0E-40	AI988562.1	EST_HUMAN	Homo sapiens proteasome (prosome, macropain) subunit, alpha type, 7 (PSMA7) mRNA, and translated products
2135	11333	20552	1.8	2.0E-40	5453592	NT	w80a11.x1 NCI_CGAP_GC8 Homo sapiens cDNA clone IMAGE:2514716 3' similar to TR:Q91929 Q91929 ZINC FINGER PROTEIN. ;
							Homo sapiens adenyl cyclase-associated protein 2 (CAP2) mRNA

Table 4

## Single Exon Probes Expressed in HELA Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3090	12326	21449	4.72	2.0E-40	5453592	NT	Homo sapiens adenyl cyclase-associated protein 2 (CAP2) mRNA
4922	14110	23208	1.68	2.0E-40	AL163280.2	NT	Homo sapiens chromosome 21 segment HS21C080
4922	14110	23207	1.68	2.0E-40	AL163280.2	NT	Homo sapiens chromosome 21 segment HS21C080
893	10128		1.72	1.0E-40	AA225989.1	EST_HUMAN	nc08a09.s1 NCI_CGAP_P1 Homo sapiens cDNA clone IMAGE:1007608
2584	11770	20680	4.35	1.0E-40	BF036881.1	EST_HUMAN	601460375F1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3863803 5'
2846	11829		2.98	1.0E-40	BE018348.1	EST_HUMAN	bb78a10.y1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3048570 5' similar to TR:Q9Z158 Q9Z158
3267	12500		1.01	1.0E-40	4507142	NT	SYNTAXIN 17.1
4611	13605	22896	5.6	1.0E-40	4508012	NT	Homo sapiens sorting nexin 3 (SNX3) mRNA
6120	15304	24736	2.37	1.0E-40	AA573201.1	EST_HUMAN	Homo sapiens zinc finger protein 200 (ZNF200) mRNA, and translated products
6120	15304	24737	2.37	1.0E-40	AA573201.1	EST_HUMAN	nj42804.s1 NCI_CGAP_AA1 Homo sapiens cDNA clone IMAGE:995167 3'
7491	16698	28183	6.81	1.0E-40	AU146345.1	EST_HUMAN	nj42804.s1 NCI_CGAP_AA1 Homo sapiens cDNA clone IMAGE:995167 3'
8809	18232		8.78	1.0E-40	BF334112.1	EST_HUMAN	AU149345 NT2RM4 Homo sapiens cDNA clone NT2RM4002122 3'
3791	13009	22124	0.91	9.0E-41	W01596.1	EST_HUMAN	MR2-CT0222-211069-002-010 CT0222 Homo sapiens cDNA
6433	15630	25095	2.38	8.0E-41	AL163203.2	NT	za36a02.r1 Soares fetal liver spleen 1NFS Homo sapiens cDNA clone IMAGE:284602 5'
838	11979	19233	1.42	7.0E-41	A1934384.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C003
838	11979	19234	1.42	7.0E-41	A1934384.1	EST_HUMAN	wp04h04.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2463895 3'
4660	13854	22951	1.12	7.0E-41	BE389592.1	EST_HUMAN	wp04h04.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2463895 3'
4660	13854	22952	1.12	7.0E-41	BE389592.1	EST_HUMAN	601282077F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3603955 5'
5261	14434	23508	7.39	7.0E-41	11431114	NT	601282077F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3603955 5'
5658	14881	24270	3.45	7.0E-41	11419208	NT	Homo sapiens hypophyseal protein (FLJ10988), mRNA
7972	17151	26886	1.69	7.0E-41	4758445	NT	Homo sapiens a disintegrin and metalloproteinase domain 22 (ADAM22), mRNA
9250	18228		5.86	7.0E-41	11417972	NT	Homo sapiens guanine nucleotide binding protein 10 (GNG10) mRNA
285	9559	18693	1.26	6.0E-41	AB037163.1	NT	Homo sapiens pescadillo (zabrafish) homolog 1, containing BRCT domain (PES1), mRNA
2081	11281	20497	1.72	6.0E-41	7657042	NT	Homo sapiens DSCR5b mRNA, complete cds
1771	10981	20171	2.49	5.0E-41	T62628.1	EST_HUMAN	Homo sapiens Down syndrome candidate region 1 (DSCR1), mRNA
5901	15118		2.22	5.0E-41	BE087042.1	EST_HUMAN	yc03e10.s1 Stragene lung (#837210) Homo sapiens cDNA clone IMAGE:79626 3'
396	9651		1.87	4.0E-41	BE156318.1	EST_HUMAN	PM4-BT0341-251199-002-F11 BT0341 Homo sapiens cDNA
1106	10330	18480	1.12	4.0E-41	AU119344.1	EST_HUMAN	QV0-H10367-150200-114-g09 HT0367 Homo sapiens cDNA
							AU119344 HEMBA1 Homo sapiens cDNA clone HEMBA1005583 5'
1414	10627	19783	16.08	4.0E-41	A027117.1	EST_HUMAN	ow45e06.s1 Soares parathyroid tumor NbHPA Homo sapiens cDNA clone IMAGE:1649794 3' similar to TR:000597 000597 CYTOCHROME C-LIKE POLYPEPTIDE, contains LTR5.b1 LTR5 repetitive element ;

Page 193 of 382  
Table 4  
Single Exon Probes Expressed in HELA Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1414	10627	18784	16.08	4.0E-41	A1027117.1	EST_HUMAN	ow45606.s1 Soares_parathyroid_tumor_NbHPA Homo sapiens cDNA clone IMAGE:1649784 3' similar to TR:O00597 O00597 CYTOCHROME C-LIKE POLYPEPTIDE :contains LTR5.b1 LTR5 repetitive element ;
1427	10640	19811	2.73	4.0E-41	AB008881.1	NT	Homo sapiens gene for activin receptor type IIB, complete cds
1612	10825	20000	5.77	4.0E-41	A1500408.1	EST_HUMAN	hm96c04.x1 NCL_CGAP_Bm25 Homo sapiens cDNA clone IMAGE:2165958 3' similar to contains OFR.b1 OFR repetitive element ;
2841	12080	21204	4.37	4.0E-41	AJ228041.1	NT	Homo sapiens 959 kb contig between AML1 and CBR1 on chromosome 21q22; segment 1/3
2841	12080	21205	4.37	4.0E-41	AJ228041.1	NT	Homo sapiens 959 kb contig between AML1 and CBR1 on chromosome 21q22; segment 1/3
4126	13332	22430	2.46	4.0E-41	X92895.1	NT	H.sapiens DNase I hypersensitive site (HSS-3) enhancer element
5878	15088		1.77	4.0E-41	AV758295.1	EST_HUMAN	AV758295 BM Homo sapiens cDNA clone BMFBHC08 5'
6900	16168	25640	4.92	4.0E-41	BF304883.1	EST_HUMAN	601888098F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4122119 5'
8174	17306		10.3	4.0E-41	AV710480.1	EST_HUMAN	AV710480 Cu Homo sapiens cDNA clone CuAAC007 5'
8998	18121		1.78	4.0E-41	AV708431.1	EST_HUMAN	AV708431 ADC Homo sapiens cDNA clone ADCARE02 5'
9186	17977	23958	1.4	4.0E-41	BE887118.1	EST_HUMAN	601508315F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3910059 5'
955	10188	19343	2.08	3.0E-41	AB030176.1	NT	Homo sapiens PAD-H18 mRNA for peptidylarginine diaminase type II, complete cds
4327	13528	22622	3.69	3.0E-41	AB028898.1	NT	Homo sapiens DNA, DLEC1 to ORCTL4 gene region, section 1/2 (DLEC1, ORCTL3, ORCTL4 genes, complete cds)
5438	14665	23818	7.72	3.0E-41	X87689.1	NT	H.sapiens mRNA for putative p64 CLCP protein
5825	15042	24446	1.7	3.0E-41	AB037808.1	NT	Homo sapiens mRNA for KIAA1387 protein, partial cds
8220	17350	26888	1.82	3.0E-41	AJ228041.1	NT	Homo sapiens 959 kb contig between AML1 and CBR1 on chromosome 21q22; segment 1/3
8808	17762		1.85	3.0E-41	BF125922.1	EST_HUMAN	601782840F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:4026081 5'
1792	10757	19931	29.38	2.0E-41	U43701.1	NT	Human ribosomal protein L23a mRNA, complete cds
1928	11132	20327	1.52	2.0E-41	AA331940.1	EST_HUMAN	EST35818 Embryo, 8 week I Homo sapiens cDNA 5' and
2185	11382	20606	1.27	2.0E-41	D86962.1	NT	Human mRNA for KIAA0207 gene, complete cds
2233	11428	20654	5.66	2.0E-41	X89631.1	NT	G.gorilla DNA for ZNF80 gene homolog
2780	10757	19931	18.14	2.0E-41	U43701.1	NT	Human ribosomal protein L23a mRNA, complete cds
3300	12631	21663	38.48	2.0E-41	AA449549.1	EST_HUMAN	zx08004.r1 Soares_total_fetus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:785839 5'
4624	13818	22908	1.43	2.0E-41	AL163267.2	NT	Homo sapiens chromosome 21 segment HS21C067
4624	13818	22909	1.43	2.0E-41	AL163267.2	NT	Homo sapiens chromosome 21 segment HS21C067
6366	15546	25001	6.72	2.0E-41	AF038404.1	NT	Homo sapiens homolog of Nedd5 (hNedd5) mRNA, complete cds
6487	15684	25151	2.25	2.0E-41	M96944.1	NT	Human B-cell specific transcription factor (BSAP) mRNA, complete cds
6487	15684	25152	2.25	2.0E-41	M96944.1	NT	Human B-cell specific transcription factor (BSAP) mRNA, complete cds
8020	17159	26695	3.94	2.0E-41	AA372637.1	EST_HUMAN	EST84555 Colon adenocarcinoma IV Homo sapiens cDNA 5' end
3171	12406	21540	1.16	1.0E-41	BE869735.1	EST_HUMAN	601445647F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3849803 5'

Page 194 of 382  
Table 4  
Single Exon Probes Expressed in HELA Cells

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3171	12408	21541	1.16	1.0E-41	BE989735.1	EST_HUMAN	601445847F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3849803 5'
4564	13758	22855	10.99	1.0E-41	6878468	NT	Mus musculus tubulin alpha 6 (Tubae6), mRNA
8462	17517		2.57	1.0E-41	11526291	NT	Homo sapiens hypothetical protein FLJ20454 (FLJ20454), mRNA
469	9722	18653	6.13	8.0E-42	AF003530.1	NT	Homo sapiens homeobox protein CDX4 (CDX4) gene, complete cds and flanking repeat regions
2079	11279	20495	2.22	8.0E-42	AB026898.1	NT	Homo sapiens DNA, DLEC1 to ORCTL4 gene region, section 1/2 (DLEC1, ORCTL3, ORCTL4 genes, complete cds)
8508	18236		29.5	8.0E-42	AA493896.1	EST_HUMAN	nh07c02.s1 NCI_CGAP_Thy1 Homo sapiens cDNA clone IMAGE:943586 similar to TR:G434304 G434304 367BP EXPRESSED SEQUENCE TAG MRNA :
8528	18109		1.24	8.0E-42	AW089062.1	EST_HUMAN	xc97a04.x1 NCI_CGAP_Bn35 Homo sapiens cDNA clone IMAGE:2592174 3' similar to contains OFR.12
940	10173		3.09	7.0E-42	AL163285.2	NT	OFR repetitive element :
8838	18043	25507	2.35	7.0E-42	AI204358.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C085
1823	11031	20224	16.53	6.0E-42	AF012872.1	NT	qf58g12.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1754278 3'
1823	11031	20225	16.53	6.0E-42	AF012872.1	NT	Homo sapiens phosphatidylinositol 4-kinase 230 (pi4K230) mRNA, complete cds
2253	11448		2.87	6.0E-42	AW238656.1	EST_HUMAN	Homo sapiens phosphatidylinositol 4-kinase 230 (pi4K230) mRNA, complete cds
133	9416		5.67	5.0E-42	AJ271735.1	NT	xp29f08.x1 NCI_CGAP_HN10 Homo sapiens cDNA clone IMAGE:2741799 3' similar to contains L1.t1 L1 repetitive element :
444	9698	18834	1.43	5.0E-42	BE217913.1	EST_HUMAN	Homo sapiens Xq pseudocentromeric region; segment 1/2
493	9746		3.16	5.0E-42	5730038	NT	h31e11.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3175052 3'
494	9747		2.91	5.0E-42	5730038	NT	Homo sapiens SET domain and mariner transposase fusion gene (SETMAR) mRNA
5988	15280	24712	2.51	5.0E-42	11417957	NT	Homo sapiens SET domain and mariner transposase fusion gene (SETMAR) mRNA
6166	15348	24788	1.74	5.0E-42	AF071569.1	NT	Homo sapiens myotubularin related protein 3 (MTMR3), mRNA
7569	16774	26267	2.28	5.0E-42	8923162	NT	Homo sapiens multifunctional calcium/calmodulin-dependent protein kinase II delta2 isoform mRNA, complete cds
761	10002	19149	18.41	4.0E-42	AF050688.1	NT	Homo sapiens hypothetical protein FLJ20163 (FLJ20163), mRNA
761	10002	19150	18.41	4.0E-42	AF050688.1	NT	Homo sapiens MHC class 1 region
1073	10288	19448	2.86	4.0E-42	AF168011.1	NT	Homo sapiens MHC class 1 region
4176	13380	22481	1.79	4.0E-42	X59417.1	NT	Homo sapiens ribonuclease III (RN3) mRNA, complete cds
4235	13438	22631	5.5	4.0E-42	4508498	NT	H. sapiens PROS-27 mRNA
4582	13776	22869	16.6	4.0E-42	4508008	NT	Homo sapiens regulatory factor X, 4 (influences HLA class II expression) (RFK4) mRNA
5196	14372	23459	1.04	4.0E-42	7661635	NT	Homo sapiens zinc finger protein 177 (ZNF177) mRNA
7242	18462	25951	1.76	4.0E-42	AW818630.1	EST_HUMAN	Homo sapiens DKFZP564O2082 protein (DKFZP564O2082), mRNA
7242	18462	25952	1.76	4.0E-42	AW818630.1	EST_HUMAN	RC1-S10278-040400-018-h11 S10278 Homo sapiens cDNA
7951	17080	26820	3.51	4.0E-42	BF035327.1	EST_HUMAN	RC1-S10278-040400-018-h11 S10278 Homo sapiens cDNA
							601458531F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3882086 5'

Table 4

## Single Exon Probes Expressed in HELA Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1478	10889	18866	2.54	2.0E-42	BF376834.1	EST_HUMAN	RCO-TN0079-110900-024-g07 TN0079 Homo sapiens cDNA
2358	11549	20770	1.77	2.0E-42	AV680218.1	EST_HUMAN	AV680218 GKC Homo sapiens cDNA clone GKCCBB08 5'
2375	11568		3.56	2.0E-42	AW898344.1	EST_HUMAN	RC3-NN0070-270400-011-h10 NN0070 Homo sapiens cDNA
2389	11582	20769	24.12	2.0E-42	AW260059.1	EST_HUMAN	2819283.3prime NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2819283 3'
5554	14778	24145	17	2.0E-42	AW955368.1	EST_HUMAN	EST367438 MAGC resequences, MAGC Homo sapiens cDNA
5554	14778	24146	17	2.0E-42	AW955368.1	EST_HUMAN	EST367438 MAGC resequences, MAGC Homo sapiens cDNA
8229	17358	26897	2	2.0E-42	AL183246.2	NT	Homo sapiens chromosome 21 segment HS21C046
741	9981	19124	1.41	1.0E-42	X57147.1	NT	Human endogenous retrovirus pHE.1 (ERV9)
1049	10275	19428	1.78	1.0E-42	AW285809.1	EST_HUMAN	UHL-B11-aff-e-04-0-J1.s1 NCI_CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2721871 3'
1108	10333	19483	1.58	1.0E-42	AJ251818.1	NT	Homo sapiens partial C9 gene for complement component C9, exon 1
1109	10333	19484	1.58	1.0E-42	AJ251818.1	NT	Homo sapiens partial C9 gene for complement component C9, exon 1
1249	11889	19628	12.22	1.0E-42	AF087166.1	NT	Homo sapiens NADH-ubiquinone oxidoreductase AGGG subunit precursor homolog mRNA, nuclear gene encoding mitochondrial protein, complete cds
1249	11889	19628	12.22	1.0E-42	AF087166.1	NT	Homo sapiens NADH-ubiquinone oxidoreductase AGGG subunit precursor homolog mRNA, nuclear gene encoding mitochondrial protein, complete cds
1675	10887	20073	1.1	1.0E-42	11423219	NT	Homo sapiens rec (LOC51201), mRNA
2509	11698	20915	2.09	1.0E-42	5174458	NT	Homo sapiens major histocompatibility complex, class II, DM alpha (HLA-DMA) mRNA
2919	12157	21292	10.03	1.0E-42	4505524	NT	Homo sapiens origin recognition complex, subunit 5 (yeast homolog)-like (ORC5L) mRNA, and translated products
3698	12909	22028	2.23	1.0E-42	7682027	NT	Homo sapiens KIAA0255 gene product (KIAA0255), mRNA
3777	12995	22111	1.02	1.0E-42	5031610	NT	Homo sapiens Golgi vesicular membrane trafficking protein p18 (BET1) mRNA
3900	13116	22233	1.09	1.0E-42	AL163287.2	NT	Homo sapiens chromosome 21 segment HS21C067
4232	13435	22529	2.23	1.0E-42	AL163280.2	NT	Homo sapiens chromosome 21 segment HS21C080
4758	13949	23050	2.4	1.0E-42	5803122	NT	Homo sapiens chromosome 21 segment HS21C080
4758	13949	23051	2.4	1.0E-42	5803122	NT	Homo sapiens proteasome inhibitor (PI31), mRNA
4788	13977	23081	6.15	1.0E-42	4506758	NT	Homo sapiens proteasome inhibitor (PI31), mRNA
4887	14075	23173	1.22	1.0E-42	AB033114.1	NT	Homo sapiens ryanodine receptor 3 (RYR3) mRNA
7562	16767	26258	1.67	1.0E-42	11437455	NT	Homo sapiens mRNA for KIAA1288 protein, partial cds
7104	16281	25761	6.25	9.0E-43	4757869	NT	Homo sapiens chromatin-specific transcription elongation factor, 140 kDa subunit (FACTP140), mRNA
7607	16810	26305	3.42	9.0E-43	AA435719.1	EST_HUMAN	Homo sapiens chromodomain protein, Y chromosome-like (CDYL) mRNA
658	8904	19030	14.02	8.0E-43	AV736824.1	EST_HUMAN	z179a07.s1 Soares testis NHT Homo sapiens cDNA clone IMAGE:728532 3'
658	8904	19031	14.02	8.0E-43	AV736824.1	EST_HUMAN	AV736824 CB Homo sapiens cDNA clone CBLAKH08 5'
707	8949	19085	4.54	8.0E-43	8823276	NT	AV736824 CB Homo sapiens cDNA clone CBLAKH08 5'
							Homo sapiens hypothetical protein FLJ20287 (FLJ20287), mRNA



PCT/US01/00670

Table 4

## Single Exon Probes Expressed in HELA Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
707	9949	19086	4.54	8.0E-43	8923276	NT	Homo sapiens hypothetical protein FLJ20287 (FLJ20287), mRNA
707	9949	19087	4.64	8.0E-43	8923276	NT	Homo sapiens hypothetical protein FLJ20287 (FLJ20287), mRNA
3620	12841	21960	8	7.0E-43	AW249442.1	EST_HUMAN	2822251.5prime NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2822251 5'
6707	16802		6.35	7.0E-43	A1938748.1	EST_HUMAN	wp69b01.x1 NCI_CGAP_Bm25 Homo sapiens cDNA clone IMAGE:2466985 3' similar to TR:O15475 O15475 UNNAMED HERV-H PROTEIN ; contains LTR7.b1 LTR7 repetitive element ; ne72d06.s1 NCI_CGAP_Ew1 Homo sapiens cDNA clone IMAGE:909803 similar to gb.L05085 60S
1351	10566		18.5	6.0E-43	AA491890.1	EST_HUMAN	RIBOSOMAL PROTEIN L30 (HUMAN);
2552	11740		2.84	6.0E-43	AV708201.1	EST_HUMAN	AV708201 ADC Homo sapiens cDNA clone ADCACC10 5'
5783	15010	24414	2.46	6.0E-43	9955873	NT	Homo sapiens ATP-binding cassette, sub-family C (CFTR/MRP), member 3 (ABCC3), transcript variant MRP3B, mRNA
6045	15213	24633	1.97	6.0E-43	AW468897.1	EST_HUMAN	hd30b04.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2910991 3' similar to contains MER1.13 MER1 MER1 repetitive element ;
7666	18665		6.52	6.0E-43	AL119158.1	EST_HUMAN	DKFZp761L1712.1 761 (synonym: ham2) Homo sapiens cDNA clone DKFZp761L1712 5'
140	9422		2.31	5.0E-43	AL163213.2	NT	Homo sapiens chromosome 21 segment HS21C013
509	9761	18887	2.47	5.0E-43	AA382780.1	EST_HUMAN	EST196033 Testis 1 Homo sapiens cDNA 5' and
2788	12039	21161	1.47	5.0E-43	AV732578.1	EST_HUMAN	AV732578 HTF Homo sapiens cDNA clone HTFANC08 5'
6868	16090	25557	5	5.0E-43	AA465288.1	EST_HUMAN	aa33d08.r1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:815055 5' oo52c10.x5 NCI_CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1569810 3' similar to TR:P80591 P80591 PV14 GENE ;
7187	16364	25944	2.95	5.0E-43	A1733244.1	EST_HUMAN	MR2-SN0007-290400-004-c02 SN0007 Homo sapiens cDNA
7348	16364	26053	5.41	5.0E-43	AW863007.1	EST_HUMAN	55a4 Human retina cDNA randomly primed sublibrary Homo sapiens cDNA
7542	16747	26241	1.68	5.0E-43	W28011.1	EST_HUMAN	Human mRNA for alpha-actinin
7993	16428	25915	2.26	5.0E-43	X15804.1	NT	Homo sapiens X-linked anhidrotic ectodermal dysplasia protein gene (EDA), exon 2 and flanking repeat regions
980	11943	19367	9.87	4.0E-43	AF003528.1	NT	Homo sapiens protocadherin beta 6 (PCDH6), mRNA
8131	15315		2.02	4.0E-43	11416793	NT	q176a02.x1 NCI_CGAP_Ki43 Homo sapiens cDNA clone IMAGE:1865354 3' similar to contains MER10.13 MER10 repetitive element ;
6519	15715	25180	4.94	4.0E-43	A1244341.1	EST_HUMAN	q176a02.x1 NCI_CGAP_Ki43 Homo sapiens cDNA clone IMAGE:1865354 3' similar to contains MER10.13 MER10 repetitive element ;
6519	15715	25181	4.94	4.0E-43	A1244341.1	EST_HUMAN	q176a02.x1 NCI_CGAP_Ki43 Homo sapiens cDNA clone IMAGE:1865354 3' similar to contains MER10.13 MER10 repetitive element ;
7852	17042	26559	1.73	4.0E-43	777380.1	EST_HUMAN	yd7zh10.r1 Soares fetal liver spleen 1NFSL Homo sapiens cDNA clone IMAGE:113827 5' yp06b05.r1 Soares infant brain 1NIB Homo sapiens cDNA clone IMAGE:31363 5' similar to contains MER10 repetitive element ;
8438	17502		3.09	4.0E-43	R20950.1	EST_HUMAN	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced
1221	10439		2.8	3.0E-43	AF223391.1	NT	

PL 1 / US 01 / 006 / 0

Page 197 of 382  
Table 4  
Single Exon Probes Expressed in HELA Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1870	10883	20087	4.5	3.0E-43	X97869.1	NT	H. sapiens gene encoding La autoantigen
3547	12770	21898	1.47	3.0E-43	S69002.1	NT	AML1-EVI-1=AML1-EVI-1 fusion protein (rearranged translocation) [human, leukemic cell line SKH1, mRNA Mutant, 5938 nt]
4277	13480	22578	1.1	3.0E-43	AA548154.1	EST_HUMAN	nk55d06.s1 NCL_CGAP_P7 Homo sapiens cDNA clone IMAGE:1017419
5875	15189	24808	4.19	3.0E-43	U65487.1	NT	Human ribosomal RNA upstream binding transcription factor (UBTF) gene, partial cds
6513	15709		8.19	3.0E-43	AA458824.1	EST_HUMAN	aa88f11.s1 Stratagene fetal retina 937202 Homo sapiens cDNA clone IMAGE:838413 3' similar to contains THR.12 THR repetitive element;
6724	15919	25378	2.48	3.0E-43	7661721	NT	Homo sapiens SET domain and mariner transposase fusion gene (SETMAR) mRNA
8218	17347	26887	2.04	3.0E-43	5730038	NT	qd61c09.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1733988 3' similar to contains PTR7.13 PTR7 PTR7 repetitive element;
188	9467		10.09	2.0E-43	AI180764.1	EST_HUMAN	Human ribosomal protein L23a mRNA, complete cds
6563	15759		7.03	2.0E-43	U43701.1	NT	FB1G5 Fetal brain, Stratagene Homo sapiens cDNA clone FB1G5 3' end similar to LINE-1
7752	16948		8.09	2.0E-43	T03007.1	EST_HUMAN	Homo sapiens Ras-like GTP-binding protein (RAB27A) gene, exons 1b and 2
1627	10840	20018	4.81	1.0E-43	AF154838.1	NT	Homo sapiens Ras-like GTP-binding protein (RAB27A) gene, exons 1b and 2
1627	10840	20017	4.81	1.0E-43	AF154838.1	NT	Homo sapiens Ras-like GTP-binding protein (RAB27A) gene, exons 1b and 2
1680	10892	20078	2.93	1.0E-43	AL163284.2	NT	Homo sapiens chromosome 21 segment HS21C084
2683	11865	21077	3.71	1.0E-43	BF348283.1	EST_HUMAN	602022313F1 NCL_CGAP_Bim87 Homo sapiens cDNA clone IMAGE:4157668 5'
5839	15155	24566	7.68	1.0E-43	4507168	NT	Homo sapiens Sp4 transcription factor (SP4) mRNA
5839	15155	24567	7.68	1.0E-43	4507168	NT	Homo sapiens Sp4 transcription factor (SP4) mRNA
6071	14518	23560	1.79	1.0E-43	R19751.1	EST_HUMAN	y940e01.r1 Soares infant brain 1N1B Homo sapiens cDNA clone IMAGE:34732 5' similar to SP-BD38 MOUSE P28658 BRAIN PROTEIN DN38 ;
6488	15883		2.86	1.0E-43	AF188490.1	NT	Homo sapiens 8q22.1 region and MTG8 (CBFA2T1) gene, partial cds
6730	15925	25384	39.18	1.0E-43	AW963676.1	EST_HUMAN	EST1375749 IMAGE resequences, MAGH Homo sapiens cDNA
7535	16740	26231	7.71	1.0E-43	AI984961.1	EST_HUMAN	wr87h01.x1 NCL_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2494705 3'
7905	17120	26651	3.87	1.0E-43	11424378	NT	Homo sapiens calcium channel, voltage-dependent, alpha 1E subunit (CACNA1E), mRNA
8379	17464		3.42	1.0E-43	AL137864.1	EST_HUMAN	DKFZ6761D1015_r1.761 (synonym: hamy2) Homo sapiens cDNA clone DKFZ6761D1015 5'
8685	17954	23980	2.23	1.0E-43	AI675416.1	EST_HUMAN	wb98b04.x1 NCL_CGAP_P228 Homo sapiens cDNA clone IMAGE:2313775 3'
8814	17802	23927	3.14	8.0E-44	11418322	NT	Homo sapiens cadherin EGF LAG seven-pass G-type receptor 1 (CELSR1), mRNA
900	10135	19287	7.56	8.0E-44	AI222985.1	EST_HUMAN	qh23g01.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1845552 3'
900	10135	19288	7.56	8.0E-44	AI222985.1	EST_HUMAN	qh23g01.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1845552 3'
7723	16922	26431	3.57	8.0E-44	Y10498.2	NT	Homo sapiens mRNA for thymidine kinase, partial
8185	17317	26861	2.01	8.0E-44	L29139.1	NT	Homo sapiens myosin mRNA, partial cds
8636	17825	23974	3.72	8.0E-44	11527389	NT	Homo sapiens polymerase (RNA) II (DNA directed) polypeptide F (POLR2F), mRNA
8878	17960	23864	1.44	8.0E-44	11418086	NT	Homo sapiens putative nuclear protein (HRIHFB2122), mRNA

Table 4

## Single Exon Probes Expressed in HELA Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9048	18142	23749	2.3	8.0E-44	11418099	NT	Homo sapiens protein kinase C, alpha binding protein (PRKCABP), mRNA
665	9811		0.83	7.0E-44	R06035.1	EST_HUMAN	yes89e01.1 Soares fetal liver spleen 1NLS Homo sapiens cDNA clone IMAGE:124920 5'
2200	11397	20621	1.86	7.0E-44	5031886	NT	Homo sapiens LIM domain-containing preferred translocation partner in lipoma (LPP) mRNA
2921	12159	21263	1.71	7.0E-44	AF048728.1	NT	Homo sapiens minisatellite ms32 repeat region
2921	12159	21284	1.71	7.0E-44	AF048728.1	NT	Homo sapiens minisatellite ms32 repeat region
3844	13061	22175	2.85	7.0E-44	AL163284.2	NT	Homo sapiens chromosome 21 segment HS21C084
4227	13430	22522	1.29	7.0E-44	AF231918.1	NT	Homo sapiens chromosome 21 unknown mRNA
4227	13430	22523	1.29	7.0E-44	AF231918.1	NT	Homo sapiens chromosome 21 unknown mRNA
6524	15720	25184	4.61	7.0E-44	AU159839.1	EST_HUMAN	AU159839 Y79AA1 Homo sapiens cDNA clone Y79AA1000496 3'
8248	17375	26909	3.42	6.0E-44	AW954050.1	EST_HUMAN	EST366120 MAGEA1 Homo sapiens cDNA clone MAGEA1000496 3'
308	9581		2.5	5.0E-44	AJ289880.1	NT	Homo sapiens KIAA0851 gene (partial), X13 gene and LZTFL1 gene
337	9605		2.23	5.0E-44	AJ289880.1	NT	Homo sapiens KIAA0851 gene (partial), X13 gene and LZTFL1 gene
6424	15621	25085	4.3	5.0E-44	AI688523.1	EST_HUMAN	tr40d02.x1 NCL CGAP_Brn25 Homo sapiens cDNA clone IMAGE:2170083 3' similar to contains OFR.11
6872	16094		2.33	5.0E-44	AU124571.1	EST_HUMAN	OFR OFR repetitive element ;
3392	12619	21750	2.73	4.0E-44	AL163303.2	NT	AU124571 NT2RM4 Homo sapiens cDNA clone NT2RM4000218 5'
5039	14223		1.73	4.0E-44	AI435225.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C103
7789	16983	26497	3.15	4.0E-44	U90878.1	NT	Bt1402.x1 NCL CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2130147 3'
1756	10967		1.21	3.0E-44	6912477	NT	Homo sapiens carboxyl terminal LIM domain protein (CLIM1) mRNA, complete cds
2497	11686	20905	3.27	3.0E-44	BE880626.1	EST_HUMAN	Homo sapiens karyopherin alpha 6 (importin alpha 7) (KPNAB), mRNA
3063	12269	21423	6.4	3.0E-44	AA169851.1	EST_HUMAN	601491529F1 NIH_MGC_69 Homo sapiens cDNA clone IMAGE:3893839 5'
1056	10282	19432	2.91	2.0E-44	4826685	NT	zp18505.1 Stragene fetal retina 937202 Homo sapiens cDNA clone IMAGE:609777 5'
1056	10282	19433	2.91	2.0E-44	4826685	NT	Homo sapiens DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 1 (DDX1) mRNA
1216	10433	19589	5.8	2.0E-44	5803200	NT	Homo sapiens DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 1 (DDX1) mRNA
1215	10433	19590	5.8	2.0E-44	5803200	NT	Homo sapiens transmembrane trafficking protein (TMP21), mRNA
1319	10534	19698	2.92	2.0E-44	AF133588.1	NT	Homo sapiens transmembrane trafficking protein (TMP21), mRNA
1376	10580	19756	1.34	2.0E-44	BE465325.1	EST_HUMAN	Homo sapiens RAB36 (RAB36) mRNA, complete cds
2120	11319	20537	1.6	2.0E-44	AF070651.1	NT	hw14g06.x1 NCL CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3182838 3' similar to SW:OXYB_HUMAN
2571	11796		1.59	2.0E-44	5901833	NT	P22059 OXYSTEROL-BINDING PROTEIN ;
3447	12672	21807	1.06	2.0E-44	D87875.1	NT	Homo sapiens tissue-type bone marrow zinc finger protein 4 mRNA, complete cds
4567	13761	22857	1.87	2.0E-44	AW864379.1	EST_HUMAN	Homo sapiens adaptor-related protein complex 4, sigma 1 subunit (CLAPS4), mRNA
6256	15437	24876	4.1	2.0E-44	114192226	NT	Homo sapiens DNA for amyloid precursor protein, complete cds
6256	15437	24877	4.1	2.0E-44	114192226	NT	PM4-SN0016-120500-003-004 SN0016 Homo sapiens cDNA
							Homo sapiens glutamate receptor, metabotropic 3 (GRM3), mRNA
							Homo sapiens glutamate receptor, metabotropic 3 (GRM3), mRNA

Page 199 of 382  
Table 4  
Single Exon Probes Expressed in HELA Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8283	17389		1.56	2.0E-44	BE244802.1	EST_HUMAN	TCBAP1E2785 Pediatric pre-B cell acute lymphoblastic leukemia Baylor-HGSC project=TC8A Homo sapiens cDNA clone TCBAP2795
54	9351	18486	5.21	1.0E-44	7657334	NT	Homo sapiens Misschapan/NIK-related kinase (MINK), mRNA
54	9351	18487	5.21	1.0E-44	7657334	NT	Homo sapiens Misschapan/NIK-related kinase (MINK), mRNA
587	9835	18954	2.08	1.0E-44	AW653132.1	EST_HUMAN	RC1-CT0249-030300-026-h12 CT0249 Homo sapiens cDNA
1205	10424		1.61	1.0E-44	AW684803.1	EST_HUMAN	RC1-BN0039-110300-012-b01 BN0039 Homo sapiens cDNA
1553	10767		6.02	1.0E-44	AL163303.2	NT	Homo sapiens chromosome 21 segment HS21C103
2191	11388	20610	4.39	1.0E-44	AA434554.1	EST_HUMAN	zw53402.r1 Soares_tet1_tet1_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:773763 5' similar to contains THR13 THR repetitive element ;
2191	11388	20611	4.39	1.0E-44	AA434554.1	EST_HUMAN	zw53402.r1 Soares_tet1_tet1_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:773763 5' similar to contains THR13 THR repetitive element ;
2715	11894	21111	1.46	1.0E-44	AF198779.1	NT	Homo sapiens transcription factor (GHM enhancer 3, JM11 protein, JM4 protein, JM5 protein, T54 protein, JM10 protein, A4 differentiation-dependent protein, triple LIM domain protein 6, and synaptophysin genes, complete cds; and L-type calcium channel a2)
3706	12928		4.68	1.0E-44	AA458869.1	EST_HUMAN	aa01c09.s1 Soares_Nhi-IMPu_S1 Homo sapiens cDNA clone IMAGE:811984 3'
7584	16789		11.94	1.0E-44	AV714608.1	EST_HUMAN	AV714608 DCB Homo sapiens cDNA clone DCBBYE03 5'
8061	17186	26735	4.59	1.0E-44	10092664	NT	Homo sapiens Sush1 domain (SCR repeat) containing (BK55A6.2), mRNA
8117	17251	26781	3.02	1.0E-44	AW846967.1	EST_HUMAN	RC1-CT0198-150999-011-C08 CT0198 Homo sapiens cDNA
8117	17251	26792	3.02	1.0E-44	AW846967.1	EST_HUMAN	RC1-CT0198-150999-011-C08 CT0198 Homo sapiens cDNA
4576	13770	22865	1.21	9.0E-45	8922391	NT	Homo sapiens hypothetical protein FLJ10379 (FLJ10379), mRNA
4576	13770	22866	1.21	9.0E-45	8922391	NT	Homo sapiens hypothetical protein FLJ10379 (FLJ10379), mRNA
2490	11680	20897	16.54	8.0E-45	5174718	NT	Homo sapiens TRK-fused gene (NOTE: non-standard symbol and name) (TFG) mRNA
5112	14292	23379	7.98	8.0E-45	5174718	NT	Homo sapiens TRK-fused gene (NOTE: non-standard symbol and name) (TFG) mRNA
2811	12149		1.44	7.0E-45	AL160131.1	NT	Novel human gene mapping to chromosome 22
3956	13171		7.02	6.0E-45	AW157570.1	EST_HUMAN	au83h07.x1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2782809 3' similar to SW:R13A_HUMAN P40429 60S RIBOSOMAL PROTEIN L13A ;
9008	18340		1.27	6.0E-45	11418213	NT	Homo sapiens ADP-ribosylation factor GTPase activating protein 1 (ARFGAP1), mRNA
802	10137		1.9	5.0E-45	AL163203.2	NT	Homo sapiens chromosome 21 segment HS21C003
1971	11175	20381	4.35	5.0E-45	BF333627.1	EST_HUMAN	CM4-CN0044-180200-515-f01 CN0044 Homo sapiens cDNA
3176	12411	21547	2	5.0E-45	AI523766.1	EST_HUMAN	tg94f07.x1 NCJ_CGAP_GLI.1 Homo sapiens cDNA clone IMAGE:2116453 3' similar to SW:PAX1_MOUSE
5445	14671	23829	8.89	5.0E-45	AA397781.1	EST_HUMAN	P09084 PAIRED BOX PROTEIN PAX-1 ;
6778	15873	25430	2.31	5.0E-45	4759223	NT	z172d03.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:727677 3' similar to contains element TAR1 repetitive element ;
							Homo sapiens programmed cell death 5 (PDCD5), mRNA

Table 4  
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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8192	17324	26867	2.63	5.0E-45	8923698	NT	Homo sapiens golgin-like protein (GLP), mRNA
1152	10374	19525	11.82	4.0E-45	X95828.1	NT	H. sapiens ART4 gene
2255	11450	20669	3.36	4.0E-45	BE265622.1	EST_HUMAN	601184440F1 NIH_MGC 7 Homo sapiens cDNA clone IMAGE:3538425 5'
							h036h04.x1 NCL_CGAP_U01 Homo sapiens cDNA clone IMAGE:3039511 3' similar to contains MER28.b3
8261	17388		1.68	4.0E-45	BE044076.1	EST_HUMAN	MER28 repetitive element.
8298	18265	23684	2.19	4.0E-45	11435947	NT	Homo sapiens chromosome 12 open reading frame 3 (C12ORF3), mRNA
8907	17798		2.18	4.0E-45	BF676077.1	EST_HUMAN	602084052F1 NIH_MGC 83 Homo sapiens cDNA clone IMAGE:4248253 5'
3305	12535		0.97	3.0E-45	171480.1	EST_HUMAN	y435107.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:110245 5'
4063	12535		0.95	3.0E-45	171480.1	EST_HUMAN	y435107.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:110245 5'
5244	14417		1.88	3.0E-45	AJ269473.1	NT	Homo sapiens mRNA for TRAF and TNF receptor associated protein (trap gene)
6713	15908	25367	2.57	3.0E-45	4758451	NT	Homo sapiens golgi autoantigen, golgin subfamily a, 2 (GOLGA2) mRNA
7168	16345	25824	16.25	3.0E-45	AL163227.2	NT	Homo sapiens chromosome 21 segment HS21C027
7168	16345	25825	16.25	3.0E-45	AL163227.2	NT	Homo sapiens chromosome 21 segment HS21C027
9127	18274		1.98	3.0E-45	X89211.1	NT	H. sapiens DNA for endogenous retroviral like element
2466	11657		1.59	2.0E-45	AL163218.2	NT	Homo sapiens chromosome 21 segment HS21C018
2998	12234	21364	0.96	2.0E-45	AJ243213.1	NT	Homo sapiens partial 5-HT4 receptor gene, exons 2 to 5
5888	15103	24514	5.4	2.0E-45	L01865.1	NT	Human eosinophil Charcot-Leyden crystal (CLC) protein (lysophospholipase) gene, promoter and exon 1
7381	18077	26084	21.36	2.0E-45	BE634350.1	EST_HUMAN	MRO-HT0923-190800-201-e02 HT0923 Homo sapiens cDNA
							aa87112.r1 Strategene fetal refina 837202 Homo sapiens cDNA clone IMAGE:838319 5' similar to
7732	16929	26437	4.48	2.0E-45	AA458770.1	EST_HUMAN	TR:G1144569 G1144569 R-SLY1.
8037	17173	26712	2.46	2.0E-45	AW270280.1	EST_HUMAN	xp72a03.x1 NCL_CGAP_Ov40 Homo sapiens cDNA clone IMAGE:2745868 3'
8037	17173	26713	2.46	2.0E-45	AW270280.1	EST_HUMAN	xp72a03.x1 NCL_CGAP_Ov40 Homo sapiens cDNA clone IMAGE:2745868 3'
9169	17964		2.9	2.0E-45	11418157	NT	Homo sapiens calcium channel, voltage-dependent, alpha 1I subunit (CACNA1I), mRNA
122	9688		3.43	1.0E-45	BE388855.1	EST_HUMAN	601284360F1 NIH_MGC 44 Homo sapiens cDNA clone IMAGE:3606183 5'
415	9688		3.92	1.0E-45	BE388855.1	EST_HUMAN	601284360F1 NIH_MGC 44 Homo sapiens cDNA clone IMAGE:3606183 5'
479	9731	18865	0.96	1.0E-45	4506412	NT	Homo sapiens RAP1A, member of RAS oncogene family (RAP1A), mRNA
1182	10403	19557	1.87	1.0E-45	7857290	NT	Homo sapiens Langerhans cell specific c-type lectin (LANGERIN), mRNA
3087	12303	21426	12.47	1.0E-45	U32188.1	NT	Human pro-a2 chain of collagen type XI (COL11A2) gene, complete cds
3487	12692	21826	0.69	1.0E-45	8659558	NT	Homo sapiens chromosome 21 open reading frame 1 (C21orf4), mRNA
4473	13671	22762	6.02	1.0E-45	BE386633.1	EST_HUMAN	601289116F1 NIH_MGC 8 Homo sapiens cDNA clone IMAGE:3618903 5'
6814	16009	25472	4.31	1.0E-45	BE687843.1	EST_HUMAN	601511228F1 NIH_MGC 71 Homo sapiens cDNA clone IMAGE:3912535 5'
8502	17541	24029	4.45	1.0E-45	11418099	NT	Homo sapiens protein kinase C, alpha binding protein (PRKCABP), mRNA
8696	17664		7.85	1.0E-45	11526281	NT	Homo sapiens hypothetical protein FLJ20454 (FLJ20454), mRNA

Table 4

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8702	17667		6.94	1.0E-45	11418177	NT	Homo sapiens Ran GTPase activating protein 1 (RANGAP1), mRNA
9133	17942	23881	2.75	1.0E-46	11418157	NT	Homo sapiens calcium channel, voltage-dependent, alpha 1I subunit (CAGNA1I), mRNA
6664	15659		11.57	9.0E-46	AL163209.2	NT	Homo sapiens chromosome 21 segment HS21C009
7210	16387	25869	8.54	9.0E-46	AW246864.1	EST_HUMAN	2822449.5 prime NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2822449 5'
2405	11587	20817	20.16	8.0E-46	AI433261.1	EST_HUMAN	ts2208.x1 NCL_CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2132196 3' similar to gb:J00314_ma2
2405	11587	20818	20.16	8.0E-46	AI433261.1	EST_HUMAN	ts2208.x1 NCL_CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2132196 3' similar to gb:J00314_ma2
6482	15678		5.81	8.0E-46	BE167244.1	EST_HUMAN	TUBULIN BETA-1 CHAIN (HUMAN);
8165	17287		3.37	8.0E-46	11418729	NT	ROS-HT0506-280200-012-C12 HT0506 Homo sapiens cDNA
4578	13772		10.04	7.0E-46	BE386165.1	EST_HUMAN	Homo sapiens ribosomal protein L44 (RPL44), mRNA
4820	14009		1.25	7.0E-46	BE094386.1	EST_HUMAN	601277292F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3618119 5'
5682	14802	24295	3.83	7.0E-46	8922708	NT	RC4-BT0310-110300-015-f10 BT0310 Homo sapiens cDNA
8832	17743		1.33	7.0E-46	AL163246.2	NT	Homo sapiens hypothetical protein FLJ10847 (FLJ10847), mRNA
2711	11890	21107	6.12	6.0E-46	AI884381.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C046
2711	11890	21108	6.12	6.0E-46	AI884381.1	EST_HUMAN	wn31108.x1 NCL_CGAP_U14 Homo sapiens cDNA clone IMAGE:2437575 3' similar to contains MER19.12
5724	14942	24338	9.61	6.0E-46	AI635448.1	EST_HUMAN	MER19 repetitive element;
7828	16404		2.87	6.0E-46	BE784971.1	EST_HUMAN	wn31108.x1 NCL_CGAP_U14 Homo sapiens cDNA clone IMAGE:2437575 3' similar to contains MER19.12
209	9489		6.85	5.0E-46	AL163210.2	NT	MER19 repetitive element;
3502	12728	21862	1.86	5.0E-46	BE677194.1	EST_HUMAN	ts58h10.x1 NCL_CGAP_Kid8 Homo sapiens cDNA clone IMAGE:2232635 3' similar to TR:O60363 O60363
3502	12728	21863	1.86	5.0E-46	BE677194.1	EST_HUMAN	SA GENE;
5977	15191	24608	1.87	5.0E-46	BF590442.1	EST_HUMAN	601478409F1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3880895 5'
6059	15249	24871	4.32	5.0E-46	BF347229.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C010
647	9693		2.39	4.0E-46	AA601143.1	EST_HUMAN	7d81g01.x1 Lupski_dorsal_root_ganglion Homo sapiens cDNA clone IMAGE:3279408 3'
1678	10891	20077	8.19	4.0E-46	AW770544.1	EST_HUMAN	7d81g01.x1 Lupski_dorsal_root_ganglion Homo sapiens cDNA clone IMAGE:3279408 3'

Page 202 of 382  
Table 4  
Single Exon Probes Expressed in HELA Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1679	10891	20078	8.19	4.0E-46	AW770544.1	EST_HUMAN	m186c03.x1 NCL_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3008638 3' similar to gb:X14008_ma1 LYSOZYME C PRECURSOR (HUMAN); contains element MER37 repetitive element :
2698	11878	21080	18.7	4.0E-46	M18048.1	NT	Human endogenous retrovirus RTV-LH2
5411	14639	23768	2.3	4.0E-46	M36852.1	NT	Human Ig germline gamma-3 heavy-chain gene V region, partial cds
5411	14639	23769	2.3	4.0E-46	M36852.1	NT	Human Ig germline gamma-3 heavy-chain gene V region, partial cds
8956	17829	23907	1.88	4.0E-46	AB002059.1	NT	Homo sapiens DNA for Human P2XM, complete cds
2250	11445	20667	1.82	3.0E-46	7657203	NT	Homo sapiens acidic 82 kDa protein mRNA (HSU15552), mRNA
2392	11585	20803	2.31	3.0E-46	AF160212.1	NT	Homo sapiens VAMP-associated 33 kDa protein mRNA, complete cds
6701	15896	25357	6.58	3.0E-46	AI831462.1	EST_HUMAN	wj49c04.x1 NCL_CGAP_Lu19 Homo sapiens cDNA clone IMAGE:2406150 3' similar to contains THR.b2 THR repetitive element :
8105	17239	26777	2.69	3.0E-46	D31765.1	NT	Human mRNA for KIAA0081 gene, partial cds
847	10084	19243	6.45	2.0E-46	AA486846.1	EST_HUMAN	ne06a09.s1 NCL_CGAP_Cc3 Homo sapiens cDNA clone IMAGE:880408 3' similar to contains THR.b2 THR repetitive element :
1544	10758		1.74	2.0E-46	AA678246.1	EST_HUMAN	z127a11.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:431898 3'
1818	10831	20008	4.27	2.0E-46	U78027.1	NT	Homo sapiens Bruton's tyrosine kinase (BTK), alpha-D-galactosidase A (GLA), L44-like ribosomal protein (L44L) and FTP3 (FTP3) genes, complete cds
4964	14181	23270	1.44	2.0E-46	AA399288.1	EST_HUMAN	z159a02.r1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:726850 5' similar to SW:RSP1_MOUSE Q01730 RSP-1 PROTEIN :
6285	15466	24807	7.31	2.0E-46	8910569	NT	Mus musculus sperm tail associated protein (Slap), mRNA
6488	15885		4.32	2.0E-46	BE889151.1	EST_HUMAN	601445137F1 NIH_MGC_85 Homo sapiens cDNA clone IMAGE:3849297 5'
7798	16991		1.77	2.0E-46	7657233	NT	Homo sapiens small acidic protein (IMAGE145052), mRNA
8422	18241		2	2.0E-46	BF028854.1	EST_HUMAN	601785225F1 NIH_MGC_53 Homo sapiens cDNA clone IMAGE:3997328 5'
8689	18135		1.33	2.0E-46	H48391.1	EST_HUMAN	y032d01.r1 Soares_fetal_liver_spleen_1NFLS Homo sapiens cDNA clone IMAGE:206877 5'
8727	17678		1.27	2.0E-46	AA001788.1	EST_HUMAN	zh84f12.r1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:428015 5'
9031	18127	23812	5.9	2.0E-46	AW277214.1	EST_HUMAN	xq78h03.x1 NCL_CGAP_Lu34 Homo sapiens cDNA clone IMAGE:2756789 3'
1240	10458	19815	7.9	1.0E-46	4502694	NT	Homo sapiens cell division cycle 10 (homologous to CDC10 of S. cerevisiae) (CDC10) mRNA
2246	11441	20665	4.25	1.0E-46	AW978516.1	EST_HUMAN	EST380825 MAGE resequences, MAGP Homo sapiens cDNA
2364	11557	20778	3.53	1.0E-46	H97930.1	EST_HUMAN	EST48b095 WATM1 Homo sapiens cDNA clone 48b095
3216	12450	21582	4.7	1.0E-46	AA631812.1	EST_HUMAN	np78b02.s1 NCL_CGAP_P12 Homo sapiens cDNA clone IMAGE:1132385 similar to gb:X78717 H.sapiens MT-11 mRNA. (HUMAN);
4890	14078		2.9	1.0E-46	AB023197.1	NT	Homo sapiens mRNA for KIAA0080 protein, partial cds
5535	14759	24128	5.85	1.0E-46	BF194707.1	EST_HUMAN	7a92b01.x1 NCL_CGAP_Ov18 Homo sapiens cDNA clone IMAGE:3643705 3'
5643	18080	24250	5.13	1.0E-46	8923762	NT	Homo sapiens centaurin-alpha 2 protein (HSA272185), mRNA

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Table 4

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5643	18060	24251	5.13	1.0E-46	8923762	NT	Homo sapiens centaurin-alpha 2 protein (HSA272195), mRNA
7439	14759	24126	4.91	1.0E-46	BF184707.1	EST_HUMAN	7692b01.x1 NCI_CGAP_Ov18 Homo sapiens cDNA clone IMAGE:3643705 3'
8451	17509	24017	1.5	1.0E-46	BF531102.1	EST_HUMAN	602072284F1 NCI_CGAP_Bm87 Homo sapiens cDNA clone IMAGE:4215388 5'
8451	17509	24018	1.5	1.0E-46	BF531102.1	EST_HUMAN	602072284F1 NCI_CGAP_Bm87 Homo sapiens cDNA clone IMAGE:4215388 5'
8244	18015		1.63	1.0E-46	AV715377.1	EST_HUMAN	AV715377 DCB Homo sapiens cDNA clone DCBAIE03 5'
775	10014		4.91	9.0E-47	AJ271735.1	NT	Homo sapiens Xq pseudautosomal region, segment 1/2
4952	14139	23233	2.1	9.0E-47	AW770928.1	EST_HUMAN	h83a04.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3009534 3' similar to TR:O75703 O75703
8979	18228	23689	1.93	9.0E-47	11417988	NT	HYPOTHETICAL 12.4 KD PROTEIN.
1777	10987	20179	44.01	8.0E-47	Y18536.1	NT	Homo sapiens SEC14 (S. cerevisiae)-like 2 (SEC14L2), mRNA
1777	10987	20180	44.01	8.0E-47	Y18536.1	NT	Homo sapiens HLA-C gene, exon 5, individual 19323
2676	11858	21073	1.3	8.0E-47	5453955	NT	Homo sapiens HLA-C gene, exon 5, individual 19323
2889	12226	21360	2.14	8.0E-47	AJ228043.1	NT	Homo sapiens protein phosphatase 2, regulatory subunit B (B56), epsilon isoform (PPP2R5E) mRNA
2513	11702	20917	3.72	8.0E-47	AL163248.2	NT	Homo sapiens 959 kb contig between AML1 and CBR1 on chromosome 21q22, segment 3/3
6947	16036	25500	5.32	6.0E-47	AI895189.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C046
5918	15133	24542	5.84	5.0E-47	11423972	NT	t588h02.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2298659 3'
7375	16591		6.37	5.0E-47	M78590.1	EST_HUMAN	Homo sapiens ODC37 (cell division cycle 37, S. cerevisiae, homolog) (CDC37), mRNA
1404	10617	19783	4.3	4.0E-47	4557558	NT	EST00738 Fetal brain, Striatum (cat8930206) Homo sapiens cDNA clone HFB07
8151	17283		6.74	4.0E-47	AW515509.1	EST_HUMAN	Homo sapiens E1A binding protein p300 (EP300) mRNA
551	9802	18928	2.54	3.0E-47	BE907634.1	EST_HUMAN	x86b07.x1 NCI_CGAP_Lym12 Homo sapiens cDNA clone IMAGE:2848597 3' similar to SW:INT6_MOUSE
551	9802	18928	2.54	3.0E-47	BE907634.1	EST_HUMAN	Q64252 VIRAL INTEGRATION SITE PROTEIN INT-6, [1]
828	10066	19219	7.18	3.0E-47	N57483.1	EST_HUMAN	601497639F1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3899721 5'
953	10186	19342	10.62	3.0E-47	AL163284.2	EST_HUMAN	601497639F1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3899721 5'
3273	12506	21637	0.76	3.0E-47	4504116	NT	y54b04.s1 Soares_multiple_sclerosis_2NblMSP Homo sapiens cDNA clone IMAGE:277327 3'
3943	13159		6.42	3.0E-47	U93181.1	NT	Homo sapiens chromosome 21 segment HS21C084
4356	13558	22653	1.87	3.0E-47	M12059.1	NT	Homo sapiens glutamate receptor, ionotropic, kainate 1 (GRIK1) mRNA
5982	14985	24273	4.5	3.0E-47	AW408800.1	EST_HUMAN	Homo sapiens nuclear dual-specificity phosphatase (Sbf1) mRNA, partial cds
5982	14985	24274	4.5	3.0E-47	AW408800.1	EST_HUMAN	Human T-cell receptor active alpha-chain mRNA from JM cell line, complete cds
5907	15124		1.87	3.0E-47	AI222413.1	EST_HUMAN	UI-HF-BM0-adv-d-07-Q-J1.r1 NIH_MGC_38 Homo sapiens cDNA clone IMAGE:3063205 5'
150	9432	18566	1.51	2.0E-47	4505318	NT	UI-HF-BM0-adv-d-07-Q-J1.r1 NIH_MGC_38 Homo sapiens cDNA clone IMAGE:3063205 5'
975	10207	19381	2.74	2.0E-47	AL163209.2	NT	qf04e07.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1843716 3'
976	10207	19382	2.74	2.0E-47	AL163209.2	NT	Homo sapiens myosin phosphatase, target subunit 2 (MYPT2), mRNA
							Homo sapiens chromosome 21 segment HS21C009
							Homo sapiens chromosome 21 segment HS21C009



Page 204 of 382  
Table 4  
Single Exon Probes Expressed in HELA Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1573	10786	18861	1.75	2.0E-47	7662109	NT	Homo sapiens KIAA0428 gene product (KIAA0428), mRNA
1652	10868	20048	4.28	2.0E-47	AA524514.1	EST_HUMAN	ng43h12.s1 NCI_CGAP_Co3 Homo sapiens cDNA clone IMAGE:937607 3'
4340	13542	22633	2.14	2.0E-47	4504868	NT	Homo sapiens ring finger protein (C3HC4 type) 8 (RNF8), mRNA
4378	13580	22679	1.96	2.0E-47	AA568592.1	EST_HUMAN	m23g07.s1 NCI_CGAP_P1 Homo sapiens cDNA clone IMAGE:914652
4378	13580	22680	1.96	2.0E-47	AA568592.1	EST_HUMAN	m23g07.s1 NCI_CGAP_P1 Homo sapiens cDNA clone IMAGE:914652
4508	13704	22788	2.32	2.0E-47	5174648	NT	Homo sapiens Rev/Rex activation domain binding protein-related (RAB-R) mRNA
4827	14018	23115	1.05	2.0E-47	AW965166.1	EST_HUMAN	EST377239 IMAGE resequencing, MAGI Homo sapiens cDNA
5187	14348		0.78	2.0E-47	A041126.1	EST_HUMAN	ov61h03.x1 Soares testis_NHT Homo sapiens cDNA clone IMAGE:1641845 3'
6447	15644	25111	3	2.0E-47	D87675.1	NT	Homo sapiens DNA for amyloid precursor protein, complete cds
6447	15644	25112	3	2.0E-47	D87675.1	NT	Homo sapiens DNA for amyloid precursor protein, complete cds
8489	18272	23679	2.83	2.0E-47	R42423.1	EST_HUMAN	yf82e08.s1 Soares infant brain 1NIB Homo sapiens cDNA clone IMAGE:28868 3' similar to contains OFR repetitive element;
1409	10622	19788	6.74	1.0E-47	A133429.1	EST_HUMAN	qp99h03.x1 Soares_fetal_lung_NbHL19W Homo sapiens cDNA clone IMAGE:1931189 3'
3812	13030	22139	0.92	1.0E-47	BE280477.1	EST_HUMAN	601155321F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3138893 5'
3812	13030	22140	0.92	1.0E-47	BE280477.1	EST_HUMAN	601155321F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3138893 5'
5106	14286	23371	2.55	1.0E-47	AW813806.1	EST_HUMAN	RC3-ST0197-130400-017-H02 ST0197 Homo sapiens cDNA
6102	15196	24614	8.41	1.0E-47	A1880886.1	EST_HUMAN	at19e08.x1 Barstead aorta HPLRB8 Homo sapiens cDNA clone IMAGE:2355588 3' similar to gb:M22895
6738	15933		6.84	1.0E-47	AW684648.1	EST_HUMAN	RAS-RELATED PROTEIN RAP-1A (HUMAN);
1591	10804	18979	4.07	9.0E-48	AF223391.1	NT	h84a11.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2878972 3' similar to gb:M26328
3531	12754	21887	0.75	8.0E-48	BF359947.1	EST_HUMAN	KERATIN, TYPE I CYTOSKELETAL 18 (HUMAN);
7677	16876	26381	3.33	9.0E-48	BE393813.1	EST_HUMAN	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced
1257	10473		2.18	8.0E-48	4501800	NT	CNV2-MT0100-310700-290-405 MT0100 Homo sapiens cDNA
1258	10473		1.89	8.0E-48	4501800	NT	601310478F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3632083 5'
3100	12336	21463	3.19	8.0E-48	AW768477.1	EST_HUMAN	Homo sapiens aminocyclase 1 (ACY1), mRNA
3100	12336	21464	3.19	8.0E-48	AW768477.1	EST_HUMAN	h61b03.x1 NCI_CGAP_Lym12 Homo sapiens cDNA clone IMAGE:3001133 3' similar to gb:X64707
497	9750		1.35	7.0E-48	AB033035.1	NT	BREAST BASIC CONSERVED PROTEIN 1 (HUMAN);
498	9760		17.36	7.0E-48	AB033035.1	NT	BREAST BASIC CONSERVED PROTEIN 1 (HUMAN);
1488	10701	19875	1.1	7.0E-48	6912718	NT	Homo sapiens mRNA for KIAA1209 protein, partial cds
1614	10827	20002	4.69	7.0E-48	5730038	NT	Homo sapiens tousel-like kinase 1 (TLK1), mRNA
							Homo sapiens SET domain and mariner transposase fusion gene (SETMAR) mRNA

Table 4

## Single Exon Probes Expressed in HELA Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5903	15120	24531	24.65	7.0E-48	11418831	NT	Homo sapiens histidyl-RNA synthetase (HARS), mRNA
3576	12789	21025	0.7	6.0E-48	A1761111.1	EST_HUMAN	wf69h03.x1 NCI_CGAP_Kid12 Homo sapiens cDNA clone IMAGE:2388613 3'
6832	16125	25591	2.22	6.0E-48	11427428	NT	Homo sapiens hypothetical protein FLJ11008 (FLJ11008), mRNA
6888	16166	25638	3.11	6.0E-48	AA189080.1	EST_HUMAN	zq45b06.s1 Stratigene hNT neuron (#837233) Homo sapiens cDNA clone IMAGE:682627 3' similar to contains Alu repetitive element;
3280	14466	21842	1.56	5.0E-48	4826891	NT	Homo sapiens phosphodiesterase 1A, calmodulin-dependent (PDE1A), mRNA
7529	16734	26224	4.02	4.0E-48	A1620420.1	EST_HUMAN	bu47a02.x1 NCI_CGAP_P28 Homo sapiens cDNA clone IMAGE:2254154 3'
1391	10605	19769	1.14	3.0E-48	AV690964.1	EST_HUMAN	AV690964 GKG Homo sapiens cDNA clone GKCDRE12 5'
1945	11149	20350	24.96	3.0E-48	4885170	NT	Homo sapiens chromosome X open reading frame 6 (CXORF6) mRNA
1945	11149	20351	24.96	3.0E-48	4885170	NT	Homo sapiens chromosome X open reading frame 6 (CXORF6) mRNA
3396	12623	21754	1	3.0E-48	AF172453.1	NT	Homo sapiens opioid growth factor receptor mRNA, complete cds
3609	12630	21951	0.78	3.0E-48	AW664531.1	EST_HUMAN	h14b12.x1 NCI_CGAP_GU1 Homo sapiens cDNA clone IMAGE:2872255 3' similar to SW:DCRB_HUMAN
4233	13436		0.69	3.0E-48	AA009541.1	EST_HUMAN	P56555 DOWN SYNDROME CRITICAL REGION PROTEIN B.1
5611	14835	24210	2.35	3.0E-48	BE084571.1	EST_HUMAN	MR4-BT0657-060400-201-e10 BT0657 Homo sapiens cDNA
7451	16659	26148	10.07	3.0E-48	BF514170.1	EST_HUMAN	UIH-BW1-ani-a-10-Q-UI.s1 NCI_CGAP_Sub7 Homo sapiens cDNA clone IMAGE:3082287 3'
47	9344	18454	1.14	2.0E-48	AA631940.1	EST_HUMAN	fmc67 Regional genomic DNA specific cDNA library Homo sapiens cDNA clone CR17-28
4528	13725	22822	1.16	2.0E-48	BE246085.1	EST_HUMAN	TCBAP1D3842 Pediatric pre-B cell acute lymphoblastic leukemia Baylor-HGSC project-TCBA Homo sapiens cDNA clone TCBAP3842
6298	15478	24921	4.24	2.0E-48	AB040834.1	NT	Homo sapiens mRNA for KIAA1501 protein, partial cds
6298	15478	24922	4.24	2.0E-48	AB040834.1	NT	Homo sapiens mRNA for KIAA1501 protein, partial cds
6304	15485	24929	3.75	2.0E-48	11498238	NT	Homo sapiens v-rel avian reticuloendotheliosis viral oncogene homolog A (nuclear factor of kappa light polypeptide gene enhancer in B-cells 3 (p65)) (RELA), mRNA
8448	14481	23532	2.71	2.0E-48	AA485007.1	EST_HUMAN	z880c03.r1 Soares ovary tumor NbHOT Homo sapiens cDNA clone IMAGE:810052 5'
8789	18191	23760	1.52	2.0E-48	BE737154.1	EST_HUMAN	801305064F1 NIH_MGC_39 Homo sapiens cDNA clone IMAGE:3639782 5'
58	8354	18471	3.21	1.0E-48	7706534	NT	Homo sapiens cisplatin resistance-associated overexpressed protein (LOC51747), mRNA
883	10119	19281	12.45	1.0E-48	4502166	NT	Homo sapiens amyloid beta (A4) precursor protein (protease nexin-II, Alzheimer disease) (APP), mRNA
1083	10308	19456	2.62	1.0E-48	7857430	NT	Homo sapiens EBNA-2 co-activator (100kD) (p100), mRNA
1083	10308	19460	2.62	1.0E-48	7857430	NT	Homo sapiens EBNA-2 co-activator (100kD) (p100), mRNA
1303	10519	19878	3.47	1.0E-48	5032032	NT	Homo sapiens RNA binding motif protein 6 (RBM6) mRNA
1884	11091	20282	18.8	1.0E-48	AL163302.2	NT	Homo sapiens chromosome 21 segment HS21C102
3463	12688	21824	1.05	1.0E-48	AL163246.2	NT	Homo sapiens chromosome 21 segment HS21C046
5163	14342	23431	1.34	1.0E-48	MT0976.1	NT	Human endogenous retroviral DNA (4-1), complete retroviral segment

Page 206 of 382  
Table 4  
Single Exon Probes Expressed in HELA Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6189	16371	24812	2.4	1.0E-48	4755137	NT	Homo sapiens huntingtin (Huntington disease) (HD) mRNA
6843	16032	25487	6.77	1.0E-48	AB033071.1	NT	Homo sapiens mRNA for KIAA1245 protein, partial cds
8411	18216		1.41	1.0E-48	W26785.1	EST_HUMAN	15d6 Human retina cDNA randomly primed sublibrary Homo sapiens cDNA
1978	11179	20387	1.76	8.0E-49	AB026497.1	NT	Mus musculus MysPDZ mRNA for myosin containing PDZ domain, complete cds
5690	14910	24303	3.04	8.0E-49	10048417	NT	Mus musculus T-box 20 (Tbx20), mRNA
5690	14910	24304	3.04	8.0E-49	10048417	NT	Mus musculus T-box 20 (Tbx20), mRNA
6558	15754	25217	5.17	8.0E-49	U23850.1	NT	Human inositol 1,4,5 triphosphate receptor type 1 mRNA, partial cds
7433	16042	26134	1.69	8.0E-49	AI623722.1	EST_HUMAN	ts38d12.x1 NCI_CGAP_U14 Homo sapiens cDNA clone IMAGE:2230871 3' similar to contains Alu repetitive element; contains element PTR5 repetitive element;
136	9853	18788	2.75	7.0E-49	5729990	NT	Homo sapiens proteasome (prosome, macropain) 26S subunit, ATPase, 4 (PSMC4) mRNA
136	9853	18788	2.75	7.0E-49	5729990	NT	Homo sapiens proteasome (prosome, macropain) 26S subunit, ATPase, 4 (PSMC4) mRNA
398	9853	18788	2.43	7.0E-49	5729990	NT	Homo sapiens proteasome (prosome, macropain) 26S subunit, ATPase, 4 (PSMC4) mRNA
398	9853	18788	2.43	7.0E-49	5729990	NT	Homo sapiens proteasome (prosome, macropain) 26S subunit, ATPase, 4 (PSMC4) mRNA
399	9853	18788	3.56	7.0E-49	5729990	NT	Homo sapiens proteasome (prosome, macropain) 26S subunit, ATPase, 4 (PSMC4) mRNA
399	9853	18788	3.56	7.0E-49	5729990	NT	Homo sapiens proteasome (prosome, macropain) 26S subunit, ATPase, 4 (PSMC4) mRNA
1228	10446	19602	3.33	7.0E-49	AL163284.2	NT	Homo sapiens chromosome 21 segment HS21C084
5424	14851	23787	1.65	7.0E-49	AI807191.1	EST_HUMAN	wf23h04.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2355663 3' similar to TR:O54923 O54923 RSEC15;
202	9482	18615	52.05	6.0E-49	AW731740.1	EST_HUMAN	ba55g05.x1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:2800504 3' similar to gb:X17206.40S RIBOSOMAL PROTEIN S4 (HUMAN); gb:M20632 Mouse LLRep3 protein mRNA from a repetitive element, complete (MOUSE);
4093	13301	22401	0.65	6.0E-49	AL162091.1	EST_HUMAN	DKFp761A138.s1 761 (synonym: hamy2) Homo sapiens cDNA clone DKFp761A138 3'
7828	17020	26535	2.57	6.0E-49	AW452218.1	EST_HUMAN	UI-H-BI3-alc-a-05-0-U1.s1 NCI_CGAP_Sub5 Homo sapiens cDNA clone IMAGE:3068048 3'
8166	17298	26840	3.61	6.0E-49	AA368556.1	EST_HUMAN	EST177525 Pancreas tumor III Homo sapiens cDNA 5' end
8166	17298	26841	3.61	6.0E-49	AA368556.1	EST_HUMAN	EST177525 Pancreas tumor III Homo sapiens cDNA 5' end
8795	18104		4.03	6.0E-49	AA707587.1	EST_HUMAN	z29c08.s1 Soares_fetal_liver_spleen_INFLS_S1 Homo sapiens cDNA clone IMAGE:451694 3'
719	9961	19098	13.78	5.0E-49	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C010
719	9961	19099	13.78	5.0E-49	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C010
1763	10974	20182	7.07	5.0E-49	AA172121.1	EST_HUMAN	zp29c07.t1 Strabagene neuroepithelium (#837231) Homo sapiens cDNA clone IMAGE:810860 5' similar to TR:G233226 G233226 RTVL-H PROTEIN; contains LTR7.3 LTR7 repetitive element;
2707	11888	21103	11.9	5.0E-49	U17714.1	NT	Homo sapiens putative tumor suppressor ST13 (ST13) mRNA, complete cds
3240	12474	21605	12.59	5.0E-49	11436355	NT	Homo sapiens similar to ribosomal protein S27 (metalloproteinin 1) (H. sapiens) (LOC333362), mRNA

Page 207 of 382  
Table 4  
Single Exon Probes Expressed in HELA Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
531	9782	18904	35.35	4.0E-49	AW189533.1	EST_HUMAN	x08501.x1 NCL_CGAP_U14 Homo sapiens cDNA clone IMAGE:2675593 3' similar to WP-B0350.2B
8652	18333		3.3	4.0E-49	AA210788.1	EST_HUMAN	CE06703 ;
8742	17687		3.86	4.0E-49	AF240786.1	NT	z80005.r1 NCL_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:682977 5'
567	8817	18939	1.66	3.0E-49	X68968.1	NT	Homo sapiens glutathione S-transferase theta 2 (GSTT2) and glutathione S-transferase theta 1 (GSTT1) genes, complete cds
2610	11794		2.65	3.0E-49	AA016131.1	EST_HUMAN	H. sapiens mRNA for acetyl-CoA carboxylase
5004	14191	23281	2.37	3.0E-49	U46999.1	NT	z631c05.r1 Soares retina N2b4HR Homo sapiens cDNA clone IMAGE:360584 5' similar to contains L1.13 L1 repetitive element ;
6259	15440	24879	10.15	3.0E-49	H39479.1	EST_HUMAN	Human type IV collagen (COL4A8) gene, exon 40
7849	17040	26557	2.43	3.0E-49	AA337561.1	EST_HUMAN	EST25e12 WATM1 Homo sapiens cDNA clone 25e12
667	9913		2.86	2.0E-49	BE165980.1	EST_HUMAN	EST42572 Endometrial tumor Homo sapiens cDNA 5' end
3188	12423	21556	1.34	2.0E-49	N28446.1	EST_HUMAN	MR3-HT0487-150200-113-g01 HT0487 Homo sapiens cDNA
4823	14012	23111	0.61	2.0E-49	BF511946.1	EST_HUMAN	yw23406.r1 Soares melanocyte 2Nbr-IM Homo sapiens cDNA clone IMAGE:262571 5'
6494	15691		2.82	2.0E-49	M86033.1	EST_HUMAN	U1H-B14-aps-4-02-0-J1.s1 NCL_CGAP_Sub8 Homo sapiens cDNA clone IMAGE:3088538 3'
809	10144		5.03	1.0E-49	BF035327.1	EST_HUMAN	EST02558 Fetal brain, Stratagene (cat#836206) Homo sapiens cDNA clone HFBCY50
1538	10751	19924	47.43	1.0E-49	4557887	NT	601459531F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3862086 5'
1770	10980	20170	4.77	1.0E-49	BE255218.1	EST_HUMAN	Homo sapiens keratin 18 (KRT18) mRNA
5283	14454		1.02	1.0E-49	7708703	NT	601115769F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3356273 5'
5372	14801	23711	4.6	1.0E-49	BF131007.1	EST_HUMAN	Homo sapiens putative G-protein coupled receptor (SH120), mRNA
6175	15357	24798	3.23	1.0E-49	BE398110.1	EST_HUMAN	601820053F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:4052052 5'
6175	15357	24787	3.23	1.0E-49	BE398110.1	EST_HUMAN	601280330F1 NIH_MGC_8 Homo sapiens cDNA clone IMAGE:3620863 5'
6207	15388	24831	2.52	1.0E-49	N25884.1	EST_HUMAN	yw78g12.s1 Soares placenta_8to9weeks_2Nbr-IP8to9W Homo sapiens cDNA clone IMAGE:258406 3' similar to gb:X65873 KINESIN HEAVY CHAIN (HUMAN);
6207	15388	24832	2.52	1.0E-49	N25884.1	EST_HUMAN	yw78g12.s1 Soares placenta_8to9weeks_2Nbr-IP8to9W Homo sapiens cDNA clone IMAGE:258406 3' similar to gb:X65873 KINESIN HEAVY CHAIN (HUMAN);
7617	16820	26315	1.92	1.0E-49	AV751477.1	EST_HUMAN	AV751477 NPD Homo sapiens cDNA clone NPDAWE04 5'
7658	17048	26567	4	1.0E-49	11427366	NT	Homo sapiens brefeldin A-inhibited guanine nucleotide-exchange protein 1 (BIG1), mRNA
8280	17397		1.68	1.0E-49	BE159343.1	EST_HUMAN	MR0-HT0407-010200-006-02 HT0407 Homo sapiens cDNA
8644	17629		2.64	1.0E-49	11418322	NT	MR0-HT0407-010200-006-02 HT0407 Homo sapiens cDNA
9187	18115		1.42	1.0E-49	11418123	NT	Homo sapiens cadherin EGF LAG seven-pass G-type receptor 1 (CELSR1), mRNA
5018	14205		1.16	9.0E-50	AF101475.1	NT	Homo sapiens KIAA0063 gene product (KIAA0063), mRNA
173	9454	18585	2.7	8.0E-50	AL163202.2	NT	Homo sapiens glycine N-methyltransferase (GNMT) gene, complete cds
726	8968	19106	2	8.0E-50	X95097.2	NT	Homo sapiens chromosome 21 segment HS21C002
							Homo sapiens mRNA for VIP receptor 2

Page 208 of 382  
Table 4  
Single Exon Probes Expressed in HELA Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
726	8988	19107	2	8.0E-50	X95097.2	NT	Homo sapiens mRNA for VIP receptor 2
1734	10946	20129	3.93	8.0E-50	4501890	NT	Homo sapiens actinin, alpha 1 (ACTN1) mRNA
2444	11635	20855	1.38	8.0E-50	7706394	NT	Homo sapiens p47 (LOC51674), mRNA
2444	11635	20856	1.38	8.0E-50	7706394	NT	Homo sapiens p47 (LOC51674), mRNA
2680	11841	21055	2.33	8.0E-50	4826858	NT	Homo sapiens capping protein (actin filament) muscle Z-line, beta (CAPZB), mRNA
7947	17087	26618	1.69	8.0E-50	AA633467.1	EST_HUMAN	GLUTATHIONE S-TRANSFERASE TESTIS/BRAIN (HUMAN);
825	8870	18992	0.7	7.0E-50	BE089591.1	EST_HUMAN	GVO-BT0703-280400-211-a08 BT0703 Homo sapiens cDNA
7341	16557	26045	21.23	7.0E-50	AI872137.1	EST_HUMAN	wm55g11.x1 NCI CGAP_U02 Homo sapiens cDNA clone IMAGE:2439908 3'
4336	13537		0.72	6.0E-50	BE794381.1	EST_HUMAN	601588565F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3943577 5'
6533	15729		4.02	6.0E-50	BE044078.1	EST_HUMAN	h338h04.x1 NCI CGAP_U11 Homo sapiens cDNA clone IMAGE:3039511 3' similar to contains MER29.b3
7392	16808	26095	5.98	6.0E-50	AA312079.1	EST_HUMAN	MER29 repetitive element ;
7392	16806	26096	5.98	6.0E-50	AA312079.1	EST_HUMAN	EST182775 Jurkat T-cells Vi Homo sapiens cDNA 5' end
1782	10973	20160	0.98	5.0E-50	BF332938.1	EST_HUMAN	EST182776 Jurkat T-cells Vi Homo sapiens cDNA 5' end
1782	10973	20161	0.98	5.0E-50	BF332938.1	EST_HUMAN	CM0-BT0792-300500-398-b05 BT0792 Homo sapiens cDNA
8258	17383	26916	2.05	5.0E-50	AA403053.1	EST_HUMAN	CM0-BT0792-300500-398-b05 BT0792 Homo sapiens cDNA
927	10161		3.35	4.0E-50	AA601143.1	EST_HUMAN	z62b01.r1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:726889 5' similar to TR:G1335769
3425	12650	21780	1.59	4.0E-50	AL163248.2	NT	G1335769 GAG-POL POLYPROTEIN ;
1907	11113		5.69	3.0E-50	M18048.1	NT	no54e09.s1 NCI CGAP_SST1 Homo sapiens cDNA clone IMAGE:1104520 3' similar to gb:XS3741_ma1
2484	11674	20881	3.11	3.0E-50	BE259196.1	EST_HUMAN	FIBULIN-1, ISOFORM A PRECURSOR (HUMAN);
3288	12501	21632	1.29	3.0E-50	AA746142.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C048
3733	12953	22070	1.01	3.0E-50	AW755254.1	EST_HUMAN	Human endogenous retrovirus RTVL-H2
5259	14432	23507	0.72	3.0E-50	AW593868.1	EST_HUMAN	601109717F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3350308 5'
6354	15534	24987	4.64	3.0E-50	AF233436.2	NT	ab03f06.s1 NCI CGAP_Kid3 Homo sapiens cDNA clone IMAGE:1322627 3'
6354	15534	24988	4.64	3.0E-50	AF233436.2	NT	CMYA5 Human cardiac muscle expression library Homo sapiens cDNA clone 4151935 similar to CMYA5
7687	18966	26367	1.83	3.0E-50	11436955	NT	Cardiomyopathy associated gene 5
							hg28e01.x1 NCI CGAP_GC8 Homo sapiens cDNA clone IMAGE:2946744 3' similar to SW:C1TC_HUMAN
							P11586 C-1-TETRAHYDROFOLATE SYNTHASE, CYTOPLASMIC; contains Alu repetitive element;
							Homo sapiens FYVE domain-containing dual specificity protein phosphatase FYVE-DSP1a mRNA, complete cds
							Homo sapiens FYVE domain-containing dual specificity protein phosphatase FYVE-DSP1a mRNA, complete cds
							Homo sapiens Grb2-associated binder 2 (KIA0571), mRNA

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Table 4

## Single Exon Probes Expressed in HELA Cells

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8000	18435	25922	5.8	3.0E-50	AJ245821.1	NT	Homo sapiens CTL2 gene
787	10026		5.16	2.0E-50	AF055066.1	NT	Homo sapiens MHC class 1 region
1087	10311	19464	5.21	2.0E-50	4557752	NT	Homo sapiens midline 1 (Opitz/BBB syndrome) (MID1) mRNA
3255	12488	21619	0.7	2.0E-50	AF111168.2	NT	Homo sapiens serine palmitoyl transferase, subunit II gene, complete cds; and unknown genes
4898	14088	23178	1.7	2.0E-50	AW869159.1	EST_HUMAN	MR3-SN0066-040500-008-01 SN0066 Homo sapiens cDNA
4898	14088	23180	1.7	2.0E-50	AW869159.1	EST_HUMAN	MR3-SN0066-040500-008-01 SN0066 Homo sapiens cDNA
6816	15812	25269	10.73	2.0E-50	X08956.1	NT	Human HALPHA44 gene for alpha-tubulin, exons 1-3
6816	15812	25270	10.73	2.0E-50	X08956.1	NT	Human HALPHA44 gene for alpha-tubulin, exons 1-3
8164	17286		2.75	2.0E-50	AF023861.1	NT	Macaca mulatta cyclophilin A mRNA, complete cds
488	9721	18952	2.18	1.0E-50	AL163209.2	NT	Homo sapiens chromosome 21 segment HS21C009
2333	11526		11.32	1.0E-50	AJ271735.1	NT	Homo sapiens Xq pseudautosomal region; segment 1/2
9224	18126		1.7	8.0E-51	D25217.2	NT	Homo sapiens mRNA for KIAA0027 protein, partial cds
4565	13759	22858	18.64	8.0E-51	AA610842.1	EST_HUMAN	np86608.s1 NCI CGAP_Lu1 Homo sapiens cDNA clone IMAGE:1142440 3' similar to gb:U12871_mn1
6358	15538	24992	1.97	8.0E-51	11439587	NT	HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN A1 (HUMAN);
2980	12217	21352	0.7	7.0E-51	AW274720.1	EST_HUMAN	Homo sapiens PDZ-73 protein (PDZ-73NY-CO-38), mRNA
3250	12483	21815	1.43	7.0E-51	AW889219.1	EST_HUMAN	xn34603.xt NCI CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2695564 3' similar to TR:Q9Z340
3338	12567	21705	0.77	7.0E-51	AW274720.1	EST_HUMAN	QV4-NT0028-200400-180-d05 NT0028 Homo sapiens cDNA
4149	13355	22457	1.26	7.0E-51	AL079628.1	EST_HUMAN	xn34603.xt NCI CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2695564 3' similar to TR:Q9Z340
4148	13355	22458	1.26	7.0E-51	AL079628.1	EST_HUMAN	Q9Z340 ATYPICAL PKC SPECIFIC BINDING PROTEIN ;
4344	13546	22637	2.74	7.0E-51	AW295603.1	EST_HUMAN	Q9Z340 ATYPICAL PKC SPECIFIC BINDING PROTEIN ;
8183	17315	26858	2	7.0E-51	AF161449.1	NT	DKFZp434B2229 t1 434 (synonym: hhes3) Homo sapiens cDNA clone DKFZp434B2229 5'
1513	10727	19899	1.08	6.0E-51	6878763	NT	DKFZp434B2229 t1 434 (synonym: hhes3) Homo sapiens cDNA clone DKFZp434B2229 5'
1948	11152	20354	8.26	6.0E-51	7657266	NT	UI-H-BW0-elp-b-05-Q-U1 s1 NCI CGAP_Sub6 Homo sapiens cDNA clone IMAGE:2728817 3'
3450	12675	21810	15.12	6.0E-51	7657266	NT	Homo sapiens HSPC331 mRNA, partial cds
4288	13497	22592	0.65	6.0E-51	9810553	NT	Homo sapiens putative DNA binding protein (M88), mRNA
4298	13497	22593	0.65	6.0E-51	9810553	NT	Homo sapiens KIAA0929 protein Mix2 interacting nuclear target (MINT) homolog (KIAA0929), mRNA
5653	14878	24263	6.45	6.0E-51	AF070083.1	NT	Homo sapiens KIAA0929 protein Mix2 interacting nuclear target (MINT) homolog (KIAA0929), mRNA
5853	14878	24264	6.45	6.0E-51	AF070083.1	NT	Homo sapiens KIAA0929 protein Mix2 interacting nuclear target (MINT) homolog (KIAA0929), mRNA
6070	14517	23559	2.46	6.0E-51	11428665	NT	Homo sapiens KIAA0929 protein Mix2 interacting nuclear target (MINT) homolog (KIAA0929), mRNA

Page 210 of 382  
Table 4  
Single Exon Probes Expressed in HELA Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7808	17001	26513	2.12	6.0E-51	11528289	NT	Homo sapiens interleukin 17 receptor (IL17R), mRNA
8060	17195	26733	1.75	6.0E-51	5453949	NT	Homo sapiens protein phosphatase 2, regulatory subunit B (B56), alpha isoform (PPP2R5A) mRNA
8060	17195	26734	1.75	6.0E-51	5453949	NT	Homo sapiens protein phosphatase 2, regulatory subunit B (B56), alpha isoform (PPP2R5A) mRNA
801	10040	19191	10.27	5.0E-51	AL163203.2	NT	Homo sapiens chromosome 21 segment HS21C003
813	10051	19205	1.85	5.0E-51	4507500	NT	Homo sapiens T-cell lymphoma invasion and metastasis 1 (TIAM1) mRNA
888	11983	18384	0.97	5.0E-51	AL133204.1	NT	Novel human gene mapping to chromosome X
1587	10900	19978	1.72	5.0E-51	5031980	NT	Homo sapiens 26S proteasome-associated pad1 homolog (POH1) mRNA
2553	11741	20957	8.99	5.0E-51	AJ007558.1	NT	Homo sapiens mRNA for nucleoporin 155
3920	13136	22253	2.4	5.0E-51	M30938.1	NT	Human Ku (p70/p80) subunit mRNA, complete cds
3920	13136	22254	2.4	5.0E-51	M30938.1	NT	Human Ku (p70/p80) subunit mRNA, complete cds
5104	14284	23368	2.25	5.0E-51	AB037832.1	NT	Homo sapiens mRNA for KIAA1411 protein, partial cds
7829	17021	26536	4.86	5.0E-51	5803136	NT	Homo sapiens RNA binding motif protein 3 (RBM3), mRNA
132	9415	18550	20.31	3.0E-51	AI587348.1	EST_HUMAN	h61c09.x1 NCI_CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2224720 3' similar to gb:M263328
1184	10405	19559	34.42	3.0E-51	AI587348.1	EST_HUMAN	KERATIN, TYPE I CYTOSKELETAL 18 (HUMAN);
4318	13519	22614	2.02	3.0E-51	AL159142.1	NT	KERATIN, TYPE I CYTOSKELETAL 18 (HUMAN);
8972	17842		1.46	3.0E-51	AF003528.1	NT	Novel human gene mapping to chromosome 22
371	9637	18770	1.81	2.0E-51	4507798	NT	Homo sapiens X-linked anhidrotic ectodermal dysplasia protein gene (EDA), exon 2 and flanking repeat regions
695	9938	19088	0.84	2.0E-51	BE391063.1	EST_HUMAN	Homo sapiens ubiquitin protein ligase E3A (human papilloma virus E6-associated protein, Angelman syndrome) (UBE3A) mRNA
695	9938	19089	0.84	2.0E-51	BE391063.1	EST_HUMAN	Homo sapiens ubiquitin protein ligase E3A (human papilloma virus E6-associated protein, Angelman syndrome) (UBE3A) mRNA
1663	10876	20081	10.64	2.0E-51	AA233352.1	EST_HUMAN	601285694F1 NIH_MGC 44 Homo sapiens cDNA clone IMAGE:3607463 5'
3713	12933	22051	3.07	2.0E-51	AI492415.1	EST_HUMAN	601285694F1 NIH_MGC 44 Homo sapiens cDNA clone IMAGE:3607463 5'
4493	13691	22784	0.62	2.0E-51	AW137826.1	EST_HUMAN	601285694F1 NIH_MGC 44 Homo sapiens cDNA clone IMAGE:3607463 5'
5684	14866	24276	3.73	2.0E-51	BE782015.1	EST_HUMAN	601285694F1 NIH_MGC 44 Homo sapiens cDNA clone IMAGE:3607463 5'
6917	16110	25576	2.68	2.0E-51	AI917078.1	EST_HUMAN	601285694F1 NIH_MGC 44 Homo sapiens cDNA clone IMAGE:3607463 5'
6964	16142	25611	8.5	2.0E-51	BE165980.1	EST_HUMAN	601285694F1 NIH_MGC 44 Homo sapiens cDNA clone IMAGE:3607463 5'

Page 211 of 382  
Table 4

## Single Exon Probes Expressed in HELA Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7871	14840	23770	9	2.0E-51	AI732851.1	EST_HUMAN	cd34f09.x5 NCL CGAP_Kid5 Homo sapiens cDNA clone IMAGE:1326609 3' similar to SW:NME1_MOUSE P35436 GLUTAMATE [NMDA] RECEPTOR SUBUNIT EPSILON 1 PRECURSOR ;
7871	14840	23771	9	2.0E-51	AI732851.1	EST_HUMAN	cd34f09.x5 NCL CGAP_Kid5 Homo sapiens cDNA clone IMAGE:1326609 3' similar to SW:NME1_MOUSE P35436 GLUTAMATE [NMDA] RECEPTOR SUBUNIT EPSILON 1 PRECURSOR ;
8987	17837	23911	1.62	2.0E-51	11419159	NT	Homo sapiens myeloid lymphoid or mixed-lineage leukemia (trithorax (Drosophila) homolog); translocated to, 4 (MLLT4), mRNA
114	9402	18531	19.07	1.0E-51	4503528	NT	Homo sapiens eukaryotic translation initiation factor 4A, isoform 1 (EIF4A1) mRNA
1495	10898		45.14	1.0E-51	AV742248.1	EST_HUMAN	AV742248 CB Homo sapiens cDNA clone CBFBCG12 5'
5048	14230	23314	0.93	1.0E-51	BE779039.1	EST_HUMAN	601464995F1 NIH_MGC_87 Homo sapiens cDNA clone IMAGE:3868246 5'
5391	14920	23734	3.38	1.0E-51	T18962.1	EST_HUMAN	b120561 Testis 1 Homo sapiens cDNA clone b120561
8248	18392		3.62	1.0E-51	AV760590.1	EST_HUMAN	AV760590 MDS Homo sapiens cDNA clone MDSB802 5'
7280	18499	25991	1.97	9.0E-52	R91638.1	EST_HUMAN	yq10h04.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:186567 5' similar to SP:YGAF_ECOLI_P37339 HYPOTHETICAL PROTEIN IN GABP 3'REGION ;
7280	18499	25992	1.97	9.0E-52	R91638.1	EST_HUMAN	yq10h04.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:186567 5' similar to SP:YGAF_ECOLI_P37339 HYPOTHETICAL PROTEIN IN GABP 3'REGION ;
8737	17683		4.59	9.0E-52	AA777621.1	EST_HUMAN	z85a07.s1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:186567 5' similar to contains THR.13 THR repetitive element ;
155	9437	18571	6.6	8.0E-52	AA720574.1	EST_HUMAN	nm21g02.s1 NCL CGAP_GC80 Homo sapiens cDNA clone IMAGE:1241138 3' similar to contains THR.13 THR repetitive element ;
1487	10700	19874	1.22	8.0E-52	X84900.1	NT	H. sapiens mRNA for laminin-5, alpha3b chain
1630	10843	20020	2.78	8.0E-52	11968028	NT	Homo sapiens hypothetical protein FLJ13556 similar to N-myc downstream regulated 3 (FLJ13556), mRNA
1630	10843	20021	2.78	8.0E-52	11968028	NT	Homo sapiens hypothetical protein FLJ13556 similar to N-myc downstream regulated 3 (FLJ13556), mRNA
3971	10843	20020	8.23	8.0E-52	11968028	NT	Homo sapiens hypothetical protein FLJ13556 similar to N-myc downstream regulated 3 (FLJ13556), mRNA
3971	10843	20021	8.23	8.0E-52	11968028	NT	Homo sapiens hypothetical protein FLJ13556 similar to N-myc downstream regulated 3 (FLJ13556), mRNA
1185	10415		2.09	6.0E-52	BE072405.1	EST_HUMAN	QV3-BT0537-271289-049-407 BT0537 Homo sapiens cDNA
1669	10882	20068	7.15	6.0E-52	AF109807.1	NT	Homo sapiens S164 gene, partial cds; PS1 and hypothetical protein genes, complete cds; and S171 gene, partial cds
7761	16957	28468	2.04	6.0E-52	BE048172.1	EST_HUMAN	tz46h04.y1 NCL CGAP_Bm52 Homo sapiens cDNA clone IMAGE:2291671 5' similar to SW:PGBM_MOUSE_Q05793 BASEMENT MEMBRANE-SPECIFIC HEPARAN SULFATE PROTEOGLYCAN CORE PROTEIN PRECURSOR ;



Table 4  
Single Exon Probes Expressed in HELA Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4433	13633	22728	1.94	5.0E-52	Z78898.1	NT	H sapiens flow-sorted chromosome 6 HindIII fragment, SC6pA18H7
1637	10851	20029	1.58	4.0E-52	AF257318.1	NT	Homo sapiens SH3-containing protein SH3GLB1 mRNA, complete cds
1758	10969	20154	1.94	4.0E-52	47588.43	NT	Homo sapiens nucleoporin 155kD (NUP155) mRNA
3801	13117	22234	0.6	4.0E-52	4507500	NT	Homo sapiens T-cell lymphoma invasion and metastasis 1 (TIAM1) mRNA
4650	13844	22935	0.97	4.0E-52	5174590	NT	Homo sapiens 5,10-methylenetetrahydrofolate dehydrogenase, 5,10-methylenetetrahydrofolate cyclohydrolase, 10-formyltetrahydrofolate synthetase (MTHFD) mRNA
6632	15828	25280	4.42	4.0E-52	11417035	NT	Homo sapiens hydroxysteroid (17-beta) dehydrogenase 4 (HSD17B4), mRNA
8564	17584		5.5	4.0E-52	11418177	NT	Homo sapiens Ran GTPase activating protein 1 (RANGAP1), mRNA
9083	17905		6.29	4.0E-52	AB002059.1	NT	Homo sapiens DNA for Human P20M, complete cds
4068	13278		14.34	3.0E-52	11437042	NT	Homo sapiens hypothetical protein FLJ10875 (FLJ10875), mRNA
569	9819	18940	2.3	2.0E-52	M10976.1	NT	Human endogenous retroviral DNA (4-1), complete retroviral segment
569	9819	18941	2.3	2.0E-52	M10976.1	NT	Human endogenous retroviral DNA (4-1), complete retroviral segment
2463	11654	20876	15.22	2.0E-52	BE207575.1	EST_HUMAN	bb66b07.y1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3030421 5' similar to gb:X16493 M.musculus. mRNA for Zfp-1 zinc finger protein (MOUSE);
2693	11873		25.07	2.0E-52	BF677892.1	EST_HUMAN	602084710F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4248891 5'
4997	14184	23272	4.01	2.0E-52	AL137188.3	NT	Novel human gene mapping to chromosome 20, similar to membrane transporters
5038	14222	23309	1.36	2.0E-52	AI141802.1	EST_HUMAN	qa56a05.s1 Soares_NHMPu_S1 Homo sapiens cDNA clone IMAGE:1690784 3'
5038	14222	23307	1.36	2.0E-52	AI141802.1	EST_HUMAN	qa56a05.s1 Soares_NHMPu_S1 Homo sapiens cDNA clone IMAGE:1690784 3'
5537	14761	24128	3.39	2.0E-52	AW848041.1	EST_HUMAN	IL3-CT0214-231289-053-E12 CT0214 Homo sapiens cDNA
5819	15036	24437	1.65	2.0E-52	11141868	NT	Homo sapiens interleukin 21 receptor (IL21R), mRNA
6669	15894		10.62	2.0E-52	AF147880.1	NT	Macaca mulatta beta-tubulin mRNA, complete cds
7116	16293	25774	5.48	2.0E-52	5730038	NT	Homo sapiens SET domain and mariner transposase fusion gene (SETMAR) mRNA
7116	16293	25775	5.48	2.0E-52	5730038	NT	Homo sapiens SET domain and mariner transposase fusion gene (SETMAR) mRNA
7756	16952	28458	6.11	2.0E-52	AI831482.1	EST_HUMAN	wj49e04.x1 NCI_CGAP_Lu19 Homo sapiens cDNA clone IMAGE:2408150 3' similar to contains THR.b2 THR repetitive element;
7756	16952	28459	6.11	2.0E-52	AI831482.1	EST_HUMAN	wj49e04.x1 NCI_CGAP_Lu19 Homo sapiens cDNA clone IMAGE:2408150 3' similar to contains THR.b2 THR repetitive element;
7769	16965	28478	3.72	2.0E-52	AV715377.1	EST_HUMAN	AV715377 DCB Homo sapiens cDNA clone DCBAIE03 5'
7892	17108		2.13	2.0E-52	W70260.1	EST_HUMAN	zd49g12.r1 Soares_fetal_heart_NCHH19W Homo sapiens cDNA clone IMAGE:344038 5'
8140	17272		3.66	2.0E-52	11417960	NT	Homo sapiens LIM domain kinase 2 (LIMK2), mRNA
8365	18375	23561	12.95	2.0E-52	AW238297.1	EST_HUMAN	xn72e07.x1 NCI_CGAP_CML1 Homo sapiens cDNA clone IMAGE:2700036 3' similar to contains Alu repetitive element; contains element LTR2 repetitive element;
8783	17712		4.63	2.0E-52	AI809885.1	EST_HUMAN	wf87d05.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2360849 3' similar to TR:Q16859 Q16859 CARBOXYLESTERASE;

Table 4

## Single Exon Probes Expressed in HELA Cells

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
539	9790	18914	1.76	1.0E-52	AA634445.1	EST_HUMAN	zu75h12.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:743879 3'
1378	10583	19759	3.28	1.0E-52	4504026	NT	Homo sapiens glutamate-aminotransferase (glutamate synthase) (GLUL) mRNA
3024	12280	21388	1.82	1.0E-52	S61070.1	NT	pol=reverse transcriptase homolog (retroviral element) [human, endogenous retroviral element RTVL-Hp1, Genomic, 680 nt]
5355	14585	23681	3.88	1.0E-52	M29426.1	NT	Human P-glycoprotein (MDR1) gene, exon 4
5827	15044	24448	2.75	1.0E-52	U38964.1	NT	Human PMS2 related (hPMSR2) gene, complete cds
6264	15445	24894	2.57	1.0E-52	X07292.1	NT	Human aldolase C gene for fructose-1,6-bisphosphate aldolase
7350	16568	26056	15.82	1.0E-52	U48296.1	NT	Homo sapiens protein tyrosine phosphatase PTPCAAX1 (hPTPCAAX1) mRNA, complete cds
7413	16825	22106	2.87	1.0E-53	11426321	NT	Homo sapiens proteasome (prosome, macropain) subunit, beta type, 2 (PSMB2), mRNA
3773	12991	22106	0.85	9.0E-53	4506064	NT	Homo sapiens protein kinase, cAMP-dependent, regulatory, type II, beta (PRKAR2B) mRNA
8614	17611		3.78	7.0E-53	BF238465.1	EST_HUMAN	60180477F1 NIH_MGC_54 Homo sapiens cDNA clone IMAGE:4132783 5'
9057	18245		6.71	7.0E-53	AK421782.1	EST_HUMAN	944f07.x1 NCI_CGAP_Bim23 Homo sapiens cDNA clone IMAGE:2086077 3' similar to contains THR.t1 THR repetitive element;
4078	13286	22384	6.55	5.0E-53	4758543	NT	Homo sapiens heterogeneous nuclear ribonucleoprotein C (C1/C2) (HNRPC) mRNA
8668	17642		1.81	5.0E-53	AW813563.1	EST_HUMAN	RC3-ST0197-151099-011-g10 ST0197 Homo sapiens cDNA
51	9348	18481	2.25	4.0E-53	AL163285.2	NT	Homo sapiens chromosome 21 segment HS21C085
51	9348	18482	2.25	4.0E-53	AL163285.2	NT	Homo sapiens chromosome 21 segment HS21C085
7768	16982	28473	3.53	4.0E-53	BF12870.1	EST_HUMAN	601810669F1 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4053977 5'
7768	16982	28474	3.53	4.0E-53	BF12870.1	EST_HUMAN	601810669F1 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4053977 5'
2822	11806	21023	1.8	3.0E-53	AB026898.1	NT	Homo sapiens DNA, DLEC1 to ORCTL4 gene region, section 1/2 (DLEC1, ORCTL3, ORCTL4 genes, complete cds)
3712	12832	22050	1.7	3.0E-53	AW060836.1	EST_HUMAN	wr22c07.x1 Soares_Dieckgraefe_colon_NHCD Homo sapiens cDNA clone IMAGE:2558796 3'
4588	13782	22874	0.61	3.0E-53	AW803563.1	EST_HUMAN	IL2-JM0081-240300-055-D03 UM0081 Homo sapiens cDNA
6582	15758	25221	5.16	3.0E-53	S72043.1	NT	GIF=growth inhibitory factor [human, brain, Genomic, 2015 nt]
6786	15983		8.94	3.0E-53	5801953	NT	Homo sapiens FGFR1 oncogene partner (FOP), mRNA
8493	17536		1.41	3.0E-53	11428423	NT	Homo sapiens acetyl-Coenzyme A carboxylase alpha (ACACA), mRNA
484	9717		5.34	2.0E-53	AA368558.1	EST_HUMAN	EST177525 Pancreas tumor III Homo sapiens cDNA 5' end
2286	11491	20711	43.99	2.0E-53	U78027.1	NT	Homo sapiens Bruton's tyrosine kinase (BTK), alpha-D-galactosidase A (GLA), L44-like ribosomal protein (L44L), and FTP3 (FTP3) genes, complete cds
2501	11690		11.69	2.0E-53	4502316	NT	Homo sapiens ATPase, H+ transporting, lysosomal (vacuolar proton pump) 31kD; Vacuolar proton-ATPase, subunit E; V-ATPase, subunit E (ATP8E), mRNA
3212	12446	21579	0.8	2.0E-53	AF083822.1	NT	Homo sapiens dihydropyridine receptor alpha 2 subunit (CACNA2D1) gene, exon 6
4036	13246	22349	2.27	2.0E-53	M61873.1	NT	Human Krueppel-related DNA-binding protein (TF34) gene, partial cds
5408	14834	23749	2.32	2.0E-53	BF33740.1	EST_HUMAN	PM1-CT0398-170800-001-g03 CT0398 Homo sapiens cDNA

Page 214 of 382  
Table 4  
Single Exon Probes Expressed in HELA Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5408	14634	23747	2.32	2.0E-53	BF334740.1	EST_HUMAN	PM1-CT0398-170800-001-g03 CT0398 Homo sapiens cDNA
6880	16071		6.07	2.0E-53	AW245678.1	EST_HUMAN	2822665.5prime NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2822665 5'
1447	10860	19835	1.18	1.0E-53	AJ271738.1	NT	Homo sapiens Xq pseudautosomal region; segment 2/2
3387	12614	21747	1.42	1.0E-53	AB026898.1	NT	Homo sapiens DNA, DLEC1 to ORCTL4 gene region, section 1/2 (DLEC1, ORCTL3, ORCTL4 genes, complete cds)
4884	14171	23261	1.03	1.0E-53	BE296388.1	EST_HUMAN	601178725F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3531919 5'
6801	15896	25454	12.97	1.0E-53	X79536.1	NT	H. sapiens mRNA for hnRNPcore protein A1
8359	17451	26581	1.49	1.0E-53	AW245422.1	EST_HUMAN	2822943.3prime NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2822943 3'
3218	12452	21585	0.82	9.0E-54	4504116	NT	Homo sapiens glutamate receptor, ionotropic, kainate 1 (GRIK1) mRNA
5330	18050	23634	5.28	9.0E-54	4508786	NT	Homo sapiens IQ motif containing GTPase activating protein 1 (IQGAP1) mRNA
212	9492	18624	5.45	8.0E-54	BE398785.1	EST_HUMAN	601272863F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3614031 5'
1803	11012	20205	2.01	8.0E-54	4504810	NT	Homo sapiens insulin-like growth factor 2 receptor (IGF2R) mRNA
4747	13938	23041	0.71	8.0E-54	4507848	NT	Homo sapiens ubiquitin specific protease 13 (isopeptidase T-3) (USP13) mRNA
4747	13938	23042	0.71	8.0E-54	4507848	NT	Homo sapiens ubiquitin specific protease 13 (isopeptidase T-3) (USP13) mRNA
5129	13938	23041	0.72	8.0E-54	4507848	NT	Homo sapiens ubiquitin specific protease 13 (isopeptidase T-3) (USP13) mRNA
5129	13938	23042	0.72	8.0E-54	4507848	NT	Homo sapiens ubiquitin specific protease 13 (isopeptidase T-3) (USP13) mRNA
5631	14855	24238	22.45	8.0E-54	6005700	NT	Homo sapiens ATP-binding cassette, sub-family A (ABC1), member 8 (ABCA8), mRNA
389	9683	18820	1.42	7.0E-54	AA812537.1	EST_HUMAN	ai79c12.s1 Soares_testis_NHT Homo sapiens cDNA clone 1377046 3' similar to contains MER30.13 MER30 repetitive element ;
1798	11007	20200	1.3	7.0E-54	Y16845.1	NT	Homo sapiens mRNA for monocytic chemotactic protein-2
2171	11368	20589	8.45	7.0E-54	N27177.1	EST_HUMAN	yw68d12.s1 Soares_placenta_8to8weeks_2NBHP8to8W Homo sapiens cDNA clone IMAGE:257398 3' similar to contains LTR7.b3 LTR7 repetitive element ;
7668	16867	26368	2.02	7.0E-54	8923698	NT	Homo sapiens golgin-like protein (GLP), mRNA
7668	16867	26369	2.02	7.0E-54	8923698	NT	Homo sapiens golgin-like protein (GLP), mRNA
7839	17031		6.58	7.0E-54	AI160189.1	EST_HUMAN	qb67g03.x1 Soares_fetal_heart_NbH110W Homo sapiens cDNA clone IMAGE:1705204 3' similar to contains OFR.11 OFR repetitive element ;
24	9320	18424	4.02	6.0E-54	AB003618.1	NT	Homo sapiens DNA for MICB, exon 4, 5 and partial cds
390	9684	18821	1.74	6.0E-54	8922148	NT	Homo sapiens hypothetical protein DKFZp434M035 (DKFZp434M035), mRNA
390	9684	18822	1.74	6.0E-54	8922148	NT	Homo sapiens hypothetical protein DKFZp434M035 (DKFZp434M035), mRNA
3251	12484	21616	1.3	6.0E-54	8922148	NT	Homo sapiens hypothetical protein DKFZp434M035 (DKFZp434M035), mRNA
3981	13195	22303	1.16	6.0E-54	4502872	NT	Homo sapiens chloride channel 6 (CLON6) mRNA
4457	13655	22749	0.75	6.0E-54	AV754748.1	EST_HUMAN	AV754748 TP Homo sapiens cDNA clone TPGAAC10 5'
4891	14079		1.7	6.0E-54	Y09846.1	NT	H. sapiens shc pseudogene, p86 isoform
5024	14079		2.37	6.0E-54	Y09846.1	NT	H. sapiens shc pseudogene, p86 isoform

Table 4

## Single Exon Probes Expressed in HELA Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7990	18425	25912	4.04	6.0E-54	AW813587.1	EST_HUMAN	RC3-ST0197-151099-011-408 ST0197 Homo sapiens cDNA
2119	11318	20536	3.92	5.0E-54	P51523	SWISSPROT	ZINC FINGER PROTEIN 84 (ZINC FINGER PROTEIN HPF2)
187	9466		74.6	4.0E-54	AF110103.1	NT	Tupaiia belangeri beta-actin mRNA, partial cds
983	10186	19351	100.21	4.0E-54	AA306764.1	EST_HUMAN	EST177698 Jurkat T-cells VI Homo sapiens cDNA 5' end similar to glyceraldehyde-3-phosphate dehydrogenase
1774	10984	20175	3.46	4.0E-54	D38521.1	NT	Human mRNA for KIAA0077 gene, partial cds
1774	10984	20176	3.46	4.0E-54	D38521.1	NT	Human mRNA for KIAA0077 gene, partial cds
3168	12403		1.94	4.0E-54	AI935086.1	EST_HUMAN	wd26d11.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2329269 3' similar to TR:O02711
83	9386	18515	11.44	3.0E-54	AA313487.1	EST_HUMAN	O02711 PRO-POL-OUTPASE POLYPROTEIN ;
2587	11773		1.32	3.0E-54	AI908757.1	EST_HUMAN	EST185371 Colon carcinoma (HCC) cell line Homo sapiens cDNA 5' end
7652	16852	26350	4.71	3.0E-54	BF345600.1	EST_HUMAN	IL-BT189-180399-007 BT189 Homo sapiens cDNA
7908	17123	26854	3.14	3.0E-54	AA39362.1	EST_HUMAN	602019408F1 NCI_CGAP_Bm87 Homo sapiens cDNA clone IMAGE:4155121 5'
8464	17519	24022	2.69	3.0E-54	AW954559.1	EST_HUMAN	z70f12.1 Soares testis NHT Homo sapiens cDNA clone IMAGE:727727 5' similar to TR:G191315
8512	18337		2.75	3.0E-54	AW748965.1	EST_HUMAN	G191315 ANDROGEN-DEPENDENT EXPRESSED PROTEIN ;
648	9894	18018	8.02	2.0E-54		NT	EST366828 MAGE resequences, MAGC Homo sapiens cDNA
1373	10587	19753	1.05	2.0E-54	5031900	NT	RC1-BT0313-131199-011-509 BT0313 Homo sapiens cDNA
2504	11692	20912	2.47	2.0E-54	AW163175.1	EST_HUMAN	Homo sapiens killer cell lectin-like receptor subfamily G, member 1 (KLRG1), mRNA
2560	11746	20866	2.11	2.0E-54	AL163210.2	NT	Homo sapiens nuclear antigen Sp100 (SP100) mRNA
2847	12086	21215	1.44	2.0E-54	AW057524.1	EST_HUMAN	au92g03.y1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2783784 5' similar to SW:CUL1_HUMAN Q13616 CULLIN HOMOLOG 1 ;
3523	12747		6.73	2.0E-54	AA532925.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C0010
4187	13391		3.92	2.0E-54	4502642	NT	wy60b12.x1 Soares_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:2552927 3' similar to TR:Q82084 Q82084 PHOSPHOLIPASE C NEIGHBORING ;
4434	13634		1.21	2.0E-54	AF208161.1	NT	W45g09.a1 NCI_CGAP_P8 Homo sapiens cDNA clone IMAGE:895488 similar to gb:X63777 60S
4438	13638		1.27	2.0E-54	AL163201.2	NT	RIBOSOMAL PROTEIN L23 (HUMAN);
5166	14345	23434	0.6	2.0E-54	AL163201.2	NT	Homo sapiens cheparonin containing T-complex subunit 6 (CCT6) mRNA
5556	14780	24148	4.56	2.0E-54		NT	Homo sapiens synovial precursor, mRNA, complete cds
5595	14819	24195	12.42	2.0E-54	AB046811.1	NT	Homo sapiens chromosome 21 segment HS21C0001
5595	14819	24196	12.42	2.0E-54	AB046811.1	NT	Homo sapiens KIAA0100 gene product (KIAA0100), mRNA
6128	15312	24746	7.59	2.0E-54	11428544	NT	Homo sapiens mRNA for KIAA1591 protein, partial cds
						NT	Homo sapiens neurofibromin 1 (neurofibromatosis, von Recklinghausen disease, Watson disease) (NF1), mRNA

Table 4

## Single Exon Probes Expressed in HELA Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6973	16151	25622	4.05	2.0E-54	AB001026.1	NT	Homo sapiens mRNA for brain ryanodine receptor, complete cds
8217	17348		4.24	2.0E-54	7657454	NT	Homo sapiens pascadillo (zebrafish) homolog 1, containing BRCT domain (PES1), mRNA
8931	17853	23887	1.8	2.0E-54	8567387	NT	Homo sapiens perforin (Drosophila) homolog 3 (PER3), mRNA
4461	13659		1.8	1.0E-54	BF316418.1	EST_HUMAN	601889230F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4128535 5'
9168	17963		3.74	1.0E-54	AU077341.1	EST_HUMAN	AU077341 Sugano cDNA library Homo sapiens cDNA clone Zv6C880 similar to 5'-end region of Human gamma-glutamyl transpeptidase mRNA, 5 end
1322	10537		0.87	8.0E-55	Y07828.2	NT	Homo sapiens RFB30 gene for RING finger protein
1325	10540		2.14	8.0E-55	Y07829.2	NT	Homo sapiens RFB30 gene for RING finger protein
7750	16946		2.46	8.0E-55	AW409714.1	EST_HUMAN	h02a02.x1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:2660807 5'
1089	10313	19487	1.07	7.0E-55	R06346.1	EST_HUMAN	yf26a04.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:127998 5' similar to SP-C561 BOVIN P10897 CYTOCHROME
7762	16958	26467	15.56	7.0E-55	AI581056.1	EST_HUMAN	tq29f09.x1 NCI_CGAP_U11 Homo sapiens cDNA clone IMAGE:2210249 3'
7762	16958	26468	15.58	7.0E-55	AI581056.1	EST_HUMAN	tq29f09.x1 NCI_CGAP_U11 Homo sapiens cDNA clone IMAGE:2210249 3'
8987	17851		1.49	7.0E-55	H23396.1	EST_HUMAN	ym57g07.r1 Soares infant brain 1N1B Homo sapiens cDNA clone IMAGE:52444 5'
9136	18283		5.18	7.0E-55	H23396.1	EST_HUMAN	ym57g07.r1 Soares infant brain 1N1B Homo sapiens cDNA clone IMAGE:52444 5'
8046	17182	26722	2.17	8.0E-55	AB040834.1	NT	Homo sapiens mRNA for KIAA1501 protein, partial cds
1740	10952	20134	1.32	5.0E-55	AA704871.1	EST_HUMAN	z95b09.s1 Soares fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:462617 3'
1740	10952	20135	1.32	5.0E-55	AA704871.1	EST_HUMAN	z95b09.s1 Soares fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:462617 3'
4782	13971	23074	1.49	5.0E-55	AW206021.1	EST_HUMAN	UI-H-B11-afy-g-09-0-UJ.st NCI_CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2723536 3'
5898	15115	24526	1.68	5.0E-55	4502240	NT	Homo sapiens arylsulfatase E (chondrodysplasia punctata 1) (ARSE), mRNA
5898	15115	24527	1.68	5.0E-55	4502240	NT	Homo sapiens arylsulfatase E (chondrodysplasia punctata 1) (ARSE), mRNA
6781	15978	25434	2.25	5.0E-55	4506302	NT	Homo sapiens protein tyrosine phosphatase, receptor type, alpha polypeptide (PTPRA) mRNA
8555	17577		3.35	5.0E-55	11417972	NT	Homo sapiens pascadillo (zebrafish) homolog 1, containing BRCT domain (PES1), mRNA
57	11958	18470	3.36	4.0E-55	AW067894.1	EST_HUMAN	EST370084 IMAGE resequences, IMAGE Homo sapiens cDNA
678	9922	19053	46.87	4.0E-55		NT	Homo sapiens RNA binding motif protein, Y chromosome, family 1, member A1 (RBM1A1) mRNA
1442	10656	19830	1.18	4.0E-55	7661713	NT	Homo sapiens predicted osteoblast protein (GS3786), mRNA
1442	10656	19831	1.18	4.0E-55	7661713	NT	Homo sapiens predicted osteoblast protein (GS3786), mRNA
1503	10718		1.45	4.0E-55	BF061411.1	EST_HUMAN	Homo sapiens predicted osteoblast protein (GS3786), mRNA
1994	11197	20406	2.71	4.0E-55	4506180	NT	contains L1 L2 L1 repetitive element
1994	11197	20407	2.71	4.0E-55	4506180	NT	Homo sapiens proteasome (prosome, macropain) subunit, alpha type, 2 (PSMA2) mRNA
2055	11256	20469	8.48	4.0E-55	4503314	NT	Homo sapiens proteasome (prosome, macropain) subunit, alpha type, 2 (PSMA2) mRNA
2055	11256	20470	8.48	4.0E-55	4503314	NT	Homo sapiens diacylglycerol kinase, gamma (60kD) (DGKG) mRNA
2276	11471	20693	7.25	4.0E-55	4507794	NT	Homo sapiens diacylglycerol kinase, gamma (60kD) (DGKG) mRNA
							Homo sapiens ubiquitin-conjugating enzyme E2 variant 1 (UBE2V1) mRNA

Table 4

## Single Exon Probes Expressed in HELA Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2550	11738		0.88	4.0E-55	AJ271735.1	NT	Homo sapiens Xq pseudautosomal region; segment 1/2
3247	12480	21812	0.94	4.0E-55	AL163300.2	NT	Homo sapiens chromosome 21 segment HS21C100
6578	15774		5.57	4.0E-55	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C010
7781	16878		5.6	4.0E-55	W28189.1	EST_HUMAN	43c5 Human retina cDNA randomly primed sublibrary Homo sapiens cDNA
8466	17520		7.9	4.0E-55	BF303941.1	EST_HUMAN	601886575F2 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4120338 5'
8402	17480		3.27	3.0E-55	BE178519.1	EST_HUMAN	PM1-HT0603-080300-001-g08 HT0603 Homo sapiens cDNA
9181	17973		1.68	3.0E-55	AL163284.2	NT	Homo sapiens chromosome 21 segment HS21C084
382	9848	18781	2.24	2.0E-55	X57147.1	NT	Human endogenous retrovirus pHE.1 (ERV9)
558	9808		1.09	2.0E-55	M10978.1	NT	Human endogenous retroviral DNA (4-1), complete retroviral segment
655	9801	19027	3.36	2.0E-55	4507288	NT	Homo sapiens syntaxin-binding protein 1 (STXBP1) mRNA, and translated products
2813	12151	21286	0.82	2.0E-55	4507788	NT	Homo sapiens ubiquitin protein ligase E3A (human papilloma virus E6-associated protein, Angelman syndrome) (UBE3A) mRNA
4785	13974	23077	2.73	2.0E-55	BE178988.1	EST_HUMAN	GM1-HT0876-150800-357-g03 HT0876 Homo sapiens cDNA
6819	18013		2.85	2.0E-55	AI028336.1	EST_HUMAN	am98h05.s1 Strategene schizo brain S11 Homo sapiens cDNA clone IMAGE:1684185 3' similar to contains
7523	16728	26219	2.48	2.0E-55	AU119344.1	EST_HUMAN	THR b2 THR repetitive element
98	9389	18518	1.2	1.0E-55	4505060	NT	AU119344 HEMBA1 Homo sapiens cDNA clone HEMBA1005583 5'
194	9474	18505	60.19	1.0E-55	U09823.1	NT	Homo sapiens mannose-6-phosphate receptor (cation dependent) (M6PR) mRNA
581	9830	18948	0.67	1.0E-55	AI026718.1	EST_HUMAN	Oryctolagus cuniculus New Zealand white elongation factor 1 alpha (Rabefla2) mRNA, complete cds
1158	10380	18532	5.24	1.0E-55	AB020710.1	NT	ov65g09.x1 Soares testis_NHT Homo sapiens cDNA clone IMAGE:1644180 3'
1921	11125	20320	2.45	1.0E-55	BE277861.1	EST_HUMAN	Homo sapiens mRNA for KIAA0603 protein, partial cds
1921	11125	20321	2.45	1.0E-55	BE277861.1	EST_HUMAN	601120118F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:2867027 5'
2293	11488		8.1	1.0E-55	5803174	NT	601120118F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:2867027 5'
2483	11673	20890	79.35	1.0E-55	X13111.1	NT	Homo sapiens SMA3 (SMA3), mRNA
2520	11708	20923	5.19	1.0E-55	AB007866.2	NT	Human mRNA for HLA-A11E, a MHC class I molecule (major histocompatibility complex)
2520	11708	20924	5.19	1.0E-55	AB007866.2	NT	Homo sapiens mRNA for KIAA0406 protein, partial cds
2573	11758	20978	8.98	1.0E-55	LS4057.1	NT	Homo sapiens mRNA for KIAA0406 protein, partial cds
3887	13182	22281	3.76	1.0E-55	AL163287.2	NT	Homo sapiens CLP mRNA, partial cds
4282	13485	22584	1.09	1.0E-55	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C067
4742	13933		1.09	1.0E-55	NT7281.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C010
4845	14034	23126	1.85	1.0E-55	AB037163.1	NT	yw44g03.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:245620 5'
4845	14034	23127	1.85	1.0E-55	AB037163.1	NT	Homo sapiens DSCR5b mRNA, complete cds
5182	14341	23430	0.87	1.0E-55	8923125	NT	Homo sapiens DSCR5b mRNA, complete cds
							Homo sapiens hypothetical protein FLJ20126 (FLJ20126), mRNA

Table 4

## Single Exon Probes Expressed in HELA Cells

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5778	14996	24397	6.65	1.0E-55	11433048	NT	Homo sapiens hct domain and RLD 2 (HERC2), mRNA
5778	14996	24398	6.65	1.0E-55	11433048	NT	Homo sapiens hct domain and RLD 2 (HERC2), mRNA
7489	16993	26178	5.28	1.0E-55	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C010
7489	16993	26177	5.28	1.0E-55	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C010
7884	16419	25906	2.62	1.0E-55	U50850.1	NT	Human infant brain unknown product mRNA, complete cds
8003	16438	25925	2.12	1.0E-55	T10045.1	EST_HUMAN	seq1575 b4HB3MA C018-HAP-F1 Homo sapiens cDNA clone b4HB3MA-C018-HAP-F161 5' similar to similar to Chinese Hamster DHFR-coamplified protein mRNA
6241	15422	24863	1.68	9.0E-56	BE378074.1	EST_HUMAN	601237702F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3609552 5'
2680	11871	21085	5.74	7.0E-56	H18634.1	EST_HUMAN	Yn62g03.r1 Soares adult brain N2b5HB55Y Homo sapiens cDNA clone IMAGE:173044 5' similar to contains THR repetitive element;
6353	15533	24985	2.12	7.0E-56	AW361213.1	EST_HUMAN	RC1-CT0252-231069-013-b07 CT0252 Homo sapiens cDNA
6353	15533	24986	2.12	7.0E-56	AW361213.1	EST_HUMAN	RC1-CT0252-231099-013-b07 CT0252 Homo sapiens cDNA
1687	10880	20084	1.85	5.0E-56	AW98712.1	EST_HUMAN	RC3-BN0053-170200-011-h01 BN0053 Homo sapiens cDNA
8651	18324	23589	2.16	5.0E-56	H55099.1	EST_HUMAN	CHR220038 Chromosome 22 exon Homo sapiens cDNA clone C22_55 5'
29	9325	18428	18.75	4.0E-56	AF141349.1	NT	Homo sapiens beta-tubulin mRNA, complete cds
29	9325	18429	18.75	4.0E-56	AF141349.1	NT	Homo sapiens beta-tubulin mRNA, complete cds
2669	11850	21065	3.18	4.0E-56	4507728	NT	Homo sapiens tubulin, beta polypeptide (TUBB) mRNA
2669	11850	21066	3.18	4.0E-56	4507728	NT	Homo sapiens tubulin, beta polypeptide (TUBB) mRNA
2764	9783	18906	3.7	4.0E-56	AF003528.1	NT	Homo sapiens X-linked anhidrotic ectodermal dysplasia protein gene (EDA), exon 2 and flanking repeat regions
2785	11761	20981	1.3	4.0E-56	AI632488.1	EST_HUMAN	wb09f08.x1 NCI CGAP GC8 Homo sapiens cDNA clone IMAGE:2305191 3' similar to SW:DCOR_MUSPA
2785	11761	20982	1.3	4.0E-56	AI632488.1	EST_HUMAN	P27119 ORNITHINE DECARBOXYLASE ;
5773	14991	24391	5.54	4.0E-56	AF217508.1	NT	wb09f08.x1 NCI CGAP GC8 Homo sapiens cDNA clone IMAGE:2305191 3' similar to SW:DCOR_MUSPA
5773	14991	24392	5.54	4.0E-56	AF217508.1	NT	P27119 ORNITHINE DECARBOXYLASE ;
7497	16704	26188	11.06	4.0E-56	AI498066.1	EST_HUMAN	Homo sapiens uncharacterized bone marrow protein BM031 mRNA, complete cds
7497	16704	26189	11.06	4.0E-56	AI498066.1	EST_HUMAN	Homo sapiens uncharacterized bone marrow protein BM031 mRNA, complete cds
1349	10584	19728	4.56	3.0E-56	8924029	NT	tm85g12.x1 NCI CGAP Bm25 Homo sapiens cDNA clone IMAGE:2163046 3'
1735	10947	20130	1.43	3.0E-56	6912743	NT	tm85g12.x1 NCI CGAP Bm25 Homo sapiens cDNA clone IMAGE:2163046 3'
2118	11317	20535	1.09	3.0E-56	6912687	NT	Homo sapiens hypothetical protein PRO1304 (PRO1304), mRNA
3089	12325	21447	1.68	3.0E-56	AA325828.1	EST_HUMAN	Homo sapiens 5'-3' exoribonuclease 2 (XRN2), mRNA
3089	12325	21448	1.68	3.0E-56	AA325828.1	EST_HUMAN	Homo sapiens oncogene TC21 (TC21), mRNA
3824	13042		2.27	3.0E-56	AF055066.1	NT	EST28889 Cerebellum II Homo sapiens cDNA 5' end
							EST28889 Cerebellum II Homo sapiens cDNA 5' end
							Homo sapiens MHC class 1 region

Page 219 of 382  
Table 4  
Single Exon Probes Expressed in HELA Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3895	13111	22229	0.98	3.0E-56	BE933512.1	EST_HUMAN	601310203F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3631848 5'
4382	13583	22685	0.6	3.0E-56	7657042	NT	Homo sapiens Down syndrome candidate region 1 (DSOR1), mRNA
4416	13616	22712	5.14	3.0E-56	AL163288.2	NT	Homo sapiens chromosome 21 segment HS21C068
4570	13764	22860	2.93	3.0E-56	5902085	NT	Homo sapiens superkiller viralicidic activity 2 (S. cerevisiae homolog)-like (SKIV2L), mRNA
4817	14008		1.75	3.0E-56	BE933572.1	EST_HUMAN	601439154F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3923100 5'
5142	14321	23413	0.76	3.0E-56	6912593	NT	Homo sapiens phosphatidylinositol transfer protein, beta (PTPNB), mRNA
5528	14752	24118	1.73	3.0E-56	4759163	NT	Homo sapiens sparco/osteonectin, cwcw and kazal-like domains proteoglycan (testican) (SPOCK) mRNA
5528	14752	24119	1.73	3.0E-56	4759163	NT	Homo sapiens sparco/osteonectin, cwcw and kazal-like domains proteoglycan (testican) (SPOCK) mRNA
6030	15238	24681	5.37	3.0E-56	11421124	NT	Homo sapiens lysosomal-associated membrane protein 2 (LAMP2), mRNA
6723	15918	25377	8	3.0E-56	11418704	NT	Homo sapiens bone morphogenetic protein 5 (BMP5), mRNA
7211	16388	25870	2.39	3.0E-56	11434856	NT	Homo sapiens KIAA0317 gene product (KIAA0317), mRNA
7861	17051	26571	5.15	3.0E-56	5902013	NT	Homo sapiens nuclear pore complex interacting protein (NPIP), mRNA
7861	17051	26572	5.15	3.0E-56	5902013	NT	Homo sapiens nuclear pore complex interacting protein (NPIP), mRNA
8510	17548	23984	1.24	3.0E-56	11434876	NT	Homo sapiens caveolin 3 (CAV3), mRNA
8510	17548	23985	1.24	3.0E-56	11434876	NT	Homo sapiens caveolin 3 (CAV3), mRNA
530	9781		2.09	2.0E-56	AA189818.1	EST_HUMAN	zq52a08.st Stratogene neuroepithelium (#837231) Homo sapiens cDNA clone IMAGE:645206 3'
740	11976	19122	1.19	2.0E-56	BE064386.1	EST_HUMAN	RC4-BT0310-110300-015-f10 BT0310 Homo sapiens cDNA
740	11976	19123	1.19	2.0E-56	BE064386.1	EST_HUMAN	RC4-BT0310-110300-015-f10 BT0310 Homo sapiens cDNA
2945	12183	21316	1.53	2.0E-56	AB037835.1	NT	Homo sapiens mRNA for KIAA1414 protein, partial cds
3288	12519		0.82	2.0E-56	AB008981.1	NT	Homo sapiens gene for activin receptor type IIB, complete cds
3507	12731	21869	1.14	2.0E-56	AV703184.1	EST_HUMAN	AV703184 ADB Homo sapiens cDNA clone ADBCFG10 5'
6121	15305	24738	1.71	2.0E-56	5730038	NT	Homo sapiens SET domain and mariner transposase fusion gene (SETMAR) mRNA
987	10218		24.65	1.0E-56	AF190630.1	NT	Macaca fascicularis protein tyrosine phosphatase (PRL-1) mRNA, complete cds
3655	12876	21894	1.84	1.0E-56	AW598833.1	EST_HUMAN	hg23c11.x1 NCI_CGAP_G06 Homo sapiens cDNA clone IMAGE:2946452 3'
3655	12876	21895	1.84	1.0E-56	AW598833.1	EST_HUMAN	hg23c11.x1 NCI_CGAP_G06 Homo sapiens cDNA clone IMAGE:2946452 3'
631	9876		2.23	9.0E-57	AW890885.1	EST_HUMAN	QV0-OT0033-070300-152-h03 OT0033 Homo sapiens cDNA
7773	16988	26481	2.07	9.0E-57	AF228497.1	NT	Homo sapiens serine protease 17 (KLK4) gene, complete cds
7773	16988	26482	2.07	9.0E-57	AF228497.1	NT	Homo sapiens serine protease 17 (KLK4) gene, complete cds
8053	17189	26729	1.8	9.0E-57	AB020981.1	NT	Homo sapiens mRNA for cyclin B2, complete cds
13	9309	18411	0.69	8.0E-57	8923349	NT	Homo sapiens hypothetical protein FLJ20371 (FLJ20371), mRNA
302	9575	18708	2.41	8.0E-57	AW816405.1	EST_HUMAN	QV4-ST0234-181199-037-f05 ST0234 Homo sapiens cDNA



Page 220 of 382  
Table 4  
Single Exon Probes Expressed in HELA Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
894	10129	19281	4.82	8.0E-57	AW284598.1	EST_HUMAN	x05410.x1 NCI_CGAP_Brm53 Homo sapiens cDNA clone IMAGE:2769261 3' similar to gb:U05875
1785	10985	20181	1.75	8.0E-57	AA498109.1	EST_HUMAN	INTERFERON-GAMMA RECEPTOR BETA CHAIN PRECURSOR (HUMAN);
5060	14240	23328	0.9	8.0E-57	BE289918.1	EST_HUMAN	z51b12.11 Soares testis_NHT Homo sapiens cDNA clone IMAGE:757151 5'
5297	18235	23703	2.72	8.0E-57	11418185	NT	600844440.F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:2960884.5'
5853	15071	24481	13.17	8.0E-57	AB023177.1	NT	Homo sapiens acrinase 2, mitochondrial (ACO2), mRNA
5853	15071	24482	13.17	8.0E-57	AB023177.1	NT	Homo sapiens mRNA for KIAA0860 protein, partial cds
6396	15577	25034	2.28	8.0E-57	AB020844.1	NT	Homo sapiens mRNA for KIAA0837 protein, partial cds
6396	15577	25035	2.29	8.0E-57	AB020844.1	NT	Homo sapiens mRNA for KIAA0837 protein, partial cds
8013	8309	18411	3.51	8.0E-57	8923349	NT	Homo sapiens hypothetical protein FLJ20371 (FLJ20371), mRNA
8751	17894	23925	1.48	8.0E-57	7019528	NT	Homo sapiens monocarboxylate transporter 3 (SLC16A8), mRNA
8902	17785	23925	2.02	8.0E-57	11545732	NT	Homo sapiens SH3-domain binding protein 1 (SH3BP1), mRNA
2597	11782	21001	1.89	7.0E-57	7657592	NT	Homo sapiens smg GDS-ASSOCIATED PROTEIN (SMAP), mRNA
2597	11782	21002	1.89	7.0E-57	7657592	NT	Homo sapiens smg GDS-ASSOCIATED PROTEIN (SMAP), mRNA
3238	12472	21604	0.78	7.0E-57	6005979	NT	Homo sapiens Kruppel-like factor 8 (KLF8), mRNA
3859	13075	22180	2.25	7.0E-57	AF012872.1	NT	Homo sapiens phosphatidylinositol 4-kinase 230 (p4K230) mRNA, complete cds
3859	13075	22181	2.25	7.0E-57	AF012872.1	NT	Homo sapiens phosphatidylinositol 4-kinase 230 (p4K230) mRNA, complete cds
9253	18270		4.12	6.0E-57	AJ271736.1	NT	Homo sapiens Xq pseudautosomal region, segment 1/2
3736	12856	22072	2.71	4.0E-57	AB026898.1	NT	Homo sapiens DNA, DLEC1 to ORCTL4 gene region, section 1/2 (DLEC1, ORCTL3, ORCTL4 genes, complete cds)
814	10052	18206	1.2	3.0E-57	4507788	NT	Homo sapiens ubiquitin protein ligase E3A (human papilloma virus E6-associated protein, Angelman syndrome) (UBE3A) mRNA
1339	10553		55.7	3.0E-57	AA230278.1	EST_HUMAN	nc13f07.s1 NCI_CGAP_P71 Homo sapiens cDNA clone IMAGE:1008037 similar to SW:RS10_HUMAN
2354	11547	20768	1.09	3.0E-57	AA348335.1	EST_HUMAN	P48783 40S RIBOSOMAL PROTEIN S10. ;
2684	11845	21059	1.09	3.0E-57	BE676622.1	EST_HUMAN	EST54770 Hippocampus II Homo sapiens cDNA 5' end
2684	11845	21060	1.09	3.0E-57	BE676622.1	EST_HUMAN	7733b10.x1 NCI_CGAP_CLL1 Homo sapiens cDNA clone IMAGE:3286443 3' similar to WP:Y47H9C.2
3536	12759	21890	2.57	3.0E-57	AF232708.1	NT	CE20263 ;
3675	12886		43.08	3.0E-57	AW853984.1	EST_HUMAN	7733b10.x1 NCI_CGAP_CLL1 Homo sapiens cDNA clone IMAGE:3286443 3' similar to WP:Y47H9C.2
5719	14937	24333	3.4	3.0E-57	BE796337.1	EST_HUMAN	7733b10.x1 NCI_CGAP_CLL1 Homo sapiens cDNA clone IMAGE:3286443 3' similar to WP:Y47H9C.2
6507	15703	25169	3.32	3.0E-57	W28130.1	EST_HUMAN	CE20263 ;
6515	15711	25175	2.34	3.0E-57	11545798	NT	7733b10.x1 NCI_CGAP_CLL1 Homo sapiens cDNA clone IMAGE:3286443 3' similar to WP:Y47H9C.2
							Homo sapiens cell-line ISA201a chloride ion current inducer protein (Cln) gene, complete cds
							RC3-CT0254-110300-027-d10 CT0254 Homo sapiens cDNA
							601589896.F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3944302 5'
							4216 Human retina cDNA randomly primed sublibrary Homo sapiens cDNA
							Homo sapiens hypothetical protein FLJ11656 (FLJ11656), mRNA

Table 4

## Single Exon Probes Expressed in HELA Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6515	15711	25176	2.34	3.0E-57	11545798	NT	Homo sapiens hypothetical protein FLJ11656 (FLJ11656), mRNA
6734	15929	25388	5.84	3.0E-57	AU117659.1	EST_HUMAN	AU117659 HEMBA1 Homo sapiens cDNA clone HEMBA1001910 5'
7482	16690	26172	3.42	3.0E-57	AW248374.1	EST_HUMAN	2820473.5 prime NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2820473 5'
8517	18343	23605	6.01	3.0E-57	W23871.1	EST_HUMAN	z645411.1 Soares fetal_lung_NbHL19W Homo sapiens cDNA clone IMAGE:305549 5'
8903	18240		1.57	3.0E-57	AW178575.1	EST_HUMAN	RCO-HT0112-08099-001-C06 HT0112 Homo sapiens cDNA
1492	10705	19878	1.63	2.0E-57	AF248219.1	NT	Homo sapiens SNARE protein kinase SNAK mRNA, complete cds
1492	10705	19879	1.63	2.0E-57	AF248219.1	NT	Homo sapiens SNARE protein kinase SNAK mRNA, complete cds
2385	11558	20780	0.98	2.0E-57	BE172528.1	EST_HUMAN	MRO-HT0559-010400-009-h10 HT0559 Homo sapiens cDNA
2688	11869	21083	2.54	2.0E-57	AA845419.1	EST_HUMAN	ak02502.s1 Soares parathyroid_tumor_NbHPA Homo sapiens cDNA clone IMAGE:1404747 3' similar to
3417	12842		2.73	2.0E-57	AL163204.2	NT	contains Alu repetitive element; contains element MER22 repetitive element;
3805	13121	22239	0.65	2.0E-57	BE073264.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C004
4189	13373	22472	2.44	2.0E-57	AA018299.1	EST_HUMAN	MRO-BT0551-080300-103-503 BT0551 Homo sapiens cDNA
4169	13373	22473	2.44	2.0E-57	AA018299.1	EST_HUMAN	z640c06.r1 Soares retina N2b4HR Homo sapiens cDNA clone IMAGE:361450 5'
4511	13707	22800	6.55	2.0E-57	AL163283.2	NT	z640c06.r1 Soares retina N2b4HR Homo sapiens cDNA clone IMAGE:361450 5'
5522	14747		1.69	2.0E-57	AA018131.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C083
5674	14894		31.59	2.0E-57	BF115298.1	EST_HUMAN	z631c05.r1 Soares retina N2b4HR Homo sapiens cDNA clone IMAGE:360584 5' similar to contains L1.13 L1
7619	17012	26525	2.46	2.0E-57	11424084	NT	repetitive element;
7818	17012	26526	2.48	2.0E-57	11424084	NT	7n80f04.x1 NCI CGAP_OV18 Homo sapiens cDNA clone IMAGE:3570866 3' similar to contains TAR1.11
7860	17050	26569	1.76	2.0E-57	AJ245503.1	NT	MER22 repetitive element;
7860	17050	26570	1.76	2.0E-57	AJ245503.1	NT	Homo sapiens hypothetical protein FLJ20041 (FLJ20041), mRNA
2198	11395	20617	2.63	1.0E-57	AW503208.1	EST_HUMAN	Homo sapiens hypothetical protein FLJ20041 (FLJ20041), mRNA
6878	15873		3.15	1.0E-57	BE043031.1	EST_HUMAN	Homo sapiens partial mRNA for PEX5 related protein
8880	17650		5.46	1.0E-57	AW470791.1	EST_HUMAN	Homo sapiens partial mRNA for PEX5 related protein
8960	17832	23909	1.58	9.0E-58	BE395061.1	EST_HUMAN	UIHF-BND-akt-g-07-0-J1.1 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3078348 5'
598	9843		2.21	8.0E-58	BE868715.1	EST_HUMAN	h032a08.x1 NCI CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3039062 3' similar to TR:O00246 O00246
660	9908	19033	9.69	8.0E-58	AI798376.1	EST_HUMAN	h032a08.x1 NCI CGAP_Kid12 Homo sapiens cDNA clone IMAGE:2875499 3' similar to contains THR.b3
660	9908	19034	9.69	8.0E-58	AI798376.1	EST_HUMAN	h032a08.x1 NCI CGAP_OV23 Homo sapiens cDNA clone IMAGE:3631000 5'
							THR repetitive element;
							601309405F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3631000 5'
							601445948F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3850211 5'
							tt34b07.x1 NCI CGAP_OV23 Homo sapiens cDNA clone IMAGE:2220181 3' similar to TR:O15475 O15475
							UNNAMED HERV-H PROTEIN;
							tt34b07.x1 NCI CGAP_OV23 Homo sapiens cDNA clone IMAGE:2220181 3' similar to TR:O15475 O15475
							UNNAMED HERV-H PROTEIN;

Page 222 of 382  
Table 4  
Single Exon Probes Expressed in HELA Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1824	11032	20228	2.33	8.0E-58	11434921	NT	Homo sapiens putative protein O-mannosyltransferase (POMT2), mRNA
1824	11032	20227	2.33	8.0E-58	11434921	NT	Homo sapiens putative protein O-mannosyltransferase (POMT2), mRNA
2829	12187		2.9	8.0E-58	7708132	NT	Homo sapiens DHHC1 protein (LOC51304), mRNA
4840	14127	23223	6.17	7.0E-58	BE206903.1	EST_HUMAN	ba05g04.y1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2823510 5' similar to TR:Q61489 Q61489 DHM1 PROTEIN ;
7432	16841		7.04	7.0E-58	5174542	NT	Homo sapiens MAD5 box transcription enhancer factor 2, polypeptide B (myocyte enhancer factor 2B) (MEF2B), mRNA
7503	18710	26197	3.9	7.0E-58	AW504109.1	EST_HUMAN	UI-HF-BND-all-g-10-Q-UJ.r1 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3079887 5'
7503	18710	26188	3.9	7.0E-58	AW504109.1	EST_HUMAN	UI-HF-BND-all-g-10-Q-UJ.r1 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3079887 5'
2218	11415	20640	1.85	6.0E-58	BE395061.1	EST_HUMAN	601309465F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3631000 5'
2343	11536	20760	12.88	8.0E-58	AU130688.1	EST_HUMAN	AU130688 NT2RP3 Homo sapiens cDNA clone NT2RP3001283 5'
2853	12091	21220	1.15	6.0E-58	BE242150.1	EST_HUMAN	TCAAP1E1219 Pediatric acute myelogenous leukemia cell (FAB M1) Baylor-HGSC project-TCAA Homo sapiens cDNA clone TCAAP1219
2853	12091	21221	1.15	6.0E-58	BE242150.1	EST_HUMAN	TCAAP1E1219 Pediatric acute myelogenous leukemia cell (FAB M1) Baylor-HGSC project-TCAA Homo sapiens cDNA clone TCAAP1219
8779	17709		1.8	8.0E-58	11528281	NT	Homo sapiens hypothetical protein FLJ20454 (FLJ20454), mRNA
305	9578	18710	4.63	5.0E-58	4507334	NT	Homo sapiens synaptotagmin 1 (SYNU1), mRNA
717	9959	19097	4.77	5.0E-58	BE763984.1	EST_HUMAN	RC4-NT0057-160600-016-b05 NT0057 Homo sapiens cDNA
1202	10422	18576	3.01	5.0E-58	AW797948.1	EST_HUMAN	CM3-JM0043-240300-127-e07 UM0043 Homo sapiens cDNA
1202	10422	18577	3.01	5.0E-58	AW797948.1	EST_HUMAN	CM3-JM0043-240300-127-e07 UM0043 Homo sapiens cDNA
1203	10422	18576	2.7	5.0E-58	AW797948.1	EST_HUMAN	CM3-JM0043-240300-127-e07 UM0043 Homo sapiens cDNA
1203	10422	18577	2.7	5.0E-58	AW797948.1	EST_HUMAN	CM3-JM0043-240300-127-e07 UM0043 Homo sapiens cDNA
3295	12526	21657	4.5	5.0E-58	AA988183.1	EST_HUMAN	or88607.s1 NCI CGAP Lu6 Homo sapiens cDNA clone IMAGE:1603908 3'
4245	13448	22539	0.92	5.0E-58	A1638745.1	EST_HUMAN	ts88e07.x1 NCI CGAP GC8 Homo sapiens cDNA clone IMAGE:2238468 3' similar to SW:PRO2_ACACA P19884 PROFILIN II ;
5504	14729		2.2	5.0E-58	11489282	NT	Homo sapiens placenta-specific 1 (PLAC1), mRNA
5743	14962	24362	6	5.0E-58	H23072.1	EST_HUMAN	ym51h07.r1 Soares infant brain 1N1B Homo sapiens cDNA clone IMAGE:52071 5'
6451	15648	25116	11.24	5.0E-58	8922693	NT	Homo sapiens hypothetical protein FLJ10828 (FLJ10828), mRNA
8483	18265		2.43	5.0E-58	11528293	NT	Homo sapiens cat eye syndrome chromosome region, candidate 1 (CECR1), mRNA
9183	17980		3.41	5.0E-58	11418177	NT	Homo sapiens Ran GTPase activating protein 1 (RANGAP1), mRNA
378	9844	18778	4.45	4.0E-58	4502302	NT	Homo sapiens ATP synthase, H+ transporting, mitochondrial F1 complex, O subunit (oligomycin sensitivity conferring protein) (ATP5O), mRNA
808	10045	19188	1.31	4.0E-58	4504634	NT	Homo sapiens interleukin 10 receptor, beta (IL10RB), mRNA

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## Single Exon Probes Expressed in HELA Cells

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1464	10677	19850	1.04	4.0E-58	4503648	NT	Homo sapiens coagulation factor IX (plasma thromboplastic component, Christmas disease, hemophilia B) (F9) mRNA
2541	11729	20947	1.09	4.0E-58	AF265555.1	NT	Homo sapiens ubiquitin-conjugating BIR-domain enzyme APOLLON mRNA, complete cds
2595	11781	20969	1.73	4.0E-58	U36251.1	NT	Human beta-prime-adaptin (BAM22) gene, exon 3
3297	12528	21659	1.07	4.0E-58	D16470.1	NT	Human mRNA, Xq terminal portion
3721	12941	22058	1.23	4.0E-58	5031660	NT	Homo sapiens EGF-like repeats and discoidin-like domains 3 (EDIL3), mRNA
7883	17071	26568	10.39	4.0E-58	11424059	NT	Homo sapiens E1B-55kDa-associated protein 5 (E1B-AP5), mRNA
340	9608		1.87	3.0E-58	R17879.1	EST_HUMAN	Y910402.1 Soares Infant brain 1N1B Homo sapiens cDNA clone IMAGE:31693 5'
1393	10607	19771	1.82	3.0E-58	4758981	NT	Homo sapiens peptide YY (PYY) mRNA
2690	12227		0.76	3.0E-58	R17879.1	EST_HUMAN	Y910402.1 Soares Infant brain 1N1B Homo sapiens cDNA clone IMAGE:31693 5'
3143	12378	21508	3.37	3.0E-58	BF569848.1	EST_HUMAN	602185789F1 NIH_MGC_45 Homo sapiens cDNA clone IMAGE:4308943 5'
3143	12378	21509	3.37	3.0E-58	BF569848.1	EST_HUMAN	602185789F1 NIH_MGC_45 Homo sapiens cDNA clone IMAGE:4308943 5'
948	10181	19337	12.44	2.0E-58	AF088624.1	NT	Homo sapiens 5-aminolevulinic synthase 2 (ALAS2) gene, complete cds
1297	10512		47.14	2.0E-58	BE208532.1	EST_HUMAN	ba08b07.y1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2823733 5' similar to gb:X69391 60S RIBOSOMAL PROTEIN L8 (HUMAN); gb:X81987 M.musculus mRNA for TAX responsive element binding protein (MOUSE);
5371	18052	23678	3.36	2.0E-58	BE907186.1	EST_HUMAN	601498961F1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3901911 5'
5371	18052	23710	3.36	2.0E-58	BE907186.1	EST_HUMAN	601498961F1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3901911 5'
5717	14935	24331	1.81	2.0E-58	A1124874.1	EST_HUMAN	am57e02.x1 Johnston frontal cortex Homo sapiens cDNA clone IMAGE:1539674 3' similar to WP:ZK328.1 CE05065 UBIQUITIN CONJUGATING ENZYME1; RECOVERIN SUBFAMILY OF EF-HAND CALCIUM BINDING PROTEIN;
6145	15329	24764	3.16	2.0E-58	AF134838.1	NT	Homo sapiens endocytic receptor Endo180 (ENDO180) mRNA, complete cds
6145	15329	24765	3.16	2.0E-58	AF134838.1	NT	Homo sapiens endocytic receptor Endo180 (ENDO180) mRNA, complete cds
7327	16543	26032	12.17	2.0E-58	BF507745.1	EST_HUMAN	601890812F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4131891 5'
7536	16741	26232	1.94	2.0E-58	AW872641.1	EST_HUMAN	hm25f08.x1 NCL_CGAP_Thy4 Homo sapiens cDNA clone IMAGE:3013671 3'
728	9871	19109	0.76	1.0E-58	M85134.1	NT	Human complement component C5 mRNA, 3'end
1075	10300	19450	3.15	1.0E-58	6274549	NT	Homo sapiens NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 9 (22kD, B22) (NDUFB9), mRNA
1335	10550	19714	0.84	1.0E-58	AW957182.1	EST_HUMAN	EST369252 MAGC resequences, MAGD Homo sapiens cDNA
1335	10550	19715	0.84	1.0E-58	AW957182.1	EST_HUMAN	EST369252 MAGC resequences, MAGD Homo sapiens cDNA
1400	10814	19778	1.13	1.0E-58	AJ238093.1	NT	Homo sapiens partial AF-4 gene, exons 2 to 7 and Alu repeat elements
1839	10853	20033	1.77	1.0E-58	BE468132.1	EST_HUMAN	hy10f08.x1 NCL_CGAP_GC8 Homo sapiens cDNA clone IMAGE:3186935 3'
2615	11799	21015	1.71	1.0E-58	AF217514.1	NT	Homo sapiens uncharacterized bone marrow protein BM038 mRNA, complete cds
2754	11833	21149	2.78	1.0E-58	4759168	NT	Homo sapiens sterol regulatory element binding transcription factor 2 (SREBF2) mRNA

PCT/US 01/00670

Table 4

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2783	11181	20389	1.27	1.0E-58	5174444	NT	Homo sapiens G protein-coupled receptor 69A (GPR69A) mRNA
3511	12735	21874	0.63	1.0E-58	4758081	NT	Homo sapiens chondroitin sulfate proteoglycan 2 (versican) (CSPG2) mRNA
3511	12735	21875	0.63	1.0E-58	4758081	NT	Homo sapiens chondroitin sulfate proteoglycan 2 (versican) (CSPG2) mRNA
4990	14177	23288	5.91	1.0E-58	A1141063.1	EST_HUMAN	oz43h01.x1 Soares_NHMPu_S1 Homo sapiens cDNA clone IMAGE:1678129 3'
8245	17374		3.05	1.0E-58	X63392.1	NT	H. sapiens immunoglobulin kappa light chain variable region L14
2198	11393	20615	45.34	8.0E-59	4507378	NT	Homo sapiens TATA box binding protein (TBP) mRNA
6521	15717	25182	2.25	8.0E-59	A1781983.1	EST_HUMAN	wh50d08.x1 NCI_OGAP_Kid11 Homo sapiens cDNA clone IMAGE:2384171 3'
182	11961		2.44	8.0E-59	BF035327.1	EST_HUMAN	601458531F1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3882086 5'
4980	14167	23257	1.07	6.0E-59	AW869159.1	EST_HUMAN	MR3-SN0069-040500-008-101 SN0066 Homo sapiens cDNA
3091	12327	21450	7.79	5.0E-59	A1807484.1	EST_HUMAN	wf48c11.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2359836 3'
4661	13855	22953	7.37	5.0E-59	X83487.1	NT	H. sapiens DNA for ZNF80-linked ERV9 long terminal repeat
6084	14530	23555	8.55	5.0E-59	AW162304.1	EST_HUMAN	au86c07.x1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2781228 3' similar to contains element TAR1 repetitive element;
7481	18689	26171	3.22	5.0E-59	11434908	NT	Homo sapiens hypothetical protein (LOC57143), mRNA
803	10042	19194	4.8	4.0E-59	D80006.1	NT	Human mRNA for KIAA0184 gene, partial cds
4803	13992	23100	0.98	4.0E-59	4508759	NT	Homo sapiens ryanodine receptor 3 (RYR3) mRNA
4803	13992	23101	0.98	4.0E-59	4508759	NT	Homo sapiens ryanodine receptor 3 (RYR3) mRNA
8632	18197		2.83	4.0E-59	AF057720.1	NT	Homo sapiens 17-beta-hydroxysteroid dehydrogenase IV (HSD17B4) gene, promoter region and exon 1
9	8305		4.61	3.0E-59	AW965524.1	EST_HUMAN	EST377582 MAGE resequences, MAGI Homo sapiens cDNA
231	9509	18637	5.06	3.0E-59	7662247	NT	Homo sapiens KIAA0680 gene product (KIAA0680), mRNA
1685	10897	20084	11.45	3.0E-59	4505860	NT	Homo sapiens plasminogen activator, tissue (PLATa) mRNA
1685	10897	20085	11.45	3.0E-59	4505860	NT	Homo sapiens plasminogen activator, tissue (PLATa) mRNA
2099	11299	20512	8.64	3.0E-59	AB029035.1	NT	Homo sapiens mRNA for KIAA1112 protein, partial cds
2099	11299	20513	8.64	3.0E-59	AB029035.1	NT	Homo sapiens mRNA for KIAA1112 protein, partial cds
3093	12329	21454	3.99	3.0E-59	4502014	NT	Homo sapiens A kinase (PRKA) anchor protein 1 (AKAP1), mRNA
3093	12329	21455	3.99	3.0E-59	4502014	NT	Homo sapiens A kinase (PRKA) anchor protein 1 (AKAP1), mRNA
3815	13033	22144	1.19	3.0E-59	4508044	NT	Homo sapiens zona pellucida glycoprotein 2 (sperm receptor) (ZP2) mRNA
4692	13983	22985	2.22	3.0E-59	AL163284.2	NT	Homo sapiens chromosome 21 segment HS21C084
4859	14047	23142	1.63	3.0E-59	7427522	NT	Homo sapiens protein tyrosine phosphatase, receptor type, T (PTPRT), mRNA
5760	14979	24377	2.17	3.0E-59	8924074	NT	Homo sapiens hypothetical protein PRO1741 (PRO1741), mRNA
8236	15416	24857	1.83	3.0E-59	5454137	NT	Homo sapiens nuclear receptor co-repressor 1 (NCOR1), mRNA
8760	17701		5.3	3.0E-59	11417868	NT	Homo sapiens gamma-glutamyltransferase-like activity 1 (GGTLA1), mRNA
6975	16153		8.01	2.0E-59	AA309774.1	EST_HUMAN	EST180633 Jurkat T-cells V Homo sapiens cDNA 5' end

Page 225 of 382  
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Single Exon Probes Expressed in HELA Cells

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7407	16818	26110	2.31	2.0E-59	AW410898.1	EST_HUMAN	fh07h04.x1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:2861654 5'
7407	16818	26111	2.31	2.0E-59	AW410898.1	EST_HUMAN	fh07h04.x1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:2861654 5'
8506	17544	24030	13.36	2.0E-59	AI631809.1	EST_HUMAN	wa36c12.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2300182 3' similar to TR:Q86542
9081	18220	23693	4.11	2.0E-59	L11645.1	NT	Q86542 RTVL-H PROTEIN, contains LTR7.b1 LTR7 repetitive element ;
168	8448		12.28	1.0E-59	BE286411.1	EST_HUMAN	Homo sapiens alpha-tubulin mRNA, complete cds
2580	11768		3.15	1.0E-59	AA748468.1	EST_HUMAN	601176757F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3531927 5'
7431	15498	24943	8.28	1.0E-59	AJ130894.1	NT	ae56h11.s1 NCI_CGAP_G081 Homo sapiens cDNA clone IMAGE:1309028 3' similar to TR:Q13537
772	10012	19160	1.36	8.0E-60	AW877845.1	EST_HUMAN	Q13537 MER37 TRANSCRIPTIONAL ELEMENT, COMPLETE CONSENSUS SEQUENCE. ;
1487	10880	18853	5.94	8.0E-60	4759158	NT	Homo sapiens mRNA for transcription factor
2138	11336	20554	4.87	8.0E-60	5174858	NT	EST389949 MAGE resequencing, MAGO Homo sapiens cDNA
2138	11336	20555	4.87	8.0E-60	5174858	NT	Homo sapiens small nuclear ribonucleoprotein D3 polypeptide (18kD) (SNRPD3) mRNA
8448	15645	25113	4.12	8.0E-60	X17033.1	NT	Homo sapiens differentiation-related gene 1 (nickel-specific induction protein) (RTP) mRNA
8754	15949	25408	3.64	8.0E-60	11428949	NT	Homo sapiens mRNA for integrin alpha-2 subunit
7409	16821	28113	5.82	8.0E-60	AL163204.2	NT	Homo sapiens S-antigen, retina and pineal gland (arrestin) (SAG), mRNA
7409	16821	28114	5.82	8.0E-60	AL163204.2	NT	Homo sapiens chromosome 21 segment HS21C004
762	10003	19151	24.23	7.0E-60	AF055068.1	NT	Homo sapiens chromosome 21 segment HS21C004
763	10003	19151	103.89	7.0E-60	AF055066.1	NT	Homo sapiens MHC class 1 region
825	10063	19215	1.61	7.0E-60	4504634	NT	Homo sapiens MHC class 1 region
2098	11298	20511	4.34	7.0E-60	AF077188.1	NT	Homo sapiens interleukin 10 receptor, beta (IL10RB), mRNA
4160	13384	22484	3.55	7.0E-60	4505488	NT	Homo sapiens cullin 4A (CUL4A) mRNA, complete cds
4573	13787	22862	0.62	7.0E-60	AF264750.1	NT	Homo sapiens ornithine decarboxylase 1 (ODC1) mRNA
6879	16070	25540	3.61	7.0E-60	H58041.1	EST_HUMAN	Homo sapiens ALR-like protein mRNA, partial cds
7904	17119	26650	1.95	7.0E-60	H58041.1	EST_HUMAN	y1204.r1 Scores fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:205087 5' similar to contains
2145	11343	20561	2.1	8.0E-60	BE864874.2	EST_HUMAN	y1204.r1 Scores fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:205087 5' similar to contains
6811	15807		10.94	8.0E-60	H52456.1	EST_HUMAN	601656751RT NIH_MGC_69 Homo sapiens cDNA clone IMAGE:3886089 3'
83	9376	18505	0.9	5.0E-60	AI807917.1	EST_HUMAN	y478h09.r1 Scores fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:201953 5' similar to contains
83	9376	18506	0.9	5.0E-60	AI807917.1	EST_HUMAN	OF1 repetitive element ;
2201	11398	20622	2.69	4.0E-60	AW503208.1	EST_HUMAN	wf52c07.x1 Scores_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2359212 3'
2201	11398	20623	2.69	4.0E-60	AW503208.1	EST_HUMAN	wf52c07.x1 Scores_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2359212 3'
							UI-HF-BN0-akt-g-07-Q-UJ.r1 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3078348 5'
							UI-HF-BN0-akt-g-07-Q-UJ.r1 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3078348 5'

Page 226 of 382  
Table 4  
Single Exon Probes Expressed in HELA Cells

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2927	12165		1.39	4.0E-60	AA289037.1	EST_HUMAN	EST11498 Uterus Homo sapiens cDNA 5' and similar to similar to retrovirus-related pol
1827	11035	20230	4.76	3.0E-60	BE562611.1	EST_HUMAN	601336448F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3690395 5'
1827	11035	20231	4.76	3.0E-60	BE562611.1	EST_HUMAN	601336448F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3690395 5'
1835	11043		4.97	3.0E-60	6031190	NT	Homo sapiens prohibitin (PHB) mRNA
4451	13650	22745	1.67	3.0E-60	AJ271735.1	NT	Homo sapiens Xq pseudautosomal region; segment 1/2
5508	14731	24093	2.37	3.0E-60	AW836196.1	EST_HUMAN	RC3-LT0023-200100-012-801 LT0023 Homo sapiens cDNA
6601	15787	25253	6.71	3.0E-60	5174844	NT	Homo sapiens proline dehydrogenase (proline oxidase) (PRODH) mRNA
6601	15787	25254	6.71	3.0E-60	5174844	NT	Homo sapiens proline dehydrogenase (proline oxidase) (PRODH) mRNA
6697	15892	25353	7.68	3.0E-60	5174844	NT	Homo sapiens proline dehydrogenase (proline oxidase) (PRODH) mRNA
9140	18257		1.5	3.0E-60	AA485286.1	EST_HUMAN	ab07n04.r1 Stragene lung (#837210) Homo sapiens cDNA clone IMAGE:840151 5' similar to contains LTR10.11 LTR10 repetitive element ;
32	8328	18433		1.51	2.0E-60	AY008285.1	Homo sapiens solute carrier (SLC25A18) mRNA, complete cds; nuclear gene for mitochondrial product
1428	10841	18812	5.12	2.0E-60	Z11684.1	NT	H. sapiens 41kDa protein kinase related to rat ERK2
1698	10908	20083	1.43	2.0E-60	M24903.1	NT	Human bcr protein mRNA, 5' end
2447	11638	20859	1.02	2.0E-60	AW380450.1	EST_HUMAN	RC1-HT0268-031298-012-02 HT0268 Homo sapiens cDNA
3554	12777	21808	0.7	2.0E-60	4757887	NT	Homo sapiens v-rat murine sarcoma viral oncogene homolog B1 (BRAF) mRNA
3892	13108	22226	0.86	2.0E-60	AF231919.1	NT	Homo sapiens chromosome 21 unknown mRNA
6018	14508	23577	2.21	2.0E-60	4503044	NT	Homo sapiens corticotropin releasing hormone receptor 2 (CRHR2) mRNA
6018	14508	23578	2.21	2.0E-60	4503044	NT	Homo sapiens corticotropin releasing hormone receptor 2 (CRHR2) mRNA
8126	15310	24743	4.04	2.0E-60	AA311159.1	EST_HUMAN	EST181949 Jurkat T-cells V Homo sapiens cDNA 5' end similar to similar to prothymosin, alpha
8126	15310	24744	4.04	2.0E-60	AA311159.1	EST_HUMAN	EST181949 Jurkat T-cells V Homo sapiens cDNA 5' end similar to similar to prothymosin, alpha
6737	15932	25392	5.05	2.0E-60	L36033.1	NT	Human pre-B cell stimulating factor homologue (SDF1b) mRNA, complete cds
7065	18242	25717		2.0E-60		NT	Homo sapiens sema domain, transmembrane domain (TM), and cytoplasmic domain, (semaphorin) 8A (SEMA8A), mRNA
7065	18242	25718	4.11	2.0E-60	11991659	NT	Homo sapiens sema domain, transmembrane domain (TM), and cytoplasmic domain, (semaphorin) 8A (SEMA8A), mRNA
7861	17140	28671	1.64	2.0E-60	4507366	NT	Homo sapiens threonyl-tRNA synthetase (TARS), mRNA
7861	17140	28672	1.64	2.0E-60	4507366	NT	Homo sapiens threonyl-tRNA synthetase (TARS), mRNA
8797	17723		6	2.0E-60	11418192	NT	Homo sapiens non-histone chromosome protein 2 (S. cerevisiae)-like 1 (NHP2L1), mRNA
8838	18186		1.56	2.0E-60	AF068757.1	NT	Homo sapiens somatostatin receptor subtype 3 (SSTR3) gene, 5' flanking region and partial cds
8940	17818		1.23	2.0E-60	11418088	NT	Homo sapiens similar to HSPC022 protein (H. sapiens) (LOC63504), mRNA
8954	17828		1.25	2.0E-60	AB011399.1	NT	Homo sapiens gene for AF-6, complete cds
528	9779	18902	1.68	1.0E-60	BE178586.1	EST_HUMAN	PM3-HT0605-270200-001-e08 HT0605 Homo sapiens cDNA

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3880	13098	22213	1.79	1.0E-60	AU143388.1	EST_HUMAN	AU143388 Y79AA1 Homo sapiens cDNA clone Y79AA1001854 5'
4876	14163	23254	1.83	1.0E-60	AL163285.2	NT	Homo sapiens chromosome 21 segment HS21C085
6704	15889		3.72	1.0E-60	AA244041.1	EST_HUMAN	nc04e12.r1 NCL_CGAP_P11 Homo sapiens cDNA clone IMAGE:1007182 similar to contains L1.t1 L1 repetitive element:
1107	10331	19481	4.23	9.0E-61	AU119344.1	EST_HUMAN	AU119344 HEMBA1 Homo sapiens cDNA clone HEMBA1005583 5'
2830	11813	21031	1.13	8.0E-61	AW008478.1	EST_HUMAN	w05b10.x1 NCL_CGAP_Co3 Homo sapiens cDNA clone IMAGE:2506555 3'
2630	11813	21032	1.13	8.0E-61	AW008478.1	EST_HUMAN	w05b10.x1 NCL_CGAP_Co3 Homo sapiens cDNA clone IMAGE:2506555 3'
2803	12141		2.66	8.0E-61	X57147.1	NT	Human endogenous retrovirus pHE.1 (ERV9)
270	9545	18874	2.65	6.0E-61	BE409310.1	EST_HUMAN	601300838F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3635480 5'
821	10059	19212	1.54	6.0E-61	BE409310.1	EST_HUMAN	601300838F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3635480 5'
1329	10544	19707	12.57	6.0E-61	AF119860.1	NT	Homo sapiens PRO2014 mRNA, complete cds
1607	10820	19896	0.91	6.0E-61	BE257400.1	EST_HUMAN	601109238F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3350145 5'
1625	10838	20015	3.27	6.0E-61	AA598033.1	EST_HUMAN	nn68h09.s1 NCL_CGAP_Lar1 Homo sapiens cDNA clone IMAGE:1088897 3'
3277	12510	21640	11.97	6.0E-61	AU130689.1	EST_HUMAN	AU130689 NT2RP3 Homo sapiens cDNA clone NT2RP3001263 5'
5673	14893	24288	3.18	6.0E-61	S79248.1	NT	Ig-beta(B29=CD79b (alternatively spliced) [human, B cells, mRNA Partial, 375 nt])
8227	15408	24850	1.8	6.0E-61	U24498.1	NT	Human autosomal dominant polycystic kidney disease protein 1 (PKD1) gene
6342	15523	24971	1.88	6.0E-61	AF035737.1	NT	Homo sapiens general transcription factor 2-1 (GTF2) mRNA, complete cds
8698	10059	19212	1.62	6.0E-61	BE409310.1	EST_HUMAN	601300838F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3635480 5'
1653	10887	20049	2.83	5.0E-61	4508008	NT	Homo sapiens protein phosphatase 1, regulatory subunit 10 (PPP1R10) mRNA
3001	12237	21367	2.23	5.0E-61	AL163279.2	NT	Homo sapiens chromosome 21 segment HS21C079
3118	12351	21479	1	5.0E-61	AB020632.1	NT	Homo sapiens mRNA for KIAA0825 protein, partial cds
3182	12397	21532	1.6	5.0E-61	4502166	NT	Homo sapiens amyloid beta (A4) precursor protein (protease nexin-II, Alzheimer disease) (APP), mRNA
3958	13174		1.78	5.0E-61	AJ228041.1	NT	Homo sapiens 959 kb contig between AML1 and CBR1 on chromosome 21q22; segment 1/3
5026	8631	18763	0.7	5.0E-61	4507500	NT	Homo sapiens T-cell lymphoma invasion and metastasis 1 (TIAM1) mRNA
5275	14447	23519	1.06	5.0E-61	AF001445.1	NT	Homo sapiens core binding factor alpha1 subunit (CBFA1) gene, exon 2
5275	14447	23520	1.08	5.0E-61	AF001445.1	NT	Homo sapiens core binding factor alpha1 subunit (CBFA1) gene, exon 2
8480	17529		4.52	4.0E-61	AV731140.1	EST_HUMAN	AV731140 HTF Homo sapiens cDNA clone HTFARB01 5'
505	9757	18884	1.85	2.0E-61	8922828	NT	Homo sapiens hypothetical protein FLJ11026 (FLJ11026), mRNA
1220	10438	18594	1.84	2.0E-61	BE168410.1	EST_HUMAN	QV3-HT0513-060400-147-401 HT0513 Homo sapiens cDNA
1220	10438	18595	1.84	2.0E-61	BE168410.1	EST_HUMAN	QV3-HT0513-060400-147-401 HT0513 Homo sapiens cDNA
1841	10855	20036	1.64	2.0E-61	N53039.1	EST_HUMAN	w53d11.s1 Soares fetal liver spleen 1NFS Homo sapiens cDNA clone IMAGE:246453 3' similar to
7045	16222	25698	2.74	2.0E-61	AW500256.1	EST_HUMAN	gbL25444 60S RIBOSOMAL PROTEIN L35A (HUMAN); UHF-BNO-ekd-f-12-Q-UJ.r1 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3076774 5'



Table 4

## Single Exon Probes Expressed in HELA Cells

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7162	16328	25812	3.6	2.0E-61	11421778	NT	Homo sapiens polymerase (RNA) III (DNA directed) (38kD) (RPC39), mRNA
7461	16669		22.39	2.0E-61	11419729	NT	Homo sapiens ribosomal protein L44 (RPL44), mRNA
441	9695		0.8	1.0E-61	AL163203.2	NT	Homo sapiens chromosome 21 segment HS21C003
782	10021	18171	1.88	1.0E-61	5458829	NT	Homo sapiens origin recognition complex, subunit 2 (yeast homolog)-like (ORCZL), mRNA
1826	11034	20229	4.25	1.0E-61	605963	NT	Homo sapiens zona pellucida glycoprotein 3A (sperm receptor) (ZP3A), mRNA
2163	11361	20579	1.74	1.0E-61	AW827281.1	EST_HUMAN	XM11509.Y1 NCI_CGAP_L15 Homo sapiens cDNA clone IMAGE:2683369 5' similar to contains element
2766	12028	21155	1.09	1.0E-61	BE386363.1	EST_HUMAN	MSR1 repetitive element;
3354	12582	21722	0.79	1.0E-61	7682319	NT	601273513F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3614687 5'
4432	13632	22727	0.74	1.0E-61	4759249	NT	Homo sapiens KIAA0808 gene product (KIAA0808), mRNA
4432	13632	22728	0.74	1.0E-61	4759249	NT	Homo sapiens TRAF family member-associated NFKB activator (TANK) mRNA
4873	14081	23155	9.51	1.0E-61	AW298181.1	EST_HUMAN	Homo sapiens TRAF family member-associated NFKB activator (TANK) mRNA
4873	14081	23156	9.51	1.0E-61	AW298181.1	EST_HUMAN	UI-H-BWO-ajl-b-08-0-UI.s1 NCI_CGAP_Sub6 Homo sapiens cDNA clone IMAGE:2732871 3'
4979	14168	23256	0.79	1.0E-61	AL163210.2	NT	UI-H-BWO-ajl-b-08-0-UI.s1 NCI_CGAP_Sub6 Homo sapiens cDNA clone IMAGE:2732871 3'
6041	15209	24629	10.68	1.0E-61	M30135.1	NT	Homo sapiens chromosome 21 segment HS21C010
6504	15701	25167	4.46	1.0E-61	11034840	NT	Human P40 T-cell and mast cell growth factor (hP40) gene, complete cds
6564	15760	25222	3.39	1.0E-61	AF224669.1	NT	Homo sapiens growth hormone releasing hormone (GHRH), mRNA
6850	16039		2.62	1.0E-61	AW999728.1	EST_HUMAN	Homo sapiens mannosidase, beta A, lysosomal (MANBA) gene, and ubiquitin-conjugating enzyme E2D 3 (UBE2D3) genes, complete cds
7084	16261	25738	12.12	1.0E-61	11428892	NT	MRO-BN0070-040400-010-H01 BN0070 Homo sapiens cDNA
7229	16450	25939	3.5	1.0E-61	11425578	NT	Homo sapiens KIAA0971 protein (KIAA0971), mRNA
8414	18231	23700	3.11	1.0E-61	11430460	NT	Homo sapiens actinin, alpha 4 (ACTN4), mRNA
8414	18231	23701	3.11	1.0E-61	11430460	NT	Homo sapiens low density lipoprotein-related protein 2 (LRP2), mRNA
9115	17833	23877	7.99	1.0E-61	11418127	NT	Homo sapiens low density lipoprotein-related protein 2 (LRP2), mRNA
9280	18097	23805	1.55	1.0E-61	11430460	NT	Homo sapiens GTP binding protein 1 (GTPBP1), mRNA
4548	13743	22844	1.6	8.0E-62	AA830420.1	EST_HUMAN	Homo sapiens low density lipoprotein-related protein 2 (LRP2), mRNA
1115	10339	19489	1.36	7.0E-62	AV714334.1	EST_HUMAN	oc-68h11.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1354725 3' similar to SW:POL_MLVRK
3480	12704	21840	0.65	7.0E-62	P17480	SWISSPROT	P31795 POL POLYPROTEIN;
7890	17106	26636	4.29	7.0E-62	A1208881.1	EST_HUMAN	AV714334 DCB Homo sapiens cDNA clone DCBAMA08 5'
2956	12194		1.27	6.0E-62	U09410.1	NT	NUCLEOLAR TRANSCRIPTION FACTOR 1 (UPSTREAM BINDING FACTOR 1) (UBF-1) (AUTOANTIGEN NOR-80)
3362	12590		5.35	6.0E-62	11418255	NT	qg56a04.x1 Soares testis_NHT Homo sapiens cDNA clone IMAGE:1839150 3' similar to TR:O15103
							O15103 HYPOTHETICAL 27.3 KD PROTEIN.;
							Human zinc finger protein ZNF131 mRNA, partial cds
							Homo sapiens CGI-56 protein (CGI-56), mRNA

Table 4

## Single Exon Probes Expressed in HELA Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6346	15527	24875	3.61	6.0E-62	A1782801.1	EST_HUMAN	w04402.x1 NCI_CGAP_CLL1 Homo sapiens cDNA clone IMAGE:2389251 3'
6346	15527	24876	3.61	6.0E-62	A1782801.1	EST_HUMAN	w04402.x1 NCI_CGAP_CLL1 Homo sapiens cDNA clone IMAGE:2389251 3'
6868	16056	25523	2.47	6.0E-62	AW814383.1	EST_HUMAN	MR3-ST0203-130100-025-g09 ST0203 Homo sapiens cDNA
422	9875	18815	2.46	5.0E-62	A1950528.1	EST_HUMAN	wx51e07.x1 NCI_CGAP_Lu28 Homo sapiens cDNA clone IMAGE:2547204 3' similar to SW:GG85_HUMAN
2370	11563	20784	4.37	5.0E-62	AJ271735.1	NT	Q08379 GOLGIN-65, contains element MER22 repetitive element;
2370	11563	20785	4.37	5.0E-62	AJ271735.1	NT	Homo sapiens Xq pseudautosomal region; segment 1/2
3397	12624	21755	2.42	5.0E-62	4508758	NT	Homo sapiens Xq pseudautosomal region; segment 1/2
4319	13520	22615	1.97	5.0E-62	AA431063.1	EST_HUMAN	zw78e08.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:782344 3' similar to SW:NRDC_RAT
4668	13761	25580	1.27	5.0E-62	AW805887.1	EST_HUMAN	P47246 NARDILYSIN;
6921	16114	25580	4.84	5.0E-62	AW410687.1	EST_HUMAN	RCS-NN1088-100500-021-H03 NN1089 Homo sapiens cDNA
7815	17008	26520	2.31	5.0E-62	11425574	NT	fb07g09.x1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:2661818 5'
7815	17008	26521	2.31	5.0E-62	11425574	NT	Homo sapiens muscle specific gene (MS), mRNA
850	10087	19248	3.3	4.0E-62	AW161479.1	EST_HUMAN	au71d03.y1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2781701 5' similar to gb:M37104
850	10087	19247	3.3	4.0E-62	AW161479.1	EST_HUMAN	ATP SYNTHASE COUPLING FACTOR 6, MITOCHONDRIAL PRECURSOR (HUMAN);
851	10087	19246	3.33	4.0E-62	AW161479.1	EST_HUMAN	au71d03.y1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2781701 5' similar to gb:M37104
851	10087	19247	3.33	4.0E-62	AW161479.1	EST_HUMAN	ATP SYNTHASE COUPLING FACTOR 6, MITOCHONDRIAL PRECURSOR (HUMAN);
2421	11612	20834	27.87	4.0E-62	A1827800.1	EST_HUMAN	au71d03.y1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2781701 5' similar to gb:M37104
2421	11612	20835	27.87	4.0E-62	A1827800.1	EST_HUMAN	ATP SYNTHASE COUPLING FACTOR 6, MITOCHONDRIAL PRECURSOR (HUMAN);
3377	12605		9.57	4.0E-62	4557887	NT	au71d03.y1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2781701 5' similar to gb:M37104
5041	14225		0.96	4.0E-62	AJ243213.1	NT	wf12b08.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2350359 3' similar to
5250	14423	23500	0.91	4.0E-62	4758323	NT	gb:X57138.maf1 HISTONE H2B.2 (HUMAN);
5626	14850	24232	1.64	4.0E-62	4506878	NT	wf12b08.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2350359 3' similar to
5786	15003	24407	2.71	4.0E-62	11420854	NT	gb:X57138.maf1 HISTONE H2B.2 (HUMAN);
6151	15335	24772	1.78	4.0E-62	11421041	NT	Homo sapiens keratin 18 (KRT18) mRNA
							Homo sapiens partial 5-HT4 receptor gene, exons 2 to 5
							Homo sapiens enhancer of zeste (Drosophila) homolog 2 (EZH2) mRNA
							Homo sapiens solute carrier family 13 (sodium-dependent dicarboxylate transporter), member 2 (SLC13A2) mRNA
							Homo sapiens ubiquitin specific protease 9, X chromosome (Drosophila fat facets related) (USP9X), mRNA
							Homo sapiens phosphoribosyl pyrophosphate synthetase 2 (PRPS2), mRNA

Page 230 of 382  
Table 4  
Single Exon Probes Expressed in HELA Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6348	15528	24977	2.14	4.0E-62	7657057	NT	Homo sapiens eukaryotic translation initiation factor 2B, subunit 2 (beta, 39kD) (EIF2B2), mRNA
6348	15528	24978	2.14	4.0E-62	7657057	NT	Homo sapiens eukaryotic translation initiation factor 2B, subunit 2 (beta, 39kD) (EIF2B2), mRNA
6731	15928	25385	10.84	4.0E-62	AB033089.1	NT	Homo sapiens mRNA for KIAA1263 protein, partial cds
7582	18787	26281	2.72	4.0E-62	Z78766.1	NT	H. sapiens flow-sorted chromosome 6 HindIII fragment, SC6pA16D3
7582	18787	26282	2.72	4.0E-62	Z78766.1	NT	H. sapiens flow-sorted chromosome 6 HindIII fragment, SC6pA16D3
7779	16974	26487	22.33	4.0E-62	ST0584.1	NT	thyroid-stimulating hormone alpha subunit [human, Genomic, 268 nt, segment 3 of 4]
8399	17477	26593	2.09	4.0E-62	11418086	NT	Homo sapiens putative nuclear protein (HRIHFB2122), mRNA
8631	18190		2.62	4.0E-62	11418192	NT	Homo sapiens non-histone chromosome protein 2 (S. cerevisiae)-like 1 (NHPZL1), mRNA
8047	17920	23873	1.7	4.0E-62	11418322	NT	Homo sapiens cadherin EGF LAG seven-pass G-type receptor 1 (CELSR1), mRNA
9089	17915	23870	7.8	4.0E-62	11417962	NT	Homo sapiens calcineurin binding protein 1 (KIAA0330), mRNA
9089	17915	23871	7.8	4.0E-62	11417962	NT	Homo sapiens calcineurin binding protein 1 (KIAA0330), mRNA
9148	17952	23863	2.56	4.0E-62	11430460	NT	Homo sapiens low density lipoprotein-related protein 2 (LRP2), mRNA
74	9368	18496	1.85	3.0E-62	4557794	NT	Homo sapiens neurofibromin 2 (bilateral acoustic neuroma) (NF2) mRNA
3011	12247	21378	0.74	3.0E-62	AB040908.1	NT	Homo sapiens mRNA for KIAA1476 protein, partial cds
3011	12247	21377	0.74	3.0E-62	AB040908.1	NT	Homo sapiens mRNA for KIAA1476 protein, partial cds
3676	12897	22017	15.04	3.0E-62	X52858.1	NT	Human cyclophilin-related processed pseudogene
6835	15830	25282	6.49	3.0E-62	AI632733.1	EST_HUMAN	was33f04.x1 NCL_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2286903 3' similar to contains THR.12
1238	10455	19814	2.67	2.0E-62	AL163284.2	NT	THR repetitive element
						NT	Homo sapiens chromosome 21 segment HS21C084
7126	16303		5.65	2.0E-62	AF224689.1	NT	Homo sapiens mannosidase, beta A, lysosomal (MANBA) gene, and ubiquitin-conjugating enzyme E2D 3
8186	17318		26.63	2.0E-62	BF330676.1	EST_HUMAN	(UBE2D3) genes, complete cds
1051	10277	19430	2	1.0E-62	AF248540.1	NT	QV4-BT0257-081189-017-403 BT0257 Homo sapiens cDNA
1530	10744	19917	17.99	1.0E-62	L78810.1	NT	Homo sapiens intersectin 2 (SH3D1B) mRNA, complete cds
						NT	Homo sapiens ADP/ATP carrier protein (ANT-2) gene, complete cds
1768	10978	20167	1.58	1.0E-62	AA625207.1	EST_HUMAN	af70a11.1 Soares_NhHMPu_S1 Homo sapiens cDNA clone IMAGE:1047404 5' similar to WP:K01H12.1
2865	12103	21234	0.94	1.0E-62	AL038044.1	EST_HUMAN	CE03453
3402	12628		2.08	1.0E-62	AB040911.1	NT	DKFZp566F104_r1 566 (synonym: htkd2) Homo sapiens cDNA clone DKFZp566F104 5'
4526	13722	22818	1.26	1.0E-62	8923201	NT	Homo sapiens mRNA for KIAA1478 protein, partial cds
6136	15320	24754	2.5	1.0E-62	AA722878.1	EST_HUMAN	Homo sapiens hypothetical protein FLJ20212 (FLJ20212), mRNA
6136	15320	24755	2.5	1.0E-62	AA722878.1	EST_HUMAN	zq89f10.s1 Soares_fetal_heart_NbHH19W Homo sapiens cDNA clone IMAGE:409771 3'
6806	16001	25460	2.36	1.0E-62	X15533.1	NT	zq89f10.s1 Soares_fetal_heart_NbHH19W Homo sapiens cDNA clone IMAGE:409771 3'
6806	16001	25461	2.36	1.0E-62	X15533.1	NT	H. sapiens lysosomal acid phosphatase gene (EC 3.1.3.2) Exon 9
6940	16084	25552	3.51	1.0E-62	AA465170.1	EST_HUMAN	H. sapiens lysosomal acid phosphatase gene (EC 3.1.3.2) Exon 9

Page 231 of 382  
Table 4  
Single Exon Probes Expressed in HELA Cells

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7906	17121	26652	2.64	1.0E-62	Z78688.1	NT	H. sapiens flow-sorted chromosome 6 HindIII fragment, SC6pA14D8
8917	17804		2.3	1.0E-62	11418322	NT	Homo sapiens cadherin EGF LAG seven-pass G-type receptor 1 (CELSR1), mRNA
9129	17940	23880	3.35	1.0E-62	11430460	NT	Homo sapiens low density lipoprotein-related protein 2 (LRP2), mRNA
343	9611	18738	2.06	9.0E-63	AW816405.1	EST_HUMAN	QV4-S10234-181199-037-f05 S10234 Homo sapiens cDNA
2314	11508		1.26	9.0E-63	C18159.1	EST_HUMAN	C18159 Human placenta cDNA (TFujwara) Homo sapiens cDNA clone GEN-558C10 5'
4018	13230	22332	7.81	9.0E-63	AB002348.2	NT	Homo sapiens mRNA for KIAA0350 protein, partial cds
4018	13230	22333	7.81	9.0E-63	AB002348.2	NT	Homo sapiens mRNA for KIAA0350 protein, partial cds
5300	14487	26928	2.91	9.0E-63	11418166	NT	Homo sapiens aconitase 2, mitochondrial (ACO2), mRNA
6157	15340	24777	3.67	9.0E-63	11426885	NT	Homo sapiens nucleoprotein 88kD (NUP88), mRNA
7610	16813	26309	2	9.0E-63	BF203408.1	EST_HUMAN	601865828F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4088487 5'
2312	11508	20727	1	8.0E-63	4557734	NT	Homo sapiens monoamine oxidase A (MAOA), nuclear gene encoding mitochondrial protein, mRNA
2341	11534	20757	4.33	8.0E-63	5031810	NT	Homo sapiens IL2-inducible T-cell kinase (ITK), mRNA
3438	12683	21795	4.09	8.0E-63	AF188349.1	NT	Gallus gallus Dach2 protein (Dach2) mRNA, complete cds
3438	12683	21796	4.09	8.0E-63	AF188349.1	NT	Gallus gallus Dach2 protein (Dach2) mRNA, complete cds
4252	13455	22547	3.98	8.0E-63	AL163286.2	NT	Homo sapiens chromosome 21 segment HS21C068
837	10170		1.24	7.0E-63	A1872137.1	EST_HUMAN	w155g11.x1 NCI_CGAP_U12 Homo sapiens cDNA clone IMAGE:2439808 3'
5358	14588		21.03	6.0E-63	AA420803.1	EST_HUMAN	nc63f02.r1 NCI_CGAP_P11 Homo sapiens cDNA clone IMAGE:745947 similar to gb:Y00381 60S
3293	12524	21658	0.98	4.0E-63	AL163278.2	NT	RIBOSOMAL PROTEIN (HUMAN);
3796	13014	22126	1.48	4.0E-63	AB014607.1	NT	Homo sapiens chromosome 21 segment HS21C078
3796	13014	22127	1.48	4.0E-63	AB014607.1	NT	Homo sapiens mRNA for KIAA0707 protein, partial cds
5848	15063	24471	2.59	4.0E-63	AW750372.1	EST_HUMAN	Homo sapiens mRNA for KIAA0707 protein, partial cds
5848	15063	24472	2.59	4.0E-63	AW750372.1	EST_HUMAN	CM3-BT0595-190100-072-a09 BT0595 Homo sapiens cDNA
7692	16891	26399	2.35	4.0E-63	AW134709.1	EST_HUMAN	CM3-BT0595-190100-072-a09 BT0595 Homo sapiens cDNA
7692	16891	26400	2.35	4.0E-63	AW134709.1	EST_HUMAN	UI-H-B11-abq-a-02-Q-UI.s1 NCI_CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2712482 3'
1804	11110	20304	2.09	3.0E-63	AB018260.1	NT	UI-H-B11-abq-a-02-Q-UI.s1 NCI_CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2712482 3'
2734	11913	21126	0.97	3.0E-63	J00310.1	NT	Homo sapiens mRNA for KIAA0717 protein, partial cds
2773	10462	18623	11.76	3.0E-63	6005963	NT	Human Met-RNA-1 gene 1
5859	15077	24490	31.49	3.0E-63	11545810	NT	Homo sapiens zinc finger protein 144 (ZNF144), mRNA
196	9476	18608	1.26	2.0E-63	U07804.1	NT	Homo sapiens hepatocellular carcinoma antigen gene 520 (LOC83928), mRNA
203	9483	18616	1.81	2.0E-63	4885226	NT	Human DNA topoisomerase I mRNA, partial cds
504	9756		1.42	2.0E-63	4557624	NT	Homo sapiens eyes absent (Drosophila) homolog 2 (EYA2), mRNA
							Homo sapiens glutamate-cysteine ligase (gamma-glutamylcysteine synthetase), catalytic (72.8kD) (GLCLC) mRNA

Table 4

## Single Exon Probes Expressed in HELA Cells

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
836	10074	19231	2.04	2.0E-63	7857042	NT	Homo sapiens Down syndrome candidate region 1 (DSCR1), mRNA
1548	10762	19936	1.66	2.0E-63	AB030388.1	NT	Homo sapiens RHCE mRNA for Rh blood CE group antigen polypeptide, complete cds
1548	10762	19937	1.66	2.0E-63	AB030388.1	NT	Homo sapiens RHCE mRNA for Rh blood CE group antigen polypeptide, complete cds
1737	10949	20132	2.19	2.0E-63	BE410739.1	EST_HUMAN	601301627F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3636103 5'
3120	12355	21484	1.16	2.0E-63	4502166	NT	Homo sapiens amyloid beta (A4) precursor protein (protease nexin-II, Alzheimer disease) (APP), mRNA
3253	12486	21618	2.53	2.0E-63	AF100718.1	NT	Homo sapiens chromosome 3 subtelomeric region
3883	13099	22216	2.35	2.0E-63	L39891.1	NT	Homo sapiens polycystic kidney disease-associated protein (PKD1) gene, complete cds
4882	14070	23167	1.1	2.0E-63	AF111167.2	NT	Homo sapiens Jun dimerization protein gene, partial cds; cfos gene, complete cds; and unknown gene
5213	14388	23473	0.67	2.0E-63	6812817	NT	Homo sapiens glutamyl-peptide cyclotransferase (glutaminyl cyclase) (QPCT), mRNA
5306	18049	23542	1.88	2.0E-63	11419429	NT	Homo sapiens similar to ecdonucleotide pyrophosphatase/phosphodiesterase 3 (H. sapiens) (LOC63214), mRNA
5606	14830	24206	2.73	2.0E-63	BF373541.1	EST_HUMAN	QV1-FT0170-040700-265-c05 FT0170 Homo sapiens cDNA
5606	14830	24207	2.73	2.0E-63	BF373541.1	EST_HUMAN	QV1-FT0170-040700-265-c05 FT0170 Homo sapiens cDNA
7332	16548	26038	27.58	2.0E-63	N78945.1	EST_HUMAN	Z61805.s1 Soares_fetal_lung_NHIL19W Homo sapiens cDNA clone IMAGE:302385 3' similar to gb:X17208.40S RIBOSOMAL PROTEIN S4 (HUMAN);
7355	16571	26062	2.86	2.0E-63	AF069810.1	NT	Homo sapiens neuroxin III-alpha gene, partial cds
7355	16571	26063	2.86	2.0E-63	AF069810.1	NT	Homo sapiens neuroxin III-alpha gene, partial cds
8513	18133	23748	5.24	2.0E-63	11418185	NT	Homo sapiens aconitase 2, mitochondrial (ACO2), mRNA
4335	13536	22627	2.88	1.0E-63	F08485.1	EST_HUMAN	HSCZVD111 normalized infant brain cDNA Homo sapiens cDNA clone c-zvd11
4335	13536	22628	2.88	1.0E-63	F08485.1	EST_HUMAN	HSCZVD111 normalized infant brain cDNA Homo sapiens cDNA clone c-zvd11
6819	15815		2.88	1.0E-63	AL163247.2	NT	Homo sapiens chromosome 21 segment HS21C047
9197	18248		7.48	1.0E-63	AL163207.2	NT	Homo sapiens chromosome 21 segment HS21C007
6416	15613	25077	8.1	9.0E-64	A1478186.1	EST_HUMAN	tm50b07.x1 NCL CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2161525 3'
1053	10279		16.75	8.0E-64	BE280786.1	EST_HUMAN	601155232F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:31390338 5'
5730	14949	24348	3.59	8.0E-64	BE885755.1	EST_HUMAN	601508988F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3910336 5'
8320	17423		4.21	8.0E-64	11418177	NT	Homo sapiens Ran GTPase activating protein 1 (RANGAP1), mRNA
8374	17460		2.3	8.0E-64	T60851.1	EST_HUMAN	y688b02.r1 Striatogene lung (#637210) Homo sapiens cDNA clone IMAGE:79179 5'
3503	12727		0.98	7.0E-64	BE394321.1	EST_HUMAN	601311455F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3633204 5'
4743	13934	23037	2.89	7.0E-64	4507490	NT	Homo sapiens thimet oligopeptidase 1 (THOP1) mRNA
4743	13934	23038	2.89	7.0E-64	4507490	NT	Homo sapiens thimet oligopeptidase 1 (THOP1) mRNA
7086	16263	25741	4.75	7.0E-64	Y07848.1	NT	Homo sapiens EWS, gar/22, rrp22 and bam22 genes

Table 4

## Single Exon Probes Expressed in HELA Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1697	10909	20094	3.93	8.0E-64	AI651982.1	EST_HUMAN	wb51607.x1 NCI_CGAP_GC8 Homo sapiens cDNA clone IMAGE:2309220 3' similar to gb:M15182 BETA-GLUCURONIDASE PRECURSOR (HUMAN);
1697	10909	20095	3.93	8.0E-64	AI651982.1	EST_HUMAN	wb51607.x1 NCI_CGAP_GC8 Homo sapiens cDNA clone IMAGE:2309220 3' similar to gb:M15182 BETA-GLUCURONIDASE PRECURSOR (HUMAN);
3086	12322	21443	4.98	8.0E-64	AW026445.1	EST_HUMAN	wv13e03.x1 NCI_CGAP_Bm23 Homo sapiens cDNA clone IMAGE:2529436 3'
3086	12322	21444	4.98	8.0E-64	AW026445.1	EST_HUMAN	wv13e03.x1 NCI_CGAP_Bm23 Homo sapiens cDNA clone IMAGE:2529436 3'
5501	14727	24087	2.09	8.0E-64	Y18933.1	NT	Homo sapiens MCP-1 gene and enhancer region
5501	14727	24088	2.09	8.0E-64	Y18933.1	NT	Homo sapiens MCP-1 gene and enhancer region
5507	14732	24094	6.03	8.0E-64	M13975.1	NT	Homo sapiens protein kinase C beta-II type (PRKCB1) mRNA, complete cds
6179	15361	24769	2.45	8.0E-64	11525879	NT	Homo sapiens mesenchyme homeo box 1 (MEOX1), mRNA
6179	15361	24800	2.45	8.0E-64	11525879	NT	Homo sapiens mesenchyme homeo box 1 (MEOX1), mRNA
6861	16051	25518	8.49	8.0E-64	11420555	NT	Homo sapiens acetyl-CoA synthetase (LOC55902), mRNA
6898	16176	25647	2.76	8.0E-64	S78475.1	NT	tRc (human, brain, mRNA, 2715 nt)
7353	16569	26059	9.75	8.0E-64	11420197	NT	Homo sapiens stromal antigen 3 (STAG3), mRNA
7353	16569	26060	9.75	8.0E-64	11420197	NT	Homo sapiens stromal antigen 3 (STAG3), mRNA
7587	12322	21443	2.09	8.0E-64	AW026445.1	EST_HUMAN	wv13e03.x1 NCI_CGAP_Bm23 Homo sapiens cDNA clone IMAGE:2529436 3'
7587	12322	21444	2.09	8.0E-64	AW026445.1	EST_HUMAN	wv13e03.x1 NCI_CGAP_Bm23 Homo sapiens cDNA clone IMAGE:2529436 3'
8532	17558	23980	4.22	8.0E-64	11526198	NT	Homo sapiens Interleukin 10 receptor, beta (IL10RB), mRNA
830	10688	19222	2.38	5.0E-64	AF231919.1	NT	Homo sapiens chromosome 21 unknown mRNA
830	10688	19223	2.38	5.0E-64	AF231919.1	NT	Homo sapiens chromosome 21 unknown mRNA
1346	10561	19726	1.1	5.0E-64	AB020710.1	NT	Homo sapiens mRNA for KIAA0903 protein, partial cds
1426	10639	19809	1.34	5.0E-64	L40833.1	NT	Homo sapiens phosphoglucomutase-related protein (PGMRP) gene, complete cds
1426	10639	19810	1.34	5.0E-64	L40833.1	NT	Homo sapiens phosphoglucomutase-related protein (PGMRP) gene, complete cds
1686	10898	20086	1.97	5.0E-64	U89358.1	NT	Human (3)mbt protein homolog mRNA, complete cds
2778	10687	19862	5.41	5.0E-64	7662205	NT	Homo sapiens KIAA0618 gene product (KIAA0618), mRNA
2778	10687	19863	5.41	5.0E-64	7662205	NT	Homo sapiens KIAA0618 gene product (KIAA0618), mRNA
3935	13151	22287	8.01	5.0E-64	AF017433.1	NT	Homo sapiens putative transcription factor OR53 (CR53) mRNA, partial cds
4083	13262	22391	0.86	5.0E-64	AB020710.1	NT	Homo sapiens mRNA for KIAA0903 protein, partial cds
7390	16604	26093	4.15	4.0E-64	AW813783.1	EST_HUMAN	RC3-ST0197-120200-015-a03 ST0197 Homo sapiens cDNA
7390	16604	26094	4.15	4.0E-64	AW813783.1	EST_HUMAN	RC3-ST0197-120200-015-a03 ST0197 Homo sapiens cDNA
2164	11362	20590	12.04	3.0E-64	C18895.1	EST_HUMAN	C18895 Human placenta cDNA (TFujwara) Homo sapiens cDNA clone GEN:598E02 5'
3221	12455	21588	0.7	3.0E-64	BE794381.1	EST_HUMAN	601589565F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3943577 5'
3420	12645	21774	1.42	3.0E-64	AV711714.1	EST_HUMAN	AV711714 DCA Homo sapiens cDNA clone DCAAMC01 5'
3420	12645	21775	1.42	3.0E-64	AV711714.1	EST_HUMAN	AV711714 DCA Homo sapiens cDNA clone DCAAMC01 5'

Page 234 of 382  
Table 4  
Single Exon Probes Expressed in HELA Cells

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5872	15090	24503	2.5	3.0E-64	BF370000.1	EST_HUMAN	RC8-FN0019-280600-011-G11 FN0019 Homo sapiens cDNA
6618	15814	25273	2.49	3.0E-64	AF248953.1	NT	Homo sapiens golgi matrix protein GM130 (GOLGA2) mRNA, complete cds
6618	15814	25274	2.49	3.0E-64	AF248953.1	NT	Homo sapiens golgi matrix protein GM130 (GOLGA2) mRNA, complete cds
6623	15819	25277	2.26	3.0E-64	BE208521.1	EST_HUMAN	bb72h12.y1 NIH_MGC_12 Homo sapiens cDNA clone IMAGE:3047975 5' similar to gb:L08069 DNAJ PROTEIN HOMOLOG 2 (HUMAN);
6623	15819	25278	2.26	3.0E-64	BE208521.1	EST_HUMAN	bb72h12.y1 NIH_MGC_12 Homo sapiens cDNA clone IMAGE:3047975 5' similar to gb:L08069 DNAJ PROTEIN HOMOLOG 2 (HUMAN);
7790	16984	26498	2.08	3.0E-64	AL163248.2	NT	Homo sapiens chromosome 21 segment HS21C046
7790	16984	26499	2.08	3.0E-64	AL163248.2	NT	Homo sapiens chromosome 21 segment HS21C046
8188	17320	28863	5.53	3.0E-64	AL163227.2	NT	Homo sapiens chromosome 21 segment HS21C027
1086	10320	19472	2.11	2.0E-64	AA609940.1	EST_HUMAN	af084008.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1031151 3'
1401	10815	19779	3.28	2.0E-64	475770.1	NT	Homo sapiens eIF4E-like cap-binding protein (4EHP) mRNA
2491	11681		2.83	2.0E-64	A1927030.1	EST_HUMAN	w087b01.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2462281 3' similar to contains element L1 repetitive element;
2496	11685	20903	8.65	2.0E-64	AL163248.2	NT	Homo sapiens chromosome 21 segment HS21C046
2496	11685	20904	8.65	2.0E-64	AL163248.2	NT	Homo sapiens chromosome 21 segment HS21C046
3105	12340	21488	2.07	2.0E-64	4504068	NT	Homo sapiens glutamic-oxaloacetic transaminase 2, mitochondrial (aspartate aminotransferase 2) (GOT2), nuclear gene encoding mitochondrial protein, mRNA
5656	14879	24269	2.65	2.0E-64	AU124387.1	EST_HUMAN	AU124387 NT2RM2 Homo sapiens cDNA clone NT2RM2002113 5'
5668	15086	24500	4.15	2.0E-64	BF688537.1	EST_HUMAN	602123474F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4280395 5'
5930	15146	24557	2.05	2.0E-64	A1078387.1	EST_HUMAN	oz28b03.x1 Soares_tetral_fetus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:1678717 3'
5964	15179	24596	4.1	2.0E-64	M77185.1	NT	H. sapiens dopamine receptor D5 pseudogene 1, partial cds
7347	16563	26052	2.91	2.0E-64	BF528114.1	EST_HUMAN	602042892F1 NCI_CGAP_Brm67 Homo sapiens cDNA clone IMAGE:4180556 5'
7619	16822	26317	5.7	2.0E-64	A1922911.1	EST_HUMAN	wn81b06.x1 NCI_CGAP_U1 Homo sapiens cDNA clone IMAGE:2452211 3'
7619	16822	26318	5.7	2.0E-64	A1922911.1	EST_HUMAN	wn81b06.x1 NCI_CGAP_U1 Homo sapiens cDNA clone IMAGE:2452211 3'
7765	16960	26493	2.13	2.0E-64	AW884773.1	EST_HUMAN	PM2-SN0018-220300-002-e12 SN0018 Homo sapiens cDNA
8446	17507	24016	1.36	2.0E-64	8567387	NT	Homo sapiens period (Drosophila) homolog 3 (PER3), mRNA
8913	17801		2.65	2.0E-64	H55162.1	EST_HUMAN	CHR220101 Chromosome 22 exon Homo sapiens cDNA clone C22_132 5'
262	9538	18667	2.22	1.0E-64	AF231919.1	NT	Homo sapiens chromosome 21 unknown mRNA
1749	10961	20143	27.24	1.0E-64	A1928419.1	EST_HUMAN	au60c01.x1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2519136 3' similar to gb:L21696_cds1 PROTHYMOSIN ALPHA (HUMAN); contains element MSR1 repetitive element;
2873	12210	21348	0.82	1.0E-64	4507334	NT	Homo sapiens synaptobrevin 1 (SYN1), mRNA

Page 235 of 382  
Table 4  
Single Exon Probes Expressed in HELA Cells

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3485	12709	21848	5.93	1.0E-04	AF198779.1	NT	Homo sapiens transcription factor IGHM enhancer 3, JM11 protein, JMA protein, JM5 protein, T54 protein, JM10 protein, A4 differentiation-dependent protein, triple LIM domain protein 6, and synapophysin genes, complete cds; and L-type calcium channel $\alpha$
3561	12784	21913	1.41	1.0E-04	AF228527.1	NT	Homo sapiens TRIAD3 mRNA, partial cds
3561	12784	21914	1.41	1.0E-04	AF228527.1	NT	Homo sapiens TRIAD3 mRNA, partial cds
3878	13094	22211	0.78	1.0E-04	8922829	NT	Homo sapiens hypothetical protein FLJ11028 (FLJ11028), mRNA
8419	17491		2.5	1.0E-04	AL163246.2	NT	Homo sapiens chromosome 21 segment HS21C048
2241	11436	20680	1.5	9.0E-05	X89211.1	NT	H. sapiens DNA for endogenous retroviral like element
2241	11436	20681	1.5	9.0E-05	X89211.1	NT	H. sapiens DNA for endogenous retroviral like element
8068	17203		35.12	9.0E-05	BF330876.1	EST_HUMAN	QV4-BT0257-081188-017-403 BT0257 Homo sapiens cDNA
8042	17178	28717	11.84	8.0E-05	A1929244.1	EST_HUMAN	eu58407.x1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2516005 3' similar to SW:RL21_HUMAN P46778 60S RIBOSOMAL PROTEIN L21.;
1063	10289	18440	2.01	8.0E-05	AV721898.1	EST_HUMAN	AV721898 HTB Homo sapiens cDNA clone HTBBZC08 5'
1890	11097		20.4	8.0E-05	AA550829.1	EST_HUMAN	rib6410 s1 NCL CGAP_P111 Homo sapiens cDNA clone IMAGE:988379 similar to gb:K03002 60S RIBOSOMAL PROTEIN L32 (HUMAN);
6700	15895	25358	3.18	8.0E-05	AW083252.1	EST_HUMAN	xc07b09.x1 NCL CGAP_Co21 Homo sapiens cDNA clone IMAGE:2583545 3' similar to TR:Q63308 Q63308 LONG INTERSPERSED REPETITIVE DNA CONTAINING 7 ORFS.; contains L1.52 L1 repetitive element;
6768	15963	25420	4.89	8.0E-05	AA427878.1	EST_HUMAN	zw53b06.s1 Soares_tadl_fetus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:773747 3'
6768	15963	25421	4.99	8.0E-05	AA427878.1	EST_HUMAN	zw53b06.s1 Soares_tadl_fetus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:773747 3'
7450	16658	26147	4.89	8.0E-05	BE567816.1	EST_HUMAN	601340485F1 NIH_MGC_53 Homo sapiens cDNA clone IMAGE:3682877 5'
8030	17167	26705	4.81	8.0E-05	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C010
637	9882	18008	0.72	5.0E-05	AF084804.1	NT	Homo sapiens KE03 protein mRNA, partial cds
1361	10576	19741	1.71	5.0E-05	7681951	NT	Homo sapiens KIAA0156 gene product (KIAA0156), mRNA
1361	10576	19742	1.71	5.0E-05	7681951	NT	Homo sapiens KIAA0156 gene product (KIAA0156), mRNA
2123	11322	20540	1.58	5.0E-05	AB033788.1	NT	Homo sapiens hPAD-colony10 mRNA for peptidylarginine deaminase type I, complete cds
3222	12456	21589	2.37	5.0E-05	4507848	NT	Homo sapiens ubiquitin specific protease 13 (isopeptidase T-3) (USP13) mRNA
3222	12456	21590	2.37	5.0E-05	4507848	NT	Homo sapiens ubiquitin specific protease 13 (isopeptidase T-3) (USP13) mRNA
188	9478	18611	2.79	4.0E-05	AL120419.1	EST_HUMAN	DKFZp761G108_r1 761 (synonym: hamy2) Homo sapiens cDNA clone DKFZp761G108 5'
753	9894	19138	1.27	4.0E-05	A1266488.1	EST_HUMAN	qm48e01.x1 Soares_placenta_8to9weeks_2NBHP8b9W Homo sapiens cDNA clone IMAGE:1891800 3'
753	9894	19139	1.27	4.0E-05	A1266488.1	EST_HUMAN	qm48e01.x1 Soares_placenta_8to9weeks_2NBHP8b9W Homo sapiens cDNA clone IMAGE:1891800 3'
1086	10310	19463	1.28	4.0E-05	4826735	NT	Homo sapiens fragile X mental retardation, autosomal homolog 1 (FXR1), mRNA



Table 4

## Single Exon Probes Expressed in HELA Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1479	10692	19867	28.34	4.0E-65	4506636	NT	Homo sapiens ribosomal protein L34 (RPL34) mRNA
2305	11489	20719	3.54	4.0E-65	BE221469.1	EST_HUMAN	hu25604.x1 NCI_CGAP_Ma15 Homo sapiens cDNA clone IMAGE:3171102 3'
2305	11489	20720	3.54	4.0E-65	BE221469.1	EST_HUMAN	hu25604.x1 NCI_CGAP_Ma15 Homo sapiens cDNA clone IMAGE:3171102 3'
3926	13142	22259	0.96	4.0E-65	AW983185.1	EST_HUMAN	RC2-BN0033-160200-013-a03 BN0033 Homo sapiens cDNA
5735	14954	24352	4.42	4.0E-65	AB033093.1	NT	Homo sapiens mRNA for KIAA1267 protein, partial cds
5735	14954	24353	4.42	4.0E-65	AB033093.1	NT	Homo sapiens hypothetical protein FLJ22087 (FLJ22087), mRNA
8173	15355	24793	2.45	4.0E-65	11545780	NT	Homo sapiens PRO1474 mRNA, complete cds
7863	18883	26365	2.72	4.0E-65	AF119848.1	NT	Homo sapiens fragile X mental retardation, autosomal homolog 1 (FXR1), mRNA
8754	10310	19463	1.88	4.0E-65	4826735	NT	Homo sapiens gene for AF-6, complete cds
8901	17794	18911	5.17	4.0E-65	AB011399.1	NT	DKFZp781G108.1 761 (synonym: hamy2) Homo sapiens cDNA clone DKFZp781G108 5'
8266	9478	18521	1.88	4.0E-65	AL120419.1	EST_HUMAN	Homo sapiens pre-B-cell colony-enhancing factor (PBEF) mRNA
97	9391	18521	1.26	3.0E-65	5031976	NT	Homo sapiens pre-B-cell colony-enhancing factor (PBEF) mRNA
98	9391	18521	1.04	3.0E-65	5031976	NT	H. sapiens HZF9 mRNA for zinc finger protein
1239	11946	18521	4.65	3.0E-65	X78932.1	NT	Homo sapiens immunoglobulin superfamily, member 3 (IGSF3) mRNA, and translated products
1543	10756	18630	0.92	3.0E-65	4504828	NT	Homo sapiens testis_NHT Homo sapiens cDNA clone IMAGE:1638173 3' similar to contains element
1781	11001	20197	1.13	3.0E-65	A000692.1	EST_HUMAN	ov23f03.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1638173 3' similar to contains element
2947	12185	21317	0.99	3.0E-65	D87078.2	NT	MSR1 repetitive element ;
3244	12477	21610	1.5	3.0E-65	4504950	NT	Homo sapiens mRNA for KIAA0235 protein, partial cds
3701	12921	22039	1.22	3.0E-65	A000692.1	EST_HUMAN	Homo sapiens laminin, beta 1 (LAMB1), mRNA
4651	13845	22636	1.56	3.0E-65	6912385	NT	Homo sapiens testis_NHT Homo sapiens cDNA clone IMAGE:781042 5'
7927	16403	25888	15.56	3.0E-65	AA430006.1	EST_HUMAN	602155082F1 NIH_MGC 83 Homo sapiens cDNA clone IMAGE:4265688 5'
3382	12609	21743	7.64	2.0E-65	BF680294.1	EST_HUMAN	602155082F1 NIH_MGC 7 Homo sapiens cDNA clone IMAGE:3534741 5'
5895	15112		5.18	2.0E-65	BE26373.1	EST_HUMAN	602134359F1 NIH_MGC 81 Homo sapiens cDNA clone IMAGE:4268295 5'
6133	15317	24750	27.19	2.0E-65	BF576922.1	EST_HUMAN	Homo sapiens SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily d, member 3 (SMARCD3), mRNA
7249	18469	25661	1.71	2.0E-65	11419247	NT	EST178755 Colon carcinoma (HCC) cell line Homo sapiens cDNA 5' and similar to endogenous retrovirus
8373	17459		11.09	2.0E-65	AA307804.1	EST_HUMAN	601854033F1 NIH_MGC 57 Homo sapiens cDNA clone IMAGE:4079769 5'
8868	18111		3.24	2.0E-65	BF246086.1	EST_HUMAN	601854033F1 NIH_MGC 20 Homo sapiens cDNA clone IMAGE:4026501 5'
90	9383		0.99	1.0E-65	BF125544.1	EST_HUMAN	Homo sapiens putative Rab5 GDP/GTP exchange factor homologue (RABEX5), mRNA
545	9786	18920	1.2	1.0E-65	7657495	NT	

Table 4

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2007	11210	20420	1.4	1.0E-65	AB040946.1	NT	Homo sapiens mRNA for KIAA1513 protein, partial cds
3351	12578	21719	0.86	1.0E-65	BE466881.1	EST_HUMAN	h224a09.x1 NCL_CGAP_GC8 Homo sapiens cDNA clone IMAGE:3208888 3'
3975	13189	22287	1.9	1.0E-65	4504082	NT	Homo sapiens glycican 4 (GPC4) mRNA
3975	13189	22288	1.9	1.0E-65	4504082	NT	Homo sapiens glycican 4 (GPC4) mRNA
4189	13383	22491	4.44	1.0E-65	AW029340.1	EST_HUMAN	wx09c09.x1 NCL_CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2543152 3'
4189	13393	22492	4.44	1.0E-65	AW029340.1	EST_HUMAN	wx09c09.x1 NCL_CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2543152 3'
4239	13442		1.11	1.0E-65	AW982813.1	EST_HUMAN	EST374888 MAGC resequences, MAGC Homo sapiens cDNA
5055	14237	23325	1.09	1.0E-65	AW238282.1	EST_HUMAN	xp20c01.x1 NCL_CGAP_HIN10 Homo sapiens cDNA clone IMAGE:2740898 3'
5055	14237	23326	1.09	1.0E-65	AW238282.1	EST_HUMAN	xp20c01.x1 NCL_CGAP_HIN10 Homo sapiens cDNA clone IMAGE:2740898 3'
6770	15965	25423	2.68	1.0E-65	AU128040.1	EST_HUMAN	AU128040 NT2RP2 Homo sapiens cDNA clone NT2RP2004714 5'
6770	15985	25424	2.68	1.0E-65	AU128040.1	EST_HUMAN	AU128040 NT2RP2 Homo sapiens cDNA clone NT2RP2004714 5'
6774	15969		4.14	1.0E-65	11431894	NT	Homo sapiens inositol 1,4,5-bisphosphate receptor, type 1 (ITPR1), mRNA
6906	16063	25529	7.42	1.0E-65	A1191716.1	EST_HUMAN	q55a02.x1 Soares testis NHT Homo sapiens cDNA clone IMAGE:1733450 3' similar to gb:M29581 ZINC
7243	16463	25953	2.12	1.0E-65	M26167.1	NT	FINGER PROTEIN 8 (HUMAN); contains MER19.11 MER19 repetitive element
7358	16574	26066	25.94	1.0E-65	4506660	NT	Human platelet factor 4 variation 1 (PF4var1) gene, complete cds
7660	16889	26398	2.8	1.0E-65	BF698707.1	EST_HUMAN	Homo sapiens ribosomal protein L7a (RPL7A) mRNA
7763	16959	26469	2.63	1.0E-65	A1621017.1	EST_HUMAN	602126239F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4283313 5'
8420	17492		2.48	1.0E-65	11418041	NT	ts76a08.x1 NCL_CGAP_GC8 Homo sapiens cDNA clone IMAGE:2237170 3' similar to gb:L16533_maf1
8524	17554	23987	5.48	1.0E-65	11418322	NT	PANCREATITIS ASSOCIATED PROTEIN 1 PRECURSOR (HUMAN);
8663	17834		1.47	1.0E-65	11418248	NT	Homo sapiens TNF-inducible protein CG12-1 (CG12-1), mRNA
71	9368	18462	0.93	9.0E-66	AL160311.1	NT	Homo sapiens cadherin EGF LAG seven-pass G-type receptor 1 (CELSR1), mRNA
71	9368	18463	0.93	9.0E-66	AL160311.1	NT	Homo sapiens sulfotransferase-related protein (SULTX3), mRNA
1362	10577	19743	2.59	9.0E-66	5031980	NT	Novel human gene mapping to chromosome 22
1362	10577	19744	2.59	9.0E-66	5031980	NT	Novel human gene mapping to chromosome 22
1477	10690		4.32	9.0E-66	M87299.1	NT	Homo sapiens 26S proteasome-associated pad1 homolog (POH1) mRNA
3677	13093	22209	0.73	9.0E-66	M72393.1	NT	Homo sapiens 26S proteasome-associated pad1 homolog (POH1) mRNA
3677	13093	22210	0.73	9.0E-66	M72393.1	NT	Human transposon-like element, partial
4699	13890	22690	0.62	9.0E-66	AL137163.1	NT	Human calcium-dependent phospholipid-binding protein (PLA2) mRNA, complete cds
7887	17103		1.9	7.0E-66	BE064410.1	EST_HUMAN	Human calcium-dependent phospholipid-binding protein (PLA2) mRNA, complete cds
4359	13561	22655	1.14	8.0E-66	A1924653.1	EST_HUMAN	Novel human gene mapping to chromosome X
							RC4-BT0311-141199-011-06 BT0311 Homo sapiens cDNA
							wn57h07.x1 NCL_CGAP_Lu19 Homo sapiens cDNA clone IMAGE:2449597 3' similar to WP:F15G9.4A
							CE16595

Table 4

## Single Exon Probes Expressed in HELA Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4359	13561	22658	1.14	6.0E-66	A924653.1	EST_HUMAN	wn57h07.x1 NCI_CGAP_Lu10 Homo sapiens cDNA clone IMAGE:2449597 3' similar to WP:F15G9.4A CE18595;
4359	13561	22657	1.14	6.0E-66	A924653.1	EST_HUMAN	wn57h07.x1 NCI_CGAP_Lu10 Homo sapiens cDNA clone IMAGE:2449597 3' similar to WP:F15G9.4A CE18595;
7719	16918	26426	9.19	6.0E-66	X69181.1	NT	H.sapiens mRNA for ribosomal protein L31
1375	10589	19755	2	5.0E-66	BE064410.1	EST_HUMAN	RC4-BT0311-141199-011-h06 BT0311 Homo sapiens cDNA
5140	14319	23410	0.97	5.0E-66	BE808644.1	EST_HUMAN	601681592F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3951791 5'
5140	14319	23411	0.97	5.0E-66	BE808644.1	EST_HUMAN	601681592F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3951791 5'
6852	16041	25505	6.48	5.0E-66	11420557	NT	Homo sapiens thyroid hormone receptor binding protein (AIB3), mRNA
800	10039	19180	1.09	4.0E-66	6670818	NT	Mus musculus fragile X mental retardation syndrome 1 homolog (Fmr1), mRNA
2245	11440	20664	4.3	4.0E-66	X89211.1	NT	H.sapiens DNA for endogenous retroviral like element
2437	11628		7.08	4.0E-66	AJ223364.1	NT	Homo sapiens germ-line DNA upstream of Ikappa locus
4793	13982		10.15	4.0E-66	9635487	NT	Human endogenous retrovirus, complete genome
5466	14692	24045	4.68	4.0E-66	11428643	NT	Homo sapiens methylene tetrahydrofolate dehydrogenase (NAD+ dependent), methenyltetrahydrofolate cyclohydrolase (MTHFD2), mRNA
6020	14510	23568	4.04	4.0E-66	AW965473.1	EST_HUMAN	EST377546 MAGE resequences, MAGI Homo sapiens cDNA
6132	15316	24749	6.3	4.0E-66	U78168.1	NT	Homo sapiens cAMP-regulated guanine nucleotide exchange factor 1 (cAMP-GEFI) mRNA, complete cds
6347	14692	24045	2.06	4.0E-66	11428643	NT	Homo sapiens methylene tetrahydrofolate dehydrogenase (NAD+ dependent), methenyltetrahydrofolate cyclohydrolase (MTHFD2), mRNA
6491	15688	25154	10.1	4.0E-66	11421638	NT	Homo sapiens hypothetical protein FLJ20116 (FLJ20116), mRNA
1430	10643	19814	37.87	3.0E-66	4502098	NT	Homo sapiens solute carrier family 25 (mitochondrial carrier, adenine nucleotide translocator), member 5 (SLC25A5), nuclear gene encoding mitochondrial protein, mRNA
1430	10643	19815	37.87	3.0E-66	4502098	NT	Homo sapiens solute carrier family 25 (mitochondrial carrier, adenine nucleotide translocator), member 5 (SLC25A5), nuclear gene encoding mitochondrial protein, mRNA
1951	11155	20357	0.92	3.0E-66	N55323.1	EST_HUMAN	yz27g12.r1 Soares_multiple_sclerosis_2Nbl-IMSP Homo sapiens cDNA clone IMAGE:284326 5' similar to SW:H2B1_TIGCA P35068 HISTONE H2B.1/H2B.2 [2] PIR:B56612;
1951	11155	20358	0.92	3.0E-66	N55323.1	EST_HUMAN	yz27g12.r1 Soares_multiple_sclerosis_2Nbl-IMSP Homo sapiens cDNA clone IMAGE:284326 5' similar to SW:H2B1_TIGCA P35068 HISTONE H2B.1/H2B.2 [2] PIR:B56612;
1951	11155	20359	0.92	3.0E-66	N55323.1	EST_HUMAN	yz27g12.r1 Soares_multiple_sclerosis_2Nbl-IMSP Homo sapiens cDNA clone IMAGE:284326 5' similar to SW:H2B1_TIGCA P35068 HISTONE H2B.1/H2B.2 [2] PIR:B56612;
2668	11849	21064	3.9	3.0E-66	11141880	NT	Homo sapiens TGF(beta)-induced transcription factor 2 (TGIF2), mRNA
3081	12317	21439	7.06	3.0E-66	7662223	NT	Homo sapiens KIAA0849 gene product (KIAA0849), mRNA
5562	14785	24155	2.1	3.0E-66	11417948	NT	Homo sapiens NIPSNAP, C. elegans, homolog 1 (NIPSNAP1), mRNA

Page 239 of 382  
Table 4  
Single Exon Probes Expressed in HELA Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5662	14785	24158	2.1	3.0E-66	11417946	NT	Homo sapiens NIPSNAP, C. elegans, homolog 1 (NIPSNAP1), mRNA
8043	17179	28718	7.97	3.0E-66	5453949	NT	Homo sapiens protein phosphatase 2, regulatory subunit B (B56), alpha isoform (PPP2R5A) mRNA
53	9350	18464	1.32	2.0E-66	7657334	NT	Homo sapiens Mischapen/NIK-related kinase (MINK), mRNA
53	9350	18465	1.32	2.0E-66	7657334	NT	Homo sapiens Mischapen/NIK-related kinase (MINK), mRNA
428	9283	18395	1.17	2.0E-66	4505524	NT	Homo sapiens origin recognition complex, subunit 5 (yeast homolog)-like (ORC5L) mRNA, and translated products
428	9283	18396	1.17	2.0E-66	4505524	NT	Homo sapiens origin recognition complex, subunit 5 (yeast homolog)-like (ORC5L) mRNA, and translated products
1794	11003	20198	4.01	2.0E-66	AL163301.2	NT	Homo sapiens chromosome 21 segment HS21C101
3747	12987	22081	0.75	2.0E-66	AL117233.1	NT	Novel human gene mapping to chromosome 1
4041	13251	22352	0.92	2.0E-66	AF108389.1	NT	Homo sapiens sodium/calcium exchanger isoform NaCa3 (NCX1) mRNA, complete cds
4247	13450	22541	1.08	2.0E-66	8923768	NT	Homo sapiens histone deacetylase 8 (HDAC8) gene (HSA277724), mRNA
4658	13852	22848	30.43	2.0E-66	AJ133267.2	NT	Homo sapiens HLA-B gene for human leukocyte antigen B
4658	13852	22849	30.43	2.0E-66	AJ133267.2	NT	Homo sapiens HLA-B gene for human leukocyte antigen B
8762	18335		2.62	2.0E-66	11418318	NT	Homo sapiens G-2 and S-phase expressed 1 (GTSE1), mRNA
1658	10871		6.34	1.0E-66	BE887173.1	EST_HUMAN	601508376F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3909631 5'
2846	12085	21213	1.61	1.0E-66	AV717817	EST_HUMAN	AV717817 DCB Homo sapiens cDNA clone DCBADC07 5'
2848	12085	21214	1.61	1.0E-66	AV717817.1	EST_HUMAN	AV717817 DCB Homo sapiens cDNA clone DCBADC07 5'
4378	12085	21213	3.84	1.0E-66	AV717817.1	EST_HUMAN	AV717817 DCB Homo sapiens cDNA clone DCBADC07 5'
4378	12085	21214	3.84	1.0E-66	AV717817.1	EST_HUMAN	AV717817 DCB Homo sapiens cDNA clone DCBADC07 5'
5387	14618	23729	5.7	1.0E-66	BF673088.1	EST_HUMAN	602152896F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4284151 5'
7516	16721	26211	2.06	1.0E-66	AF111167.2	NT	Homo sapiens jun dimerization protein gene, partial cds; cfos gene, complete cds; and unknown gene
9114	17932		1.35	1.0E-66	BE894192.1	EST_HUMAN	601437130F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3922303 5'
8530	17558		2.6	9.0E-67	11418177	NT	Homo sapiens Ran GTPase activating protein 1 (RANGAP1), mRNA
385	9679	18816	2.26	7.0E-67	AW162232.1	EST_HUMAN	au75d02.x1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2782083 3' similar to gb:M37104 ATP SYNTHASE COUPLING FACTOR 6, MITOCHONDRIAL PRECURSOR (HUMAN);
1389	10603	19768	1.83	7.0E-67	AA383416.1	EST_HUMAN	EST96812 Testis 1 Homo sapiens cDNA 5' end similar to similar to C. elegans hypothetical protein, cosmid ZK353
1539	10752	19925	1.19	7.0E-67	W85947.1	EST_HUMAN	zh56b05.r1 Soares fetal liver spleen_INFLS_S1 Homo sapiens cDNA clone IMAGE:416049 5'
1539	10752	19926	1.19	7.0E-67	W85947.1	EST_HUMAN	zh56b05.r1 Soares fetal liver spleen_INFLS_S1 Homo sapiens cDNA clone IMAGE:416049 5'
2001	11204	20414	1.12	7.0E-67	7657243	NT	Homo sapiens inositol 1,3,4-trisphosphate 5/6 kinase (ITPK1), mRNA
2001	11204	20415	1.12	7.0E-67	7657243	NT	Homo sapiens inositol 1,3,4-trisphosphate 5/6 kinase (ITPK1), mRNA

Page 240 of 382  
Table 4  
Single Exon Probes Expressed in HELA Cells

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2762	9679	18816	2.8	7.0E-67	AW162232.1	EST_HUMAN	eu75402.x1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2782083 3' similar to gb:M37104 ATP SYNTHASE COUPLING FACTOR 6, MITOCHONDRIAL PRECURSOR (HUMAN);
5777	14895	24395	1.87	7.0E-67	11425572	NT	Homo sapiens adaptor-related protein complex 2, beta 1 subunit (AP2B1), mRNA
5777	14895	24396	1.87	7.0E-67	11425572	NT	Homo sapiens adaptor-related protein complex 2, beta 1 subunit (AP2B1), mRNA
8176	17308	26851	2.1	7.0E-67	U82486.1	NT	Human cytochrome oxidase subunit VIa (COX8A1P) pseudogene, complete cds
8300	17408	26833	1.92	7.0E-67	11430460	NT	Homo sapiens low density lipoprotein-related protein 2 (LRP2), mRNA
8300	17408	26834	1.92	7.0E-67	11430460	NT	Homo sapiens low density lipoprotein-related protein 2 (LRP2), mRNA
8789	17716	23961	1.98	7.0E-67	AB011389.1	NT	Homo sapiens gene for AF-8, complete cds
566	9816	18938	2.14	6.0E-67	X68968.1	NT	H. sapiens mRNA for acetyl-CoA carboxylase
803	10044	19195	1.06	6.0E-67	Z17227.1	NT	Homo sapiens mRNA for transmembrane receptor protein
1280	10495	19654	0.98	6.0E-67	Y14320.1	NT	Homo sapiens PMP69 gene, exons 3, 4, 5, 6 & 7
3133	12388	21499	1.21	6.0E-67	4508434	NT	Homo sapiens retinoblastoma 1 (including osteosarcoma) (RB1) mRNA
3416	12841	21770	1.29	6.0E-67	4507332	NT	Homo sapiens Synapsin III (SYN3) mRNA, and translated products
3416	12841	21771	1.29	6.0E-67	4507332	NT	Homo sapiens Synapsin III (SYN3) mRNA, and translated products
4107	13314	22411	0.79	6.0E-67	AL163201.2	NT	Homo sapiens chromosome 21 segment HS21C001
4107	13314	22412	0.79	6.0E-67	AL163201.2	NT	Homo sapiens chromosome 21 segment HS21C001
4716	13907	23008	4.23	6.0E-67	7657020	NT	Homo sapiens DKFZp434P211 protein (DKFZP434P211), mRNA
4716	13907	23009	4.23	6.0E-67	7657020	NT	Homo sapiens DKFZp434P211 protein (DKFZP434P211), mRNA
3187	12422	21555	2.95	5.0E-67	AF009660.1	NT	Homo sapiens T cell receptor beta locus, TCRBV7S3A2 to TCRBV12S2 region
1336	10551	19716	0.74	4.0E-67	R90819.1	EST_HUMAN	yn02d11.11 Soares adult brain N2b4HB55Y Homo sapiens cDNA clone IMAGE:167253 5'
7630	16831		2.29	4.0E-67	AA714294.1	EST_HUMAN	mw06a01.s1 NCI_CGAP_S51 Homo sapiens cDNA clone IMAGE:1238472 3' similar to TR:O10385 O10385 PRO-POL-DUTPASE POLYPROTEIN ;
2785	9884	19009	1.15	3.0E-67	AA333788.1	EST_HUMAN	EST37903 Embryo, 9 week Homo sapiens cDNA 5' and
3431	12856	21786	1.11	3.0E-67	BE064410.1	EST_HUMAN	RC4-BT0311-141198-011-r06 BT0311 Homo sapiens cDNA
4704	13895	22894	3.38	3.0E-67	AW869159.1	EST_HUMAN	MR3-SN0068-040500-008-r01 SN0068 Homo sapiens cDNA
4734	13925		1.01	3.0E-67	AL163279.2	NT	Homo sapiens chromosome 21 segment HS21C0079
6522	15718	25183	2.27	3.0E-67	BF196068.1	EST_HUMAN	hr81f05.x1 NCI_CGAP_Kid111 Homo sapiens cDNA clone IMAGE:3134813 3' similar to SW:RHOP_MOUSE
7811	17004		24.32	3.0E-67	AA827874.1	EST_HUMAN	Q61085 GTP-RHO BINDING PROTEIN 1 ;
193	9473	18604	1.21	2.0E-67	BE348354.1	EST_HUMAN	am18b07.s1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1541365 3'
855	10091	19253	5.63	2.0E-67	AW816405.1	EST_HUMAN	hw16g08.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3183138 3' similar to WP:F23H11.9 CE09817 ;
1113	10337		1.73	2.0E-67	AF167460.1	NT	QV4-S10234-181199-037-r05 ST0234 Homo sapiens cDNA Homo sapiens double stranded RNA activated protein kinase (PKR) gene, exons 2a, 2, 3, and 4

Page 241 of 382  
Table 4  
Single Exon Probes Expressed in HELA Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1849	11056	20248	0.91	2.0E-67	BE303037.1	EST_HUMAN	ba72g05.y1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:2805976 5' similar to TR:094892 094892 KIAA0798 PROTEIN.;
1849	11056	20249	0.91	2.0E-67	BE303037.1	EST_HUMAN	ba72g05.y1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:2805976 5' similar to TR:094892 094892 KIAA0798 PROTEIN.;
2350	11543	20768	1.39	2.0E-67	AF308561.1	NT	Homo sapiens KRAB zinc finger protein ZFQR mRNA, complete cds
2395	11588	20808	3.97	2.0E-67	4758795	NT	Homo sapiens developmentally regulated GTP-binding protein 1 (DRG1), mRNA
3444	12669	21804	4.82	2.0E-67	AA625755.1	EST_HUMAN	zu91g01.s1 Soares_testis NIH_Homo sapiens cDNA clone IMAGE:745392 3'
3979	13193	22301	3.33	2.0E-67	AL163300.2	NT	Homo sapiens chromosome 21 segment HS21C100
5720	14938	24334	4.82	2.0E-67	BF240758.1	EST_HUMAN	601875351F1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:4091893 5'
5785	15002	24405	2.36	2.0E-67	AB051763.1	NT	Homo sapiens mRNA for NADPH-cytochrome P-450 reductase, complete cds
5785	15002	24408	2.36	2.0E-67	AB051763.1	NT	Homo sapiens mRNA for NADPH-cytochrome P-450 reductase, complete cds
7478	16884	26167	1.8	2.0E-67	BF685788.1	EST_HUMAN	602140470F1 NIH_MGC_46 Homo sapiens cDNA clone IMAGE:4301705 5'
7623	18390		3.79	2.0E-67	11438448	NT	Homo sapiens KIAA0985 protein (KIAA0985), mRNA
7891	18426	25913	2.14	2.0E-67	BF371769.1	EST_HUMAN	PM2-TN0103-040900-001-c02 TN0103 Homo sapiens cDNA
8665	18189	23759	2.99	2.0E-67	11418189	NT	Homo sapiens thyroid autoantigen 70kD (Ku antigen) (GZ2P1), mRNA
257	9533	18664	7.29	1.0E-67	4502168	NT	Homo sapiens amyloid beta (A4) precursor protein (protease nexin-II, Alzheimer disease) (APP), mRNA
715	9857	19095	1.12	1.0E-67	AA702794.1	EST_HUMAN	z880504.s1 Soares_fetal_liver脾脏_NFLS_S1 Homo sapiens cDNA clone IMAGE:448015 3'
4722	13913	23014	0.59	1.0E-67	BF439247.1	EST_HUMAN	hab61108.x1 Soares_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE: 3'
2142	11340	20558	1.2	8.0E-68	BE870732.1	EST_HUMAN	601448558F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3852254 5'
3851	13067	22181	5.82	8.0E-68	AA208456.1	EST_HUMAN	zq82h10.r1 Stratiene hNT neuron (#837233) Homo sapiens cDNA clone IMAGE:648163 5' similar to SW_SAV_SULAC Q07590 SAV PROTEIN.;
3851	13067	22182	5.82	8.0E-68	AA208456.1	EST_HUMAN	zq82h10.r1 Stratiene hNT neuron (#837233) Homo sapiens cDNA clone IMAGE:648163 5' similar to SW_SAV_SULAC Q07590 SAV PROTEIN.;
7197	16374	25858	2.52	6.0E-68	11422086	NT	Homo sapiens brefeldin A-inhibited guanine nucleotide-exchange protein 2 (BIG2), mRNA
8973	17943		1.37	6.0E-68	BE612554.1	EST_HUMAN	601452067F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3855761 5'
812	11942	19203	1.04	5.0E-68	AF231919.1	NT	Homo sapiens chromosome 21 unknown mRNA
812	11942	19204	1.04	5.0E-68	AF231919.1	NT	Homo sapiens chromosome 21 unknown mRNA
829	10067	19220	5.46	5.0E-68	AF231919.1	NT	Homo sapiens chromosome 21 unknown mRNA
829	10067	19221	5.46	5.0E-68	AF231919.1	NT	Homo sapiens chromosome 21 unknown mRNA
2735	11914	21127	0.97	5.0E-68	AF231919.1	NT	Homo sapiens chromosome 21 unknown mRNA
3112	12347	21475	3.04	5.0E-68	AB037852.1	NT	Homo sapiens mRNA for KIAA1431 protein, partial cds
4162	13368		0.64	5.0E-68	4826867	NT	Homo sapiens retinoblastoma-binding protein 2 (RBBP2) mRNA
4489	13687	22778	0.75	5.0E-68	AL157645.1	EST_HUMAN	DKFZ547D207_r1 547 (synonym: hfbf1) Homo sapiens cDNA clone DKFZ547D207 5'

Page 242 of 382  
Table 4  
Single Exon Probes Expressed in HELA Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2493	11683	20899	3.92	4.0E-68	11421388	NT	Homo sapiens transcription factor NRF (NRF), mRNA
2493	11683	20899	3.92	4.0E-68	11421388	NT	Homo sapiens transcription factor NRF (NRF), mRNA
4985	14182		13.93	4.0E-68	P04408	SWISSPROT	GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE, LIVER
5212	14387	23472	0.72	4.0E-68	7549804	NT	Homo sapiens deiodinase, iodothyronine, type II (DIO2), transcript variant 2, mRNA
5989	15271	24699	5.7	4.0E-68	11055991	NT	Homo sapiens serine carboxypeptidase 1 precursor protein (HSCP1), mRNA
5989	15271	24700	5.7	4.0E-68	11055991	NT	Homo sapiens serine carboxypeptidase 1 precursor protein (HSCP1), mRNA
6777	15972	25428	5.65	4.0E-68	D63479.2	NT	Homo sapiens mRNA for KIAA0145 protein, partial cds
6777	15972	25429	5.65	4.0E-68	D63479.2	NT	Homo sapiens mRNA for KIAA0145 protein, partial cds
7573	16778	26271	7.1	4.0E-68	4506282	NT	Homo sapiens protein tyrosine phosphatase type IVA, member 1 (PTP4A1) mRNA
7573	16778	26272	7.1	4.0E-68	4506282	NT	Homo sapiens protein tyrosine phosphatase type IVA, member 1 (PTP4A1) mRNA
3641	12862	21980	5.48	3.0E-68	AF236082.1	NT	Mus musculus G-protein coupled receptor GPR73 (Gpr73) mRNA, complete cds
6897	15603		5.45	3.0E-68	A1342323.1	EST_HUMAN	q138h02.x1 Soares, fetal_lung_Nhl-19W Homo sapiens cDNA clone IMAGE:1950291 3' similar to contains
9188	18108		1.41	3.0E-68	AW639485.1	EST_HUMAN	THR-12 THR repetitive element
2814	14475		26.8	2.0E-68	D00522.1	NT	Orctulus longicaudatus mRNA for EF-1 alpha, complete cds
4003	13216	22320	0.89	2.0E-68	BE675766.1	EST_HUMAN	711502.x1 NCL CGAP_CLL1 Homo sapiens cDNA clone IMAGE:3294747 3' similar to TR:O80828 O80828
4088	13878	22880	1.97	2.0E-68	AB008681.1	NT	HYPOTHETICAL 88.8 KD PROTEIN
6031	15239		8.84	2.0E-68	R45088.1	EST_HUMAN	Homo sapiens gene for activin receptor type IIB, complete cds
6110	15204	24623	4.55	2.0E-68	BF035316.1	EST_HUMAN	y838g04.s1 Soares infant brain 1N1B Homo sapiens cDNA clone IMAGE:34896 3'
79	9372	18502	2.89	1.0E-68	4506222	NT	601458514F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3882034 5'
301	8574	18707	11.39	1.0E-68	AW816405.1	EST_HUMAN	Homo sapiens meningioma (disrupted in balanced translocation) 1 (MN1), mRNA
2218	11413	20637	2.32	1.0E-68	AB011149.1	NT	QV4-ST0234-181198-037-05 ST0234 Homo sapiens cDNA
2218	11413	20638	2.32	1.0E-68	AB011149.1	NT	Homo sapiens mRNA for KIAA0577 protein, complete cds
3986	13200	22308	0.97	1.0E-68	BE286032.1	EST_HUMAN	Homo sapiens mRNA for KIAA0577 protein, complete cds
5053	14235	23322	0.64	1.0E-68	AA887943.1	EST_HUMAN	601177002F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3532344 5'
5346	14576	23653	1.69	1.0E-68	7662349	NT	aa47g12.s1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1480518 3'
7429	16639	26132	2.83	1.0E-68	11418869	NT	Homo sapiens cell recognition molecule Casp2 (KIAA0868), mRNA
7429	16639	26133	2.83	1.0E-68	11418869	NT	Homo sapiens phosphodiesterase 7B (PDE7B), mRNA
7478	16686	26168	2.64	1.0E-68	L76416.1	NT	Homo sapiens phosphodiesterase 7B (PDE7B), mRNA
7747	16943	26455	2.44	1.0E-68	11433277	NT	Homo sapiens MIF2 suppressor (HSM13) mRNA, complete cds
7847	17038	26554	2.74	1.0E-68	U50319.1	NT	Homo sapiens myosin IC (MYO1C), mRNA
7847	17038	26555	2.74	1.0E-68	U50319.1	NT	Human protein kinase C substrate 80K-H (PRKCSH) gene, exon 4-5
8169	17301	26845	1.88	1.0E-68	11418431	NT	Human protein kinase C substrate 80K-H (PRKCSH) gene, exon 4-5

Table 4

## Single Exon Probes Expressed in HELA Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8168	17301	28848	1.88	1.0E-68	11418431	NT	Homo sapiens CGI-78 protein (LOC51632), mRNA
8955	9372	18502	2.07	1.0E-68	4505222	NT	Homo sapiens meningioma (disrupted in balanced translocation) 1 (MN1), mRNA
9178	18288	23888	1.69	1.0E-68	11430460	NT	Homo sapiens low density lipoprotein-related protein 2 (LRP2), mRNA
21	9317	18418	2.67	9.0E-69	5031976	NT	Homo sapiens pre-B-cell colony-enhancing factor (PBEF) mRNA
21	9317	18420	2.67	9.0E-69	5031976	NT	Homo sapiens pre-B-cell colony-enhancing factor (PBEF) mRNA
1035	10281	19411	3.32	9.0E-69	5031980	NT	Homo sapiens 28S proteasome-associated pad1 homolog (POH1) mRNA
1035	10281	19412	3.32	9.0E-69	5031980	NT	Homo sapiens 28S proteasome-associated pad1 homolog (POH1) mRNA
4110	13317	22418	0.69	9.0E-69	4757867	NT	Homo sapiens v-rat murine sarcoma viral oncogene homolog B1 (BRAF) mRNA
7465	16673		9.68	9.0E-69	AU117241.1	EST_HUMAN	Homo sapiens HEMBA1 Homo sapiens cDNA clone HEMBA1000988 5'
3384	12592		1.39	8.0E-69	AJ237744.1	NT	Homo sapiens RIBIR gene (partial), exon 12
5814	15031	24432	5.24	7.0E-69	9986912	NT	Homo sapiens actin-related protein 3-beta (ARP3BETA), mRNA
6415	15612	25075	9.31	6.0E-69	A192784.1	EST_HUMAN	q62h01.x1 Soares_fetal_lung_NHIL19W Homo sapiens cDNA clone IMAGE:1743601 3' similar to
6415	15612	25076	9.31	6.0E-69	A192784.1	EST_HUMAN	gbL11566 60S RIBOSOMAL PROTEIN L18 (HUMAN);
9101	18262		4.5	5.0E-69	AW613417.1	EST_HUMAN	q62h01.x1 Soares_fetal_lung_NHIL19W Homo sapiens cDNA clone IMAGE:1743601 3' similar to
526	9777		1.22	4.0E-69	A1873630.1	EST_HUMAN	hh72e06.x1 NCI_CGAP_GU1 Homo sapiens cDNA clone IMAGE:2868354 3' similar to contains MER29.12
5589	14813	24187	4.72	4.0E-69	A1784973.1	EST_HUMAN	wh57b08.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2437125 3'
5946	15162	24575	3.11	4.0E-69	4557732	NT	O55137 ACYL-COA THIOESTERASE.;
5946	15162	24576	3.11	4.0E-69	4557732	NT	Homo sapiens latent transforming growth factor beta binding protein 2 (LTBP2) mRNA
391	9895	18823	2.37	3.0E-69	BE268012.1	EST_HUMAN	Homo sapiens latent transforming growth factor beta binding protein 2 (LTBP2) mRNA
618	9893	18983	1.63	3.0E-69	AF221712.1	NT	601110371F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3351352 5'
1540	10753		2.54	3.0E-69	T80514.1	EST_HUMAN	Homo sapiens Smad- and Olf-interacting zinc finger protein mRNA, partial cds
4992	14199	23259	4.28	3.0E-69	AB037732.1	NT	y048a02.r1 Soares Infant brain 1N1B Homo sapiens cDNA clone IMAGE:24880 5' similar to SP-A48838
5178	13268	22370	1.54	3.0E-69	A1765888.1	EST_HUMAN	A48836 SPEGF III-EGF REPEAT-CONTAINING FIBROPELIN-LIKE PROTEIN - SEA URCHIN;
5296	14488	26927	2.25	3.0E-69	11418185	NT	Homo sapiens mRNA for KIAA1311 protein, partial cds
6313	15484	24940	8.1	3.0E-69	AF268075.1	NT	wh66g08.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2385758 3'
6929	16122	25589	3.57	3.0E-69	X08233.1	NT	Homo sapiens aconitase 2, mitochondrial (ACO2), mRNA
7235	16456	25944	4.89	3.0E-69	11432120	NT	Homo sapiens TRAF6-binding protein T88P mRNA, complete cds
							Human mRNA for calcium-binding protein in macrophages (MRP-14) macrophage migration inhibitory factor (MIF)-related protein
							Homo sapiens ribosomal protein S15a (RPS15A), mRNA



Page 244 of 382  
Table 4

## Single Exon Probes Expressed in HELA Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7418	18630		15.56	3.0E-69	AA376398.1	EST_HUMAN	EST88807 HSC172 cells II Homo sapiens cDNA 5' end similar to similar to ribosomal protein S18
8432	17488		5.21	3.0E-69	11419157	NT	Homo sapiens HGC8.2 protein (HGC8.2), mRNA
128	9663	18802	0.98	2.0E-69	AF160252.1	NT	Homo sapiens KIAA0553 protein gene, complete cds; and alpha1b protein gene, partial cds
128	9663	18803	0.98	2.0E-69	AF160252.1	NT	Homo sapiens KIAA0553 protein gene, complete cds; and alpha1b protein gene, partial cds
410	9663	18802	4.91	2.0E-69	AF160252.1	NT	Homo sapiens KIAA0553 protein gene, complete cds; and alpha1b protein gene, partial cds
410	9663	18803	4.91	2.0E-69	AF160252.1	NT	Homo sapiens KIAA0553 protein gene, complete cds; and alpha1b protein gene, partial cds
1850	11057	20250	1.85	2.0E-69	BE257857.1	EST_HUMAN	601109444F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3350074 5'
2766	12038		3.59	2.0E-69	AA431167.1	EST_HUMAN	zw71g02.r1 Soares testis NHT Homo sapiens cDNA clone IMAGE:781682 5'
1628	10839		11.27	1.0E-69	BF330124.1	EST_HUMAN	RCO-BN0305-200600-031-05 BN0305 Homo sapiens cDNA
1678	10890	20078	2.07	1.0E-69	AF053768.1	NT	Rattus norvegicus brain specific cortactin-binding protein CBP90 mRNA, partial cds
5934	15150	24560	4.11	1.0E-69	AW393999.1	EST_HUMAN	QVQ-TT0010-031189-045-c07 TT0010 Homo sapiens cDNA
6013	15263	24687	3.25	1.0E-69	AB032973.1	NT	Homo sapiens mRNA for KIAA1147 protein, partial cds
6013	15263	24688	3.25	1.0E-69	AB032973.1	NT	Homo sapiens mRNA for KIAA1147 protein, partial cds
7127	16304	25784	4.82	1.0E-69	BE245070.1	EST_HUMAN	TCBAP1E2678 Pediatric pre-B cell acute lymphoblastic leukemia Baylor-HGSC project=TCBA Homo sapiens cDNA clone TCBAP2678
7127	16304	25785	4.82	1.0E-69	BE245070.1	EST_HUMAN	TCBAP1E2678 Pediatric pre-B cell acute lymphoblastic leukemia Baylor-HGSC project=TCBA Homo sapiens cDNA clone TCBAP2678
7449	16657		25.72	1.0E-69	4504918	NT	Homo sapiens keratin 8 (KRT8) mRNA
8369	17456	26587	1.39	1.0E-69	BF125887.1	EST_HUMAN	601762902F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:4025785 5'
8798	17724		3.22	1.0E-69	A1808894.1	EST_HUMAN	wf64a08.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2360390 3' similar to contains Alu repetitive element; contains element MIR repetitive element
2300	12014	20714	1.88	8.0E-70	AA230303.1	EST_HUMAN	nc13d12.r1 NCI_CGAP_P1 Homo sapiens cDNA clone IMAGE:1008023
4367	13569	22665	1.97	8.0E-70	L77598.1	NT	Homo sapiens DGS-1 mRNA, 3' end
1782	10992	20187	1.72	7.0E-70	A1497807.1	EST_HUMAN	hm89f01.x1 NCI_CGAP_Brn25 Homo sapiens cDNA clone IMAGE:2165305 3'
1782	10992	20188	1.72	7.0E-70	A1497807.1	EST_HUMAN	hm89f01.x1 NCI_CGAP_Brn25 Homo sapiens cDNA clone IMAGE:2165305 3'
1899	11109	20288	1.42	7.0E-70	AA282855.1	EST_HUMAN	z15104.r1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:713239 5'
2031	11232		4.62	7.0E-70	5031688	NT	Homo sapiens tumor suppressor deleted in oral cancer-related 1 (DOC-1R) mRNA
4210	13413	22508	4.25	7.0E-70	4757723	NT	Homo sapiens adenylate cyclase 3 (ADCY3) mRNA
5433	14660	23789	5.69	7.0E-70	AB032369.1	NT	Homo sapiens MIST mRNA, partial cds
5433	14660	23800	5.69	7.0E-70	AB032369.1	NT	Homo sapiens MIST mRNA, partial cds
6054	15222	24841	1.72	7.0E-70	AJ000052.1	NT	Homo sapiens gene encoding splicing factor SF1, exons 2-8
6888	15883	25342	5.2	7.0E-70	M74099.1	NT	Human displacement protein (CCAAT) mRNA
6888	15883	25343	5.2	7.0E-70	M74099.1	NT	Human displacement protein (CCAAT) mRNA
6888	15894	25056	6.49	7.0E-70	AF153716.1	NT	Homo sapiens phospholipid scramblase 1 gene, exon 1 and 5' flanking region

Page 245 of 382  
Table 4  
Single Exon Probes Expressed in HELA Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8125	17259	26801	2.19	7.0E-70	11526319	NT	Homo sapiens HIR (histone cell cycle regulation defective, S. cerevisiae) homolog A (HIRA), mRNA
8125	17259	26802	2.19	7.0E-70	11526319	NT	Homo sapiens HIR (histone cell cycle regulation defective, S. cerevisiae) homolog A (HIRA), mRNA
881	10117	19278	2.56	6.0E-70	4502166	NT	Homo sapiens amyloid beta (A4) precursor protein (protease nexin-II, Alzheimer disease) (APP), mRNA
2108	11305	20519	4.61	6.0E-70	M30838.1	NT	Human Ku (p70/p80) subunit mRNA, complete cds
2474	11685	20884	1.68	6.0E-70	8823689	NT	Homo sapiens CHIP-N-acetylneuraminic acid synthase (LOC55607), mRNA
2518	12018	20920	88.43	5.0E-70	7662307	NT	Homo sapiens KIAA0782 gene product (KIAA0782), mRNA
2518	12018	20921	88.43	5.0E-70	7662307	NT	Homo sapiens KIAA0782 gene product (KIAA0782), mRNA
8378	17463		2.24	5.0E-70	BE166034.1	EST_HUMAN	MR3-HT0487-150200-115-408 HT0487 Homo sapiens cDNA
1569	10782	19955	2.52	3.0E-70	BE071796.1	EST_HUMAN	RCO-BT0522-071299-011-412 BT0522 Homo sapiens cDNA
1569	10782	19958	2.52	3.0E-70	BE071796.1	EST_HUMAN	RCO-BT0522-071299-011-412 BT0522 Homo sapiens cDNA
40	8336	18443	0.74	2.0E-70	AF012872.1	NT	Homo sapiens phosphatidylinositol 4-kinase 230 (p4K230) mRNA, complete cds
696	9839	19070	19.57	2.0E-70	N42161.1	EST_HUMAN	Y07a10.1 Soares melanocyte 2Nblm Homo sapiens cDNA clone IMAGE:270522 5' similar to SW:D3HL_RAT P29268 3-HYDROXYISOBUTYRATE DEHYDROGENASE PRECURSOR ;
696	9839	19071	19.57	2.0E-70	N42161.1	EST_HUMAN	Y07a10.1 Soares melanocyte 2Nblm Homo sapiens cDNA clone IMAGE:270522 5' similar to SW:D3HL_RAT P29268 3-HYDROXYISOBUTYRATE DEHYDROGENASE PRECURSOR ;
712	9954	19094	3.59	2.0E-70	A1248896.1	EST_HUMAN	SW:D3HL_RAT P29268 3-HYDROXYISOBUTYRATE DEHYDROGENASE PRECURSOR ;
1028	10254	19405	2.8	2.0E-70	8823669	NT	Q51H01.x1 NCI_CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2004913 3'
1192	10412	19566	0.59	2.0E-70	7661983	NT	Homo sapiens hypothetical protein FLJ20758 (FLJ20758), mRNA
1192	10412	19567	0.59	2.0E-70	7661983	NT	Homo sapiens KIAA0193 gene product (KIAA0193), mRNA
1413	10626	19792	1.36	2.0E-70	BE467311.1	EST_HUMAN	Homo sapiens KIAA0193 gene product (KIAA0193), mRNA
1632	10846	20024	0.93	2.0E-70	AA180083.1	EST_HUMAN	h284c12.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3212758 3'
1632	10846	20025	0.93	2.0E-70	AA180083.1	EST_HUMAN	zp45h05.11 Stratagene HeLa cell c3 937216 Homo sapiens cDNA clone IMAGE:612441 5' similar to TR:G1041283 G1041283 D2085.5 ;
1716	10928	20113	1.45	2.0E-70	AL163202.2	NT	zp45h05.11 Stratagene HeLa cell c3 937216 Homo sapiens cDNA clone IMAGE:612441 5' similar to TR:G1041283 G1041283 D2085.5 ;
2286	11481		29.63	2.0E-70	AA054010.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C002
2448	11639	20860	2.97	2.0E-70	AB011173.1	NT	zf48g04.1 Soares retina N2b4HR Homo sapiens cDNA clone IMAGE:380214 5' similar to SW:GAG_HTL1A
3604	12826	21946	0.6	2.0E-70	H37988.1	EST_HUMAN	P03345 GAG POLYPROTEIN ;
3809	13027	22137	1.12	2.0E-70	AL133207.2	NT	Homo sapiens mRNA for KIAA0601 protein, partial cds
3916	13132	22250	2.14	2.0E-70	AJ246003.1	NT	Yp58p04.1 Soares fetal liver spleen 1NfLS Homo sapiens cDNA clone IMAGE:191599 5'
							Novel human gene mapping to chromosome X
							Homo sapiens Spast gene for spastin protein

Page 246 of 382  
Table 4  
Single Exon Probes Expressed in HELA Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4026	13237	22342	3.74	2.0E-70	M69181.1	NT	Human nonmuscle myosin heavy chain-B (MYH10) mRNA, partial cds
5446	14672	23830	8.15	2.0E-70	X72662.1	NT	H sapiens gene for schwannomin (CS8)
5446	14672	23831	8.15	2.0E-70	X72662.1	NT	H sapiens gene for schwannomin (CS8)
5949	15165	24578	2.25	2.0E-70	D12825.1	NT	Human mRNA for NF1 protein isoform (neurofibromin isoform), complete cds
5958	15174	24589	10.47	2.0E-70	AF123074.1	NT	Homo sapiens cytoplasmic dynein intermediate chain 1 mRNA, complete cds
5958	15174	24590	10.47	2.0E-70	AF123074.1	NT	Homo sapiens cytoplasmic dynein intermediate chain 1 mRNA, complete cds
6087	14533	23557	1.72	2.0E-70	11422842	NT	Homo sapiens sialyltransferase 6 (N-acetylglucosaminide alpha 2,3-sialyltransferase) (SIAT6), mRNA
6431	15828	25093	4.82	2.0E-70	M21741.1	NT	Human guanine nucleotide-binding protein alpha-subunit gene (G-s-alpha), exons 4 and 5
7638	16838	26334	3.48	2.0E-70	8923420	NT	Homo sapiens hypothetical protein FLJ20450 (FLJ20450), mRNA
7638	16838	26335	3.48	2.0E-70	8923420	NT	Homo sapiens hypothetical protein FLJ20450 (FLJ20450), mRNA
8154	17286	26830	10.05	2.0E-70	4503520	NT	Homo sapiens eukaryotic translation initiation factor 3, subunit 6 (48kD) (EIF3S6) mRNA
8787	17714	23958	2.3	2.0E-70	11430460	NT	Homo sapiens low density lipoprotein-related protein 2 (LRP2), mRNA
8787	17714	23959	2.3	2.0E-70	11430460	NT	Homo sapiens low density lipoprotein-related protein 2 (LRP2), mRNA
3370	12988		3.37	1.0E-70	4507478	NT	Homo sapiens transglutaminase 3 (E polypeptide, protein-glutamine-gamma-glutamyltransferase) (TGM3) mRNA
7508	18713	26201	19.02	1.0E-70	AV738538.1	EST_HUMAN	AV738538 CB Homo sapiens cDNA clone CBLBGB10 5'
5635	14859	24242	7.21	9.0E-71	AI143870.1	EST_HUMAN	q04f01.x1 Soares, testis_NHT Homo sapiens cDNA clone IMAGE:1738009 3' similar to TR:O14045
5635	14859	24243	7.21	9.0E-71	AI143870.1	EST_HUMAN	q04f01.x1 Soares, testis_NHT Homo sapiens cDNA clone IMAGE:1738009 3' similar to TR:O14045
6100	15300	24732	2.08	9.0E-71	AI654903.1	EST_HUMAN	wb52c05.x1 NCLCGAP_G08 Homo sapiens cDNA clone IMAGE:2309288 3' similar to TR:P97213 P97213
8055	15300	24732	5.42	9.0E-71	AI654903.1	EST_HUMAN	CDU2, CDU1, TCDD, TCDB, TCDE, TCDA, TCDC, CDD1, CDD2, CDD3, AND CDD4 GENES ;
8794	15989		4.09	8.0E-71	AA171451.1	EST_HUMAN	wb52c05.x1 NCLCGAP_G08 Homo sapiens cDNA clone IMAGE:2309288 3' similar to TR:P97213 P97213
8245	15428	24888	8.53	7.0E-71	AA442230.1	EST_HUMAN	CDU2, CDU1, TCDD, TCDB, TCDE, TCDA, TCDC, CDD1, CDD2, CDD3, AND CDD4 GENES ;
7875	17063	26588	5.4	7.0E-71	AL163210.2	NT	zp21d11.11 Stragene neuroepithelium (#837231) Homo sapiens cDNA clone IMAGE:610101 5' similar to
2177	11374	20598	28.52	5.0E-71	AF056322.1	NT	TR:G1143061 G1143061 STRAIN XA34 POL ;
4089	13307	22407	1.2	5.0E-71	AW1616405.1	EST_HUMAN	z460h08.11 Soares, testis_NHT Homo sapiens cDNA clone IMAGE:758075 5'
5605	14829	24205	1.82	5.0E-71	4502740	NT	Homo sapiens chromosome 21 segment HS21C010
6390	15570	25027	21.73	5.0E-71	AF072810.1	NT	Homo sapiens SP100-HMG nuclear autoantigen (SP100) mRNA, complete cds
7043	18220		3.25	5.0E-71	X13467.1	NT	QV4-ST0234-181199-037-405 ST0234 Homo sapiens cDNA
							Homo sapiens cyclin-dependent kinase 6 (CDK6) mRNA
							Homo sapiens transcription factor WSTF mRNA, complete cds
							Human PreA4 gene for Alzheimer's disease A4 amyloid protein precursor (exon 2)

Table 4

## Single Exon Probes Expressed in HELA Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7553	18758	28252	3.73	5.0E-71	11436314	NT	Homo sapiens pro-platelet basic protein (includes platelet basic protein, beta-thromboglobulin, connective tissue-activating peptide III, neutrophil-activating peptide-2) (PPBP), mRNA
7746	16942	28454	2.43	5.0E-71	11438069	NT	Homo sapiens similar to hypothetical protein FLJ20163 (H. sapiens) (LOC833326), mRNA
8692	17680		1.78	5.0E-71	11418039	NT	Homo sapiens RNA binding motif protein 9 (RBM9), mRNA
355	9623	18752	112.04	4.0E-71	AF157628.1	NT	Equus caballus glyceraldehyde-3-phosphate dehydrogenase mRNA, partial cds
355	9623	18753	112.04	4.0E-71	AF157628.1	NT	Equus caballus glyceraldehyde-3-phosphate dehydrogenase mRNA, partial cds
2839	12078	21201	1.63	4.0E-71	4506880	NT	Homo sapiens plasminogen (PLG) mRNA
4420	13620	22715	5.57	4.0E-71	AF056322.1	NT	Homo sapiens SP100-HMG nuclear autoantigen (SP100) mRNA, complete cds
5007	14184	23283	5.98	4.0E-71	7657602	NT	Homo sapiens putative heme-binding protein (SOUL), mRNA
7283	16502	25994	4.32	3.0E-71	AA557683.1	EST_HUMAN	nl45h10.s1 NCI_CGAP_P14 Homo sapiens cDNA clone IMAGE:1043883 similar to contains PTR5.13 PTR5 repetitive element.
1237	10454	19613	10.52	2.0E-71	AL163206.2	NT	Homo sapiens chromosome 21 segment HS21C006
5344	14574	23651	7.56	2.0E-71	D87482.1	NT	Human mRNA for KIAA0272 gene, partial cds
5344	14574	23652	7.56	2.0E-71	D87482.1	NT	Human mRNA for KIAA0272 gene, partial cds
6072	14519	23561	57.87	2.0E-71	AL042439.1	EST_HUMAN	DKFZp34D1721.1 434 (synonym: hies3) Homo sapiens cDNA clone DKFZp34D1721.5
7222	16399	25883	4.66	2.0E-71	AF095703.1	NT	Homo sapiens short chain L-3-hydroxyacyl-CoA dehydrogenase precursor (HADHSC) gene, nuclear gene encoding mitochondrial protein, complete cds
7222	16399	25884	4.66	2.0E-71	AF095703.1	NT	Homo sapiens short chain L-3-hydroxyacyl-CoA dehydrogenase precursor (HADHSC) gene, nuclear gene encoding mitochondrial protein, complete cds
7285	16504	25995	2.75	2.0E-71	BE018477.1	EST_HUMAN	b581a06.y1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3048754 5' similar to SW:R23B_HUMAN P54727 UV EXCISION REPAIR PROTEIN PROTEIN RAD23 HOMOLOG B:
8112	17246	26786	1.65	2.0E-71	R55626.1	EST_HUMAN	y77c11.1 Soares breast 2NblBst Homo sapiens cDNA clone IMAGE:154772 5'
8445	17506		7.28	2.0E-71	T05489.1	EST_HUMAN	y643a09.1 Soares fetal liver spleen 1NfLS Homo sapiens cDNA clone IMAGE:120520 5'
644	9890	18015	1.07	1.0E-71	A1077827.1	EST_HUMAN	ov15e03.s1 Soares, senescent, fibroblasts_NbHSF Homo sapiens cDNA clone IMAGE:1665916 3' similar to contains LOR1.b2 LOR1 repetitive element:
949	10182	19338	2.43	1.0E-71	7708281	NT	Homo sapiens neuronal cell death-related protein (LOC51616), mRNA
1108	10332	19482	6.48	1.0E-71	AF205890.1	NT	Homo sapiens disabled-2 gene, exons 2 through 15 and complete cds
1348	10563	19728	10.22	1.0E-71	AF012872.1	NT	Homo sapiens phosphatidylinositol 4-kinase 230 (p4K230) mRNA, complete cds
2051	11252	20465	2.23	1.0E-71	AB017007.1	NT	Homo sapiens PMS2L16 mRNA, partial cds
2051	11252	20466	2.23	1.0E-71	AB017007.1	NT	Homo sapiens PMS2L16 mRNA, partial cds
2653	11836	21049	4.77	1.0E-71	7657153	NT	Homo sapiens hairy/enhancer-of-split related with YRPW motif-like (HEYL), mRNA
3475	12699	21835	2	1.0E-71	AF119665.1	NT	Homo sapiens inorganic pyrophosphatase mRNA, complete cds
3574	12767	21822	7.32	1.0E-71	AF246219.1	NT	Homo sapiens SNARE protein kinase SNAK mRNA, complete cds
3574	12767	21823	7.32	1.0E-71	AF246219.1	NT	Homo sapiens SNARE protein kinase SNAK mRNA, complete cds

Table 4

## Single Exon Probes Expressed in HELA Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3827	12848	21868	0.89	1.0E-71	BE122850.1	EST_HUMAN	02_15 Human Epidermal Keratinocyte Subtraction Library: Upregulated Transcripts Homo sapiens cDNA clone 02_15 5' similar to Homo sapiens chromosome 19
3827	12848	21967	0.89	1.0E-71	BE122850.1	EST_HUMAN	02_15 Human Epidermal Keratinocyte Subtraction Library: Upregulated Transcripts Homo sapiens cDNA clone 02_15 5' similar to Homo sapiens chromosome 19
3722	12842	22059	1.54	1.0E-71	AF218904.1	NT	Homo sapiens attractin precursor (ATRIN) gene, exon 19
4468	13684	22757	2.57	1.0E-71	D28476.1	NT	Human mRNA for KIAA0045 gene, complete cds
4592	13786	22878	0.83	1.0E-71	H23176.1	EST_HUMAN	ym56h10.r1 Soares infant brain 1N1B Homo sapiens cDNA clone IMAGE:52528 5'
4810	13999		1.9	1.0E-71	AF077188.1	NT	Homo sapiens cullin 4A (CUL4A) mRNA, complete cds
6211	15392	24836	13.82	1.0E-71	U80753.1	NT	Homo sapiens CAGL79 mRNA, partial cds
6613	15809	25264	4.88	1.0E-71	8922811	NT	Homo sapiens hypothetical protein FLJ10998 (FLJ10998), mRNA
6613	15809	25265	4.99	1.0E-71	8922811	NT	Homo sapiens hypothetical protein FLJ10998 (FLJ10998), mRNA
7076	16253	25726	6.32	1.0E-71	AY007643.1	NT	Homo sapiens cytochrome c oxidase subunit VIIa-related protein gene, complete cds
7365	16581		6.66	1.0E-71	AV761217.1	EST_HUMAN	AV761217 MDS Homo sapiens cDNA clone MDSEIA03 5'
7459	16667	26155	2.12	1.0E-71	11418903	NT	Homo sapiens coagulation factor XIII, A1 polypeptide (F13A1), mRNA
7706	16905	26413	2.19	1.0E-71	11417191	NT	Homo sapiens leucylcystinyl aminopeptidase (LNPEP), mRNA
7706	16905	26414	2.19	1.0E-71	11417191	NT	Homo sapiens leucylcystinyl aminopeptidase (LNPEP), mRNA
8836	17746		6.70	1.0E-71	AB011399.1	NT	Homo sapiens gene for AF-8, complete cds
413	9668	18805	0.89	9.0E-72	A1857635.1	EST_HUMAN	wk95g03.x1 NCJ CGAP Lu19 Homo sapiens cDNA clone IMAGE:2423188 3' similar to TR:O88705 O88705
413	9668	18806	0.89	9.0E-72	A1857635.1	EST_HUMAN	HYPOTHETICAL 38.6 KD PROTEIN, contains Alu repetitive element; wk95g03.x1 NCJ CGAP Lu19 Homo sapiens cDNA clone IMAGE:2423188 3' similar to TR:O88705 O88705
4090	13298	22395	2.08	7.0E-72		NT	HYPOTHETICAL 38.6 KD PROTEIN, contains Alu repetitive element;
4090	13298	22396	2.06	7.0E-72	4501866	NT	Homo sapiens acetylase 2, mitochondrial (ACO2), nuclear gene encoding mitochondrial protein, mRNA
4090	13298	22397	2.06	7.0E-72	4501866	NT	Homo sapiens acetylase 2, mitochondrial (ACO2), nuclear gene encoding mitochondrial protein, mRNA
6129	15313	24747	2.92	7.0E-72	S41694.1	NT	Homo sapiens acetylase 2, mitochondrial (ACO2), nuclear gene encoding mitochondrial protein, mRNA
6584	17835		1.43	7.0E-72	F26259.1	EST_HUMAN	(pseudogene) PTMAP2=proboscis alpha [human, Genomic, 1192 nt, segment 2 of 3]
6583	15789		2.97	8.0E-72	AL163246.2	NT	HSPD13670 HMA3 Homo sapiens cDNA clone s400005(G02)
65	9361	18484	1.3	5.0E-72	BF333707.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C046
65	9361	18485	1.3	5.0E-72	BF333707.1	EST_HUMAN	QV0-CS0010-150900-398-e11 CS0010 Homo sapiens cDNA
66	9361	18484	9	5.0E-72	BF333707.1	EST_HUMAN	QV0-CS0010-150900-398-e11 CS0010 Homo sapiens cDNA
66	9361	18485	9	5.0E-72	BF333707.1	EST_HUMAN	QV0-CS0010-150900-398-e11 CS0010 Homo sapiens cDNA

Page 249 of 382  
Table 4  
Single Exon Probes Expressed in HELA Cells

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1147	10370		2.72	5.0E-72	L11845.1	NT	Homo sapiens alpha-tubulin mRNA, complete cds
8709	15904	25364	2.48	5.0E-72	AW161274.1	EST_HUMAN	au80c03.Y1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2782564 5' similar to
7795	16988	26502	3.23	5.0E-72	BF331571.1	EST_HUMAN	TR:Q98785 Q98785 HYPOTHETICAL 32.4 KD PROTEIN; contains element MSR1 repetitive element ;
7795	16988	26503	3.23	5.0E-72	BF331571.1	EST_HUMAN	MR4-BT0598-010600-005-d05 BT0598 Homo sapiens cDNA
8523	18323		2.09	5.0E-72	BE926645.1	EST_HUMAN	MR4-BT0598-010600-005-d05 BT0598 Homo sapiens cDNA
4838	14027		1.15	4.0E-72	11034844	NT	QV1-BT0632-280800-342-a10 BT0632 Homo sapiens cDNA
8059	17194	26732	6.71	4.0E-72	H79421.1	EST_HUMAN	Homo sapiens hypothetical protein dJ1057B20.2 (DJ1057B20.2), mRNA
8178	17310	26853	3.08	4.0E-72	T81910.1	EST_HUMAN	y28a03.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:235084 5'
8894	17768	23921	8.76	4.0E-72	AJ277546.2	NT	y28a09.s1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:109649 3'
20	9316	18418	1.29	3.0E-72	5031976	NT	Homo sapiens WEE1 gene for protein kinase and partial ZNF143 gene for zinc finger transcription factor;
913	10148		2.08	3.0E-72	AA728828.1	EST_HUMAN	Homo sapiens pre-B-cell colony-enhancing factor (PBCE) mRNA
1163	10385	19535	13.92	3.0E-72	U16306.1	NT	af63a06.s1 Soares, testis_NHT Homo sapiens cDNA clone 1310290 3'
1163	10385	19536	13.92	3.0E-72	U16306.1	NT	Human chondroitin sulfate proteoglycan versican V0 splice-variant precursor peptide mRNA, complete cds
1201	10421	19574	0.73	3.0E-72	U80228.1	NT	Human chondroitin sulfate proteoglycan versican V0 splice-variant precursor peptide mRNA, complete cds
1201	10421	19575	0.73	3.0E-72	U80228.1	NT	Human gamma-aminobutyric acid transaminase mRNA, partial cds
1507	10720	19892	1.41	3.0E-72	BE242161.1	EST_HUMAN	Human gamma-aminobutyric acid transaminase mRNA, partial cds
3040	12277	21405	11.09	3.0E-72	AJ229043.1	NT	TCAAPE1252 Pediatric acute myelogenous leukemia cell (FAB M1) Baylor-HGSC project-TCAA Homo sapiens cDNA clone TCAAP1252
3246	12479	21611	3.48	3.0E-72	8923548	NT	Homo sapiens 959 kb contig between AML1 and CBR1 on chromosome 21q22, segment 3/3
3813	13031	22141	2.14	3.0E-72	S77589.1	NT	Homo sapiens hypothetical protein FLJ20585 (FLJ20585), mRNA
4542	13737	22835	3.48	3.0E-72	11416198	NT	TCR V delta 2-C alpha = T-cell receptor delta and C alpha fusion gene (alternatively spliced, splice junction)
5846	14869	24254	1.78	3.0E-72	AF073367.1	NT	(human, precursor B-cell line REH, mRNA Partial, 211 nt)
5846	14869	24255	1.78	3.0E-72	AF073367.1	NT	Homo sapiens hypothetical protein (FLJ11127), mRNA
5738	14957	24356	4.53	3.0E-72	AB028004.1	NT	Homo sapiens growth factor receptor-bound protein 10 (GRB10) gene, exon 5
5738	14957	24357	4.53	3.0E-72	AB028004.1	NT	Homo sapiens growth factor receptor-bound protein 10 (GRB10) gene, exon 5
5940	15156	24568	3.64	3.0E-72	4826987	NT	Homo sapiens mRNA for KIAA1081 protein, partial cds
6327	15508	24954	1.78	3.0E-72	U80017.1	NT	Homo sapiens ribosomal protein L3-like (RPL3L) mRNA
							Homo sapiens basic transcription factor 2 p44 (btf2p44) gene, partial cds, neuronal apoptosis inhibitory protein (nrip) and survival motor neuron protein (smn) genes, complete cds

F1/US 01/00670

Table 4

## Single Exon Probes Expressed in HELA Cells

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7326	16542	26031	2.65	2.0E-72	AA788277.1	EST_HUMAN	qj28b08.s1 Soares_testis_NHT Homo sapiens cDNA clone 1391609 3' similar to gb:X02067 H.sapiens
8889	17784	23918	6.91	2.0E-72	AF182714.1	NT	mRNA for 7SL RNA pseudogene (HUMAN);
2043	11244	20453	0.99	1.0E-72	AA846225.1	EST_HUMAN	Rattus norvegicus putative phosphate/phosphoenolpyruvate translocator mRNA, complete cds
5559	14782	24151	4.02	1.0E-72	7657676	NT	ab34802.s1 Soares_parenchymal_tumor_NbHPA Homo sapiens cDNA clone IMAGE:1387395 3'
6350	15530	24880	3.92	1.0E-72	BE175434.1	EST_HUMAN	Homo sapiens vacuolar protein sorting 41 (yeast homolog) (VPS41), mRNA
6350	15530	24881	3.92	1.0E-72	BE175434.1	EST_HUMAN	RC4-HT0578-170300-012-g02 HT0578 Homo sapiens cDNA
6957	16135	25605	9.43	1.0E-72	AF222742.1	NT	RC4-HT0578-170300-012-g02 HT0578 Homo sapiens cDNA
6957	16135	25606	9.43	1.0E-72	AF222742.1	NT	Homo sapiens synaptic glycoprotein SC2 (SC2) mRNA, complete cds
1458	10871	19843	1.06	9.0E-73	AW374988.1	EST_HUMAN	Homo sapiens synaptic glycoprotein SC2 (SC2) mRNA, complete cds
7524	16729		34.82	9.0E-73	11424099	NT	MRO-CT0063-071099-002-h11 CT0063 Homo sapiens cDNA
							Homo sapiens ribosomal protein L13a (RPL13A), mRNA
1045	10270	19421	1.6	8.0E-73	AW071755.1	EST_HUMAN	ws55c06.x1 NCL_CGAP_Brn25 Homo sapiens cDNA clone IMAGE:2501088 3' similar to TR:Q59050
3262	12495	21625	0.62	8.0E-73	11435180	NT	Q59050 HYPOPHOSPHATE PROTEIN MJ1656 ;
5912	15128	24538	5.01	8.0E-73	11426469	NT	Homo sapiens gephyrin (GPH), mRNA
6493	15680	25155	3.2	8.0E-73	AF113129.1	NT	Homo sapiens lysosome homolog (LOC57151), mRNA
8949	17824	23904	5.07	8.0E-73	11418189	NT	Homo sapiens vacuolar ATPase isoform VA68 mRNA, complete cds
1142	10365	19516	0.74	7.0E-73	8923280	NT	Homo sapiens thyroid autoantigen 70kD (Ku antigen) (G22P1), mRNA
3270	12503	21634	1.44	7.0E-73	AL163206.2	NT	Homo sapiens hypothetical protein FLJ20309 (FLJ20309), mRNA
4963	14150		1.27	7.0E-73	AL163282.2	NT	Homo sapiens chromosome 21 segment HS21C008
161	9443		2.72	6.0E-73	AL163218.2	NT	Homo sapiens chromosome 21 segment HS21C082
6152	15338	24773	3.59	6.0E-73	BE168574.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C018
5303	14535	23539	2.11	4.0E-73	11422159	NT	QV0-HT0494-020300-137-d03 HT0494 Homo sapiens cDNA
1830	11038	20234	1.22	3.0E-73	11435913	NT	Homo sapiens HELG protein (FAM44A1), mRNA
1830	11038	20235	1.22	3.0E-73	11435913	NT	Homo sapiens heme-binding protein (HEBP), mRNA
9195	17982		1.8	3.0E-73	AL163246.2	NT	Homo sapiens heme-binding protein (HEBP), mRNA
9198	17984		1.4	3.0E-73	AW898081.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C046
861	10087	19259	3.36	2.0E-73	AF139897.1	NT	RC3-NN0068-270400-011-c04 NN0068 Homo sapiens cDNA
1915	11120		3.14	2.0E-73	AW898081.1	EST_HUMAN	Homo sapiens BASS1 (BASS1) mRNA, partial cds
2260	11455		1.58	2.0E-73	U01317.1	NT	RC3-NN0068-270400-011-c04 NN0068 Homo sapiens cDNA
3148	12381	21513	3.5	2.0E-73	4502562	NT	Human beta globin region on chromosome 11
							Homo sapiens caspase 8, apoptosis-related cysteine protease (CASP8) mRNA
3525	12749	21880	0.94	2.0E-73	7669539	NT	Homo sapiens Parkinson disease (autosomal recessive, juvenile) 2, parkin (PARK2), transcript variant 3, mRNA

Table 4

## Single Exon Probes Expressed in HELA Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3525	12748	21881	0.94	2.0E-73	7689539	NT	Homo sapiens Parkinson disease (autosomal recessive, juvenile) 2, parkin (PARK2), transcript variant 3, mRNA
4428	13628		2.51	2.0E-73	AL163283.2	NT	Homo sapiens chromosome 21 segment HS21C083
5864	15082	24495	6.18	2.0E-73	AB046811.1	NT	Homo sapiens mRNA for KIAA1591 protein, partial cds
7622	16825	26321	3.96	2.0E-73	4557612	NT	Homo sapiens galactosylceramidase (Krabbe disease) (GALC), mRNA
7622	16825	26322	3.96	2.0E-73	4557612	NT	Homo sapiens galactosylceramidase (Krabbe disease) (GALC), mRNA
7649	16849	26347	1.94	2.0E-73	AB028982.1	NT	Homo sapiens mRNA for KIAA1059 protein, partial cds
8728	11120		2.66	2.0E-73	AW898081.1	EST_HUMAN	RC3-NIN0068-270400-011-c04 NN0068 Homo sapiens cDNA
1753	10985	20150	2.16	1.0E-73	AU121585.1	EST_HUMAN	AU121585 MAMMA1 Homo sapiens cDNA clone MAMMA1000490 5'
7986	16421	25808	3.76	1.0E-73	BE385477.1	EST_HUMAN	601276071F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3817105 5'
5623	14847	24228	1.05	8.0E-74	S83194.1	NT	Homo sapiens CD39-like 4 (CD39L4) mRNA
748	9889	19132	2	8.0E-74	S83194.1	NT	Ca2+/calmodulin-dependent protein kinase IV kinase isoform [rats, brain, mRNA, 3428 nt]
5623	14847	24229	2	8.0E-74	AJ001089.1	NT	Ca2+/calmodulin-dependent protein kinase IV kinase isoform [rats, brain, mRNA, 3428 nt]
1919	11123	20318	4.63	7.0E-74	AJ001089.1	NT	Homo sapiens NKG2D gene, exon 10
3301	12632	21664	1.74	7.0E-74	AL163246.2	NT	Homo sapiens chromosome 21 segment HS21C046
8948	17823	23903	4.04	7.0E-74	BE266305.1	EST_HUMAN	Homo sapiens S164 gene, partial cds; PS1 and hypothetical protein genes, complete cds; and S171 gene, partial cds
1130	10354	19506	4.82	6.0E-74	AF109907.1	NT	partial cds
1604	10818	19983	1.07	6.0E-74	AW263177.1	EST_HUMAN	Xn78g07.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2700636 3'
2262	11477	20698	45.19	6.0E-74	BE388260.1	EST_HUMAN	60128321F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3605453 5'
2282	11477	20699	45.19	6.0E-74	BE388260.1	EST_HUMAN	60128321F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3605453 5'
2816	12055	21179	1.03	6.0E-74	AW014039.1	EST_HUMAN	UI-H-B10-aah-h-03-Q-UI.st NCI_CGAP_Sub1 Homo sapiens cDNA clone IMAGE:2708365 3'
2816	12055	21180	1.03	6.0E-74	AW014039.1	EST_HUMAN	UI-H-B10-aah-h-03-Q-UI.st NCI_CGAP_Sub1 Homo sapiens cDNA clone IMAGE:2708365 3'
3694	12914	22032	1.63	6.0E-74	BE048846.1	EST_HUMAN	hr54e11.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:3132332 3'
3694	12914	22033	1.63	6.0E-74	BE048846.1	EST_HUMAN	hr54e11.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:3132332 3'
5052	14234	23320	0.98	6.0E-74	4758135	NT	Homo sapiens DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 11 (S.cerevisiae CHL1-like helicase) (DDX11) mRNA
5052	14234	23321	0.98	6.0E-74	4758135	NT	Homo sapiens DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 11 (S.cerevisiae CHL1-like helicase) (DDX11) mRNA
5377	14608	23716	3.17	6.0E-74	11056013	NT	Homo sapiens actin filament associated protein (AFAP), mRNA
915	10150	19310	2.7	5.0E-74	AW020986.1	EST_HUMAN	df17c09.y1 Morton Fetal Cochlea Homo sapiens cDNA clone IMAGE:2483704 5'
2663	11844		8.98	5.0E-74	AW362756.1	EST_HUMAN	PMO-CT0289-271098-001-n07 CT0289 Homo sapiens cDNA
5399	14627	23741	2.11	5.0E-74	11425417	NT	Homo sapiens phosphatidylinositol glycan, class L (PIGL), mRNA
5568	14783	24166	12.05	5.0E-74	X89870.1	NT	H.sapiens mRNA for TPCR18 protein



Table 4

## Single Exon Probes Expressed in HELA Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5587	14811	24185	7.5	5.0E-74	4507868	NT	Homo sapiens VAMP (vesicle-associated membrane protein)-associated protein A (33kD) (VAPA) mRNA, and translated products
5620	14843	24221	1.93	5.0E-74	11431471	NT	Homo sapiens interleukin 4 receptor (IL4R), mRNA
5620	14843	24222	1.93	5.0E-74	11431471	NT	Homo sapiens interleukin 4 receptor (IL4R), mRNA
6038	15246	24688	3.76	5.0E-74	7662263	NT	Homo sapiens KIAA0716 gene product (KIAA0716), mRNA
6476	15673	25144	3.84	5.0E-74	11345483	NT	Homo sapiens hypothetical protein FLJ13222 (FLJ13222), mRNA
7321	16538	26026	2.02	5.0E-74	Y09420.1	NT	H. sapiens mRNA for HIP-1
7321	16538	26027	2.02	5.0E-74	Y09420.1	NT	H. sapiens mRNA for HIP-1
284	9558	18892	3.08	4.0E-74	D87875.1	NT	Homo sapiens DNA for amyloid precursor protein, complete cds
862	10088	19260	4.8	4.0E-74	AB028942.1	NT	Homo sapiens mRNA for KIAA1019 protein, partial cds
1832	11136	20331	2.56	4.0E-74	AB028888.1	NT	Homo sapiens DNA, DLEC1 to ORCTL4 gene region, section 1/2 (DLEC1, ORCTL3, ORCTL4 genes, complete cds)
1832	11136	20332	2.56	4.0E-74	AB028888.1	NT	Homo sapiens DNA, DLEC1 to ORCTL4 gene region, section 1/2 (DLEC1, ORCTL3, ORCTL4 genes, complete cds)
2040	11241	20449	8.89	4.0E-74	4506182	NT	Homo sapiens proteasome (prosome, macropain) subunit, beta type, 1 (PSMB1) mRNA
2040	11241	20450	8.89	4.0E-74	4506182	NT	Homo sapiens proteasome (prosome, macropain) subunit, beta type, 1 (PSMB1) mRNA
2102	11302	20518	1.2	4.0E-74	AB032894.1	NT	Homo sapiens mRNA for KIAA1188 protein, partial cds
3056	12292	21418	4.63	4.0E-74	AJ006976.1	NT	Homo sapiens PLP gene
3501	12725	21881	1.5	4.0E-74	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C010
4040	13250	22351	0.92	4.0E-74	AL163247.2	NT	Homo sapiens chromosome 21 segment HS21C047
4554	13749	22848	2.01	4.0E-74	7662183	NT	Homo sapiens KIAA0569 gene product (KIAA0569), mRNA
4616	13810	22801	0.75	4.0E-74	Z17227.1	NT	Homo sapiens mRNA for transmembrane receptor protein
6840	15835		21.31	3.0E-74	AA300378.1	EST_HUMAN	EST13131 Thymus tumor III Homo sapiens cDNA 5' end similar to similar to ribosomal protein L37
865	10188	18353	150.49	2.0E-74	7669491	NT	Homo sapiens glyceraldehyde-3-phosphate dehydrogenase (GAPD), mRNA
865	10188	18354	156.49	2.0E-74	7669491	NT	Homo sapiens glyceraldehyde-3-phosphate dehydrogenase (GAPD), mRNA
1183	10404	19558	1.38	2.0E-74	AF020092.1	NT	Human endogenous retrovirus HERV-K_T47D
1251	10487	19631	2.13	2.0E-74	AJ950528.1	EST_HUMAN	wx51607.X1 NCI_CGAP_Lu28 Homo sapiens cDNA clone IMAGE:2547204 3' similar to SW:GG95_HUMAN Q08379 GOLGIN-95; contains element MER22 repetitive element;
1575	10788	19663	1.77	2.0E-74	4885188	NT	Homo sapiens epidermal growth factor receptor (avian erythroblastic leukemia viral (v-erb-b) oncogene homolog) (EGFR) mRNA
1575	10788	19664	1.77	2.0E-74	4885188	NT	Homo sapiens epidermal growth factor receptor (avian erythroblastic leukemia viral (v-erb-b) oncogene homolog) (EGFR) mRNA
2682	11748	20968	11.6	2.0E-74	AJ557280.1	EST_HUMAN	PT.2.1_15_G11.1 tumor2 Homo sapiens cDNA 3'
5030	14215	23289	2.54	2.0E-74	AL355092.1	NT	Novel human gene mapping to chromosome 22

Single Exon Probes Expressed in HELA Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5030	14215	23300	2.54	2.0E-74	AL355092.1	NT	Novel human gene mapping to chromosome 22
5034	14219	23304	5.01	2.0E-74	J02863.1	NT	Human platelet glycoprotein IIb mRNA, 3' end
5571	18058	24169	1.84	2.0E-74	BE711134.1	EST_HUMAN	RC8-HT0878-220500-011-C03 HT0878 Homo sapiens cDNA
5613	18059	24212	2.23	2.0E-74	11439587	NT	Homo sapiens PDZ-73 protein (PDZ-73NY-CO-38), mRNA
5613	18059	24213	2.23	2.0E-74	11439587	NT	Homo sapiens PDZ-73 protein (PDZ-73NY-CO-38), mRNA
5638	18059	24212	2.91	2.0E-74	11439587	NT	Homo sapiens PDZ-73 protein (PDZ-73NY-CO-38), mRNA
5638	18059	24213	2.91	2.0E-74	11439587	NT	Homo sapiens PDZ-73 protein (PDZ-73NY-CO-38), mRNA
6871	16083	25561	11.56	2.0E-74	AL163204.2	NT	Homo sapiens chromosome 21 segment HS21C004
6864	17641		2.32	2.0E-74	AA198181.1	EST_HUMAN	zp98a08.s1 Stragosome muscle 937209 Homo sapiens cDNA clone IMAGE:628018 3'
9223	18002	23888	1.34	2.0E-74	BF666568.1	EST_HUMAN	602121428F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4278559 5'
55	9352	18468	1.97	1.0E-74	7657334	NT	Homo sapiens MissheperNIK-related kinase (MINK), mRNA
342	9610	18737	3.64	1.0E-74	AW816405.1	EST_HUMAN	QV4-ST0234-181189-037-05 ST0234 Homo sapiens cDNA
508	9758	18885	0.96	1.0E-74	8922829	NT	Homo sapiens hypothetical protein FLJ11028 (FLJ11028), mRNA
513	9764	18890	17.5	1.0E-74	X02344.1	NT	Homo sapiens beta 2 gene
608	9855	18974	2.28	1.0E-74	4508020	NT	Homo sapiens zinc finger protein 259 (ZNF259) mRNA
1007	10238	19390	1.74	1.0E-74	AL163246.2	NT	Homo sapiens chromosome 21 segment HS21C046
2183	11390	20613	4.9	1.0E-74	AB002059.1	NT	Homo sapiens DNA for Human P2M, complete cds
3104	12339	21467	2.47	1.0E-74	4758697	NT	Homo sapiens mannosidase, alpha, class 2A, member 1 (MAN2A1), mRNA
3945	13161	22277	8	1.0E-74	AL163268.2	NT	Homo sapiens chromosome 21 segment HS21C008
5226	14400	23483	1.29	1.0E-74	8659564	NT	Homo sapiens chromosome 21 segment HS21C008
5228	14400	23484	1.29	1.0E-74	8659564	NT	Homo sapiens chromosome 21 segment HS21C008
6719	15914	25374	2.79	1.0E-74	AF214562.1	NT	Homo sapiens tracheal epithelium enriched protein (PLUNC) gene, complete cds
8285	17401	26930	2.1	1.0E-74	11417856	NT	Homo sapiens glutathione S-transferase theta 2 (GSTT2), mRNA
8370	17457		4.1	1.0E-74	11417856	NT	Homo sapiens glutathione S-transferase theta 2 (GSTT2), mRNA
8519	11390	20613	1.42	1.0E-74	AB002059.1	NT	Homo sapiens DNA for Human P2M, complete cds
9020	17872		1.62	1.0E-74	AF240786.1	NT	Homo sapiens glutathione S-transferase theta 2 (GSTT2) and glutathione S-transferase theta 1 (GSTT1) genes, complete cds
2607	11781		3.57	8.0E-75	AF176228.1	NT	Homo sapiens DNA cytosine-5 methyltransferase 3B (DNMT3B) mRNA, complete cds
8686	17855		1.83	8.0E-75	AL163202.2	NT	Homo sapiens chromosome 21 segment HS21C002
2287	11482	20703	3.62	6.0E-75	A1817415.1	EST_HUMAN	wk38a08.x1 NCI_CGAP_P22 Homo sapiens cDNA clone IMAGE:2417854 3' similar to gb:M14123_cds4 RETROVIRUS-RELATED POL POLYPROTEIN (HUMAN);
7144	16321	25802	4.05	5.0E-75	A1638623.1	EST_HUMAN	t81c12.x1 NCI_CGAP_GC8 Homo sapiens cDNA clone IMAGE:2242390 3' similar to TR:P97361 P97361
112	9400	18529	4.44	4.0E-75	BE081333.1	EST_HUMAN	HYPOTHETICAL 20.1 KD PROTEIN ; QV1-BT0632-210200-079-602 BT0632 Homo sapiens cDNA

Page 254 of 382  
Table 4  
Single Exon Probes Expressed in HELA Cells

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
465	9718		0.83	4.0E-75	N38757.1	EST_HUMAN	y80108.t1 Soares melanocyte 2NblHM Homo sapiens cDNA clone IMAGE:268055 5'
1736	10948	20131	1.15	4.0E-75	AW897230.1	EST_HUMAN	CMO-NN0057-150400-335-a11 NN0057 Homo sapiens cDNA
2801	12041	21162	5.26	4.0E-75	BE409464.1	EST_HUMAN	601303866F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3638344 5'
3474	12698	21834	1.02	4.0E-75	8922637	NT	Homo sapiens hypothetical protein FLJ10747 (FLJ10747), mRNA
5776	14994	24394	5.66	4.0E-75	5579457	NT	Homo sapiens eukaryotic translation initiation factor 3, subunit 8 (EIF3S8), mRNA
5983	15195	24812	2.08	4.0E-75	11417948	NT	Homo sapiens NIPSNAP, C. elegans, homolog 1 (NIPSNAP1), mRNA
5983	15195	24813	2.06	4.0E-75	11417948	NT	Homo sapiens NIPSNAP, C. elegans, homolog 1 (NIPSNAP1), mRNA
7277	16496	25988	8.7	4.0E-75	7689503	NT	Homo sapiens myosin, heavy polypeptide 1, skeletal muscle, adult (MYH1), mRNA
8241	17370	26906	1.67	4.0E-75	AF039699.1	NT	Homo sapiens antigen NY-CO-37 (NY-CO-38) mRNA, complete cds
1010	10241	18393	3.38	3.0E-75	AF157623.1	NT	Homo sapiens HTRA serine protease (PRSS11) gene, complete cds
1011	10241	18393	2.18	3.0E-75	AF157623.1	NT	Homo sapiens HTRA serine protease (PRSS11) gene, complete cds
1804	11013	20208	2.02	3.0E-75	AB011153.1	NT	Homo sapiens mRNA for KIAA0581 protein, partial cds
2082	11282	20498	28.14	3.0E-75	4507334	NT	Homo sapiens synaptotagmin 1 (SYNJ1), mRNA
2387	11580	20797	5.08	3.0E-75	4759153	NT	Homo sapiens synaptsomal-associated protein, 28kD (SNAP28) mRNA
2886	12223	21356	0.81	3.0E-75	AL163201.2	NT	Homo sapiens chromosome 21 segment HS21C001
3152	12387	21519	1.02	3.0E-75	AB011153.1	NT	Homo sapiens mRNA for KIAA0581 protein, partial cds
3324	12553	21688	1.08	3.0E-75	M72393.1	NT	Human calcium-dependent phospholipid-binding protein (PLA2) mRNA, complete cds
3324	12553	21689	1.08	3.0E-75	M72393.1	NT	Human calcium-dependent phospholipid-binding protein (PLA2) mRNA, complete cds
3720	12940	22057	0.89	3.0E-75	M72393.1	NT	Human calcium-dependent phospholipid-binding protein (PLA2) mRNA, complete cds
4150	13356	22459	3.01	3.0E-75	D87675.1	NT	Homo sapiens DNA for amyloid precursor protein, complete cds
4429	13629	22723	0.77	3.0E-75	7662421	NT	Homo sapiens KIAA0971 protein (KIAA0971), mRNA
5215	14390		0.98	3.0E-75	AL163209.2	NT	Homo sapiens chromosome 21 segment HS21C009
5986	15288	24694	1.62	3.0E-75	11528319	NT	Homo sapiens HIR (histone cell cycle regulation defective, S. cerevisiae) homolog A (HIRA), mRNA
5986	15288	24695	1.62	3.0E-75	11528319	NT	Homo sapiens HIR (histone cell cycle regulation defective, S. cerevisiae) homolog A (HIRA), mRNA
6134	15318	24751	4.66	3.0E-75	7662209	NT	Homo sapiens KIAA0623 gene product (KIAA0623), mRNA
6134	15318	24752	4.66	3.0E-75	7662209	NT	Homo sapiens KIAA0623 gene product (KIAA0623), mRNA
6344	15525	24972	2.76	3.0E-75	4885632	NT	Homo sapiens Oncogene TIM (TIM) mRNA
6344	15525	24973	2.76	3.0E-75	4885632	NT	Homo sapiens Oncogene TIM (TIM) mRNA
2267	11482	20682	11.09	1.0E-75	AW168135.1	EST_HUMAN	xg90402.x1 NCI CGAP_U14 Homo sapiens cDNA clone IMAGE:2632707 3' similar to contains PTR7.11
2897	12135	21272	3.26	1.0E-75	X52221.1	NT	PTR7 repetitive element; H.sapiens ERCC2 gene, exons 1 & 2 (partial)
4698	13889	22889	1.48	1.0E-75	BE278301.1	EST_HUMAN	601157633F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3504272 5'

Page 255 of 382  
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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6605	15801		7.18	1.0E-75	AA399270.1	EST_HUMAN	z57h03.s1 Soares, testis, NHT Homo sapiens cDNA clone IMAGE:728485 3' similar to gb:M13832 40S
6887	16078	25547	5.15	1.0E-75	BF313645.1	EST_HUMAN	RIBOSOMAL PROTEIN S17 (HUMAN);
6887	16078	25548	5.15	1.0E-75	BF313645.1	EST_HUMAN	601900294F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4128678 5'
7460	16668		5.8	1.0E-75	AA684377.1	EST_HUMAN	601900294F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4128678 5'
7658	16858	26359	4.06	1.0E-75	AF223391.1	NT	ac71b08.s1 Stratagene lung (#937210) Homo sapiens cDNA clone IMAGE:868599 3'
8574	14503	23588	2.38	1.0E-75	BE894182.1	EST_HUMAN	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced
46	9343	18452	2.66	9.0E-76	AI652648.1	EST_HUMAN	601437130F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3822303 5'
46	9343	18453	2.66	9.0E-76	AI652648.1	EST_HUMAN	w630b10.x1 NCI_CGAP_G08 Homo sapiens cDNA clone IMAGE:2307163 3' similar to TR:O75235 O75235
7041	16218	25693	55.5	9.0E-76	M12937.1	NT	TRAP1;
145	9427	18561	7.27	8.0E-76	AF154830.1	NT	Human ferritin Heavy subunit mRNA, complete cds
946	10179	19334	5.48	8.0E-76	4504374	NT	Homo sapiens carboxyl phosphatase synthetase 1 mRNA, complete cds
946	10179	19335	5.48	8.0E-76	4504374	NT	Homo sapiens H factor 1 (complement) (HF1) mRNA
2862	12100	21231	1.47	8.0E-76	7708724	NT	Homo sapiens H factor 1 (complement) (HF1) mRNA
5739	14958	24358	5.1	8.0E-76	11421442	NT	Homo sapiens mediator (Sur2), mRNA
7256	16479	25971	8.45	8.0E-76	10442821	NT	Homo sapiens LIM domain kinase 1 (LIMK1), mRNA
8934	17815		1.97	8.0E-76	11417862	NT	Homo sapiens baculoviral IAP repeat-containing 8 (BIRC8), mRNA
9030	18233	23702	1.41	8.0E-76	AL365515.1	NT	Homo sapiens calcineurin binding protein 1 (KIAA0330), mRNA
							Novel human gene mapping to chromosome 22
785	10024	19174	1.91	7.0E-76	5016092	NT	Homo sapiens dihydrolipoamide dehydrogenase (E3 component of pyruvate dehydrogenase complex, 2-oxo-
3263	12496	21626	3.4	7.0E-76	AF050490.1	NT	glutarate complex, branched chain keto acid dehydrogenase complex) (DLD) mRNA
3269	12502	21633	8.15	7.0E-76	4505052	NT	Homo sapiens cAMP-specific phosphodiesterase 8A (PDE8A) mRNA, partial cds
4365	13567	22662	6.55	7.0E-76	4507184	NT	Homo sapiens lymphocyte antigen 75 (LY75) mRNA, and translated products
4365	13567	22663	6.55	7.0E-76	4507184	NT	Homo sapiens septaplatin reductase (7,8-dihydrobiopterin:NADP+ oxidoreductase) (SPR) mRNA
1241	10457		8.89	6.0E-76	BE396263.1	EST_HUMAN	Homo sapiens septaplatin reductase (7,8-dihydrobiopterin:NADP+ oxidoreductase) (SPR) mRNA
8001	16436	25923	3.25	6.0E-76	BE273201.1	EST_HUMAN	601312019F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3686757 5'
1912	11117	20312	11.44	5.0E-76	D63874.1	NT	601142253F1 NIH_MGC_14 Homo sapiens cDNA clone IMAGE:3506029 5'
1912	11117	20313	11.44	5.0E-76	D63874.1	NT	Human mRNA for HMG-1, complete cds
1912	11117	20314	11.44	5.0E-76	D63874.1	NT	Human mRNA for HMG-1, complete cds
3173	12408	21543	0.7	4.0E-76	BE814086.1	EST_HUMAN	QV3-BN0047-270700-289-g08 BN0047 Homo sapiens cDNA

Page 256 of 382  
Table 4  
Single Exon Probes Expressed in HELA Cells

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7082	16259	25734	3.98	4.0E-78	D81625.1	EST_HUMAN	HUM178G01B Human fetal brain (TFujiware) Homo sapiens cDNA clone GEN-178G01 5'
7082	16259	25735	3.98	4.0E-78	D81625.1	EST_HUMAN	HUM178G01B Human fetal brain (TFujiware) Homo sapiens cDNA clone GEN-178G01 5'
635	9880	19003	1.54	3.0E-78	BF516262.1	EST_HUMAN	UIH-BW1-anz-b-04-Q-UI s1 NCL CGAP_Sub7 Homo sapiens cDNA clone IMAGE:3083882 3'
635	9880	19004	1.54	3.0E-78	BF516262.1	EST_HUMAN	UIH-BW1-anz-b-04-Q-UI s1 NCL CGAP_Sub7 Homo sapiens cDNA clone IMAGE:3083882 3'
1579	10792	19368	10.99	3.0E-78	4503476	NT	Homo sapiens eukaryotic translation elongation factor 1 beta 2 (EEF1B2) mRNA
1579	10792	19369	10.99	3.0E-78	4503476	NT	Homo sapiens eukaryotic translation elongation factor 1 beta 2 (EEF1B2) mRNA
3407	12633	21763	5.18	3.0E-78	BF375689.1	EST_HUMAN	RC5-ST0300-180100-033-A03 ST0300 Homo sapiens cDNA
3407	12633	21764	5.18	3.0E-78	BF375689.1	EST_HUMAN	RC5-ST0300-180100-033-A03 ST0300 Homo sapiens cDNA
5294	14483	26828	2.14	3.0E-78	Z41314.1	EST_HUMAN	HSCZQD042 normalized infant brain cDNA Homo sapiens cDNA clone c-zqd04 3'
5820	15037	24438	8.16	3.0E-78	AF286598.1	NT	Homo sapiens angiotensin binding protein 1 mRNA, complete cds
6996	16174	25645	2.8	3.0E-78	AW299353.1	EST_HUMAN	xs49h01.x1 NCL CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2773009 3'
8276	18148	23752	1.8	3.0E-78	AW867894.1	EST_HUMAN	EST380059 MAGC resequences, MAGJ Homo sapiens cDNA
8382	18365	23592	4.03	3.0E-78	AW956455.1	EST_HUMAN	EST386525 MAGC resequences, MAGD Homo sapiens cDNA
286	9560	18694	1.1	2.0E-78	D84295.1	NT	Human mRNA for possible protein TPRDII, complete cds
347	9615	18741	2.93	2.0E-78	D84295.1	NT	Human mRNA for possible protein TPRDII, complete cds
347	9615	18742	2.93	2.0E-78	D84295.1	NT	Human mRNA for possible protein TPRDII, complete cds
487	9720		1.48	2.0E-78	4557682	NT	Homo sapiens immunoglobulin (CD79A) binding protein 1 (IGBP1) mRNA
597	9844	18963	1.03	2.0E-78	4503944	NT	Homo sapiens glucagon (GCG) mRNA
1036	10264	18417	0.71	2.0E-78	4758053	NT	Homo sapiens cAMP responsive element binding protein 1 (CREB1) mRNA
1522	10736	18908	2.17	2.0E-78	4504028	NT	Homo sapiens GM2 ganglioside activator protein (GM2A) mRNA
1522	10736	18909	2.17	2.0E-78	4504028	NT	Homo sapiens GM2 ganglioside activator protein (GM2A) mRNA
1897	11104	20286	1.05	2.0E-78	AA253954.1	EST_HUMAN	zs60h11.s1 Strabagene schizo brain S11 Homo sapiens cDNA clone IMAGE:701925 3'
2794	12034	21158	3.2	2.0E-78	P23266	SWISSPROT	OLFACTORY RECEPTOR-LIKE PROTEIN F5
3266	12499	21630	1.85	2.0E-78	AA445992.1	EST_HUMAN	zw64602.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:780886 3' similar to SW:ITB5_HUMAN
3266	12499	21631	1.85	2.0E-78	AA445992.1	EST_HUMAN	P18084 INTEGRIN BETA-5 SUBUNIT PRECURSOR, ;
4117	9590	18694	0.61	2.0E-78	D84295.1	NT	zw64602.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:780886 3' similar to SW:ITB5_HUMAN
4495	13693	22787	1.14	2.0E-78	11545921	NT	P18084 INTEGRIN BETA-5 SUBUNIT PRECURSOR, ;
4968	14153	23245	6.42	2.0E-78	AW879618.1	EST_HUMAN	Human mRNA for possible protein TPRDII, complete cds
5155	14334	23424	1.04	2.0E-78	5031680	NT	Homo sapiens melanoma differentiation associated protein-5 (MDA5), mRNA
5500	14726	24086	5.67	2.0E-78	AB029004.1	NT	QV3-OT0028-220300-132-511 OT0028 Homo sapiens cDNA
7162	16339	25819	4.12	2.0E-78	11437211	NT	Homo sapiens EGF-like repeats and discoidin I-like domains 3 (EDIL3), mRNA
7495	16702	28187	2.68	2.0E-78	7549807	NT	Homo sapiens KIAA1081 protein, partial cds
							Homo sapiens similar to ribosomal protein S28 (H. sapiens) (LOC63150), mRNA
							Homo sapiens HIRA interacting protein 4 (dnal-like) (HIRIP4), mRNA

Table 4

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4285	13488	22687	4.6	1.0E-76	D63874.1	NT	Human mRNA for HMG-1, complete cds
4285	13488	22588	4.6	1.0E-76	D63874.1	NT	Human mRNA for HMG-1, complete cds
5418	14646	23779	5.46	1.0E-76	BE796537.1	EST_HUMAN	601589896F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3944302 5'
6053	15221	24640	4.38	9.0E-77	BE889525.1	EST_HUMAN	601512435F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3913737 5'
9098	17814		1.36	9.0E-77	BE410354.1	EST_HUMAN	601302333F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3636753 5'
192	9471	18602	2.94	8.0E-77	R83144.1	EST_HUMAN	Yp11H02 r1 Soares breast 3NbrHst Homo sapiens cDNA clone IMAGE:187155 5' similar to
4522	13718	22813	1.3	8.0E-77	BF205181.1	EST_HUMAN	SP-ANKB_HUMAN Q01484 ANKYRIN, BRAIN VARIANT 1 ;
5420	14648	23782	2.57	8.0E-77	4506230	NT	Homo sapiens proteasome (prosome, macropain) 20S subunit, non-ATPase, 7 (Mov34 homolog) (PSMD7) mRNA
7925	17138	26669	2.71	8.0E-77	AA019770.1	EST_HUMAN	ze62a02.r1 Soares retina N2b4-HR Homo sapiens cDNA clone IMAGE:363578 5'
7825	17138	26670	2.71	8.0E-77	AA019770.1	EST_HUMAN	ze62a02.r1 Soares retina N2b4-HR Homo sapiens cDNA clone IMAGE:363578 5'
9076	17901	23901	8.5	8.0E-77	R00245.1	EST_HUMAN	ye68904.s1 Soares fetal liver spleen 1NfLS Homo sapiens cDNA clone IMAGE:123007 3' similar to contains
1898	11105	20297	2.31	7.0E-77	AA625755.1	EST_HUMAN	MER10 repetitive element ;
2374	11567	20788	12.68	7.0E-77	4505944	NT	Homo sapiens polymerase (RNA) II (DNA directed) polypeptide E (25kD) (POLR2E) mRNA
2374	11567	20789	12.68	7.0E-77	4505944	NT	Homo sapiens polymerase (RNA) II (DNA directed) polypeptide E (25kD) (POLR2E) mRNA
287	9542	18672	6.02	6.0E-77	4504800	NT	Homo sapiens interferon (alpha, beta and omega) receptor 2 (IFNAR2) mRNA
1150	10373	18524	0.7	6.0E-77	AW957753.1	EST_HUMAN	EST369823 IMAGE resequences, MAGE Homo sapiens cDNA
1529	10743	18916	2.44	6.0E-77	AI204086.1	EST_HUMAN	qe7h12.x1 Soares_fetal_lung_NbHL19W Homo sapiens cDNA clone IMAGE:1745063 3'
4949	14136	23229	0.72	6.0E-77	4557752	NT	Homo sapiens midline 1 (Optiz/BBB syndrome) (MID1) mRNA
4949	14136	23230	0.72	6.0E-77	4557752	NT	Homo sapiens midline 1 (Optiz/BBB syndrome) (MID1) mRNA
147	9429	18563	2.64	5.0E-77	AF154830.1	NT	Homo sapiens carbamyl phosphate synthetase I mRNA, complete cds
147	9429	18564	2.64	5.0E-77	AF154830.1	NT	Homo sapiens carbamyl phosphate synthetase I mRNA, complete cds
1243	10459	18618	1.8	5.0E-77	AF041015.1	NT	7 Homo sapiens glucokinase (GCK) gene, exon 2
1388	10582	18749	2.11	5.0E-77	4557250	NT	Homo sapiens disintegrin and metalloprotease domain 10 (ADAM10) mRNA
2645	11828	21043	1.52	5.0E-77	AF162688.1	NT	Homo sapiens taurine-like kinase 1 (TLK1) mRNA, complete cds
2719	11898	21114	1.44	5.0E-77	4503160	NT	Homo sapiens cullin 1 (CUL1) mRNA
3495	12718	21856	1.39	5.0E-77	8094518	NT	Homo sapiens ubiquitin specific protease 18 (USP18) mRNA
4714	13905	23005	1.88	5.0E-77	5031660	NT	Homo sapiens EGF-like repeats and discoidin I-like domains 3 (EDIL3), mRNA
4714	13905	23006	1.88	5.0E-77	5031660	NT	Homo sapiens EGF-like repeats and discoidin I-like domains 3 (EDIL3), mRNA
4956	14143	23238	2.29	5.0E-77	AL043953.1	EST_HUMAN	DKFZp434G1728_r1 434 (synonym: hsc3) Homo sapiens cDNA clone DKFZp434G1728 5'
6220	15401	24842	10.02	5.0E-77	X88296.1	NT	H. sapiens mRNA for ubiquitin hydrolase
6847	18105	25571	4.08	5.0E-77	11421928	NT	Homo sapiens sorting nexin 5 (SNX5), mRNA

Page 258 of 382  
Table 4  
Single Exon Probes Expressed in HELA Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6947	18105	25572	4.08	5.0E-77	11421928	NT	Homo sapiens sorting nexin 5 (SNX5), mRNA
3682	12903	22023	0.99	4.0E-77	AL449758.1	EST_HUMAN	AL449758 Homo sapiens fetal brain (Stavrides GS) Homo sapiens cDNA
1942	11148	20345	1.54	3.0E-77	5730038	NT	Homo sapiens SET domain and mariner transposase fusion gene (SETMAR) mRNA
1942	11148	20345	1.54	3.0E-77	5730038	NT	Homo sapiens SET domain and mariner transposase fusion gene (SETMAR) mRNA
7452	18660	28149	4.55	3.0E-77	BF356917.1	EST_HUMAN	PM3-MIT0078-080800-005-g03 MIT0078 Homo sapiens cDNA
1360	10575	18740	1.54	2.0E-77	AV764817.1	EST_HUMAN	AV764817 MDS Homo sapiens cDNA clone MDSBTF10 5'
1435	10849	19823	8.06	2.0E-77	AW89712.1	EST_HUMAN	RC3-BN0053-170200-011-h01 BN0053 Homo sapiens cDNA
2060	11261	20475	1.8	2.0E-77	L41825.1	NT	Homo sapiens CYP17 gene, 5' and
2073	11273	20488	2.86	2.0E-77	7708315	NT	Homo sapiens CGI-79 protein (LOC51634), mRNA
2554	12019	20958	1.51	2.0E-77	AB037836.1	NT	Homo sapiens mRNA for KIAA1415 protein, partial cds
2554	12019	20959	1.51	2.0E-77	AB037838.1	NT	Homo sapiens mRNA for KIAA1415 protein, partial cds
4010	13222	22323	1.48	2.0E-77	BE044316.1	EST_HUMAN	h043005.x1 Soerres_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:3040113 3' similar to SW:GAG2_HUMAN P10264 RETROVIRUS-RELATED GAG POLYPROTEIN ;
4596	13790		1.9	2.0E-77	4504068	NT	Homo sapiens glutamic-oxaloacetic transaminase 2, mitochondrial (aspartate aminotransferase 2) (GOT2), nuclear gene encoding mitochondrial protein, mRNA
4779	13968	23070	6.61	2.0E-77	AA653025.1	EST_HUMAN	ns68g12.s1 NCI CGAP Pr2 Homo sapiens cDNA clone IMAGE:1189838 similar to SW:RL29_HUMAN P47914 60S RIBOSOMAL PROTEIN L28, [1]: contains element MSR1 repetitive element ;
5637	14861	24246	1.99	2.0E-77	BE298940.1	EST_HUMAN	601119852F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3029436 5'
5740	14959	24359	1.66	2.0E-77	BE787143.1	EST_HUMAN	601476802F1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3879505 5'
6153	15337	24774	15.25	2.0E-77	AB33003.1	EST_HUMAN	a174e09.x1 Barstead colon HPLB7 Homo sapiens cDNA clone IMAGE:2377720 3' similar to TR:Q13311 Q13311 TAX1-BINDING PROTEIN TXBP151, [1]:
6928	18119	25588	4.1	2.0E-77	U50321.1	NT	Human protein kinase C substrate 80K-H (PRKCSH) gene, exon 7
6928	18119	25587	4.1	2.0E-77	U50321.1	NT	Human protein kinase C substrate 80K-H (PRKCSH) gene, exon 7
45	9341	18448	1	1.0E-77	AB033102.1	NT	Homo sapiens mRNA for KIAA1276 protein, partial cds
45	9341	18449	1	1.0E-77	AB033102.1	NT	Homo sapiens mRNA for KIAA1276 protein, partial cds
277	9552	18683	3.78	1.0E-77	4502166	NT	Homo sapiens amyloid beta (A4) precursor protein (protease nexin-II, Alzheimer disease) (APP), mRNA
277	9552	18684	3.78	1.0E-77	4502166	NT	Homo sapiens amyloid beta (A4) precursor protein (protease nexin-II, Alzheimer disease) (APP), mRNA
885	11980	19284	6.39	1.0E-77	4502166	NT	Homo sapiens amyloid beta (A4) precursor protein (protease nexin-II, Alzheimer disease) (APP), mRNA
885	11980	19285	6.39	1.0E-77	4502166	NT	Homo sapiens amyloid beta (A4) precursor protein (protease nexin-II, Alzheimer disease) (APP), mRNA

Page 259 of 382  
Table 4  
Single Exon Probes Expressed in HELA Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1885	11092	20283	1.21	1.0E-77	AW058119.1	EST_HUMAN	w83e05.x1 Soares_thymus_NHFFh Homo sapiens cDNA clone IMAGE:2536160 3'
2407	11599	20820	2.84	1.0E-77	AB028024.1	NT	Homo sapiens mRNA for KIAA1101 protein, complete cds
3010	12248	21375	2.96	1.0E-77	4903300	NT	Homo sapiens 2,4-dienyl CoA reductase 1, mitochondrial (DECOR1), mRNA
4348	13548	22840	3.77	1.0E-77	7706289	NT	Homo sapiens CGI-60 protein (LOC51626), mRNA
4523	13719	22814	20.84	1.0E-77	AJ228041.1	NT	Homo sapiens 959 kb contig between AML1 and CBR1 on chromosome 21q22; segment 1/3
4852	13846	22937	2.36	1.0E-77	6552322	NT	Homo sapiens breast cancer 1, early onset (BRCA1), transcript variant BRCA1-exon4, mRNA
4702	13893	22992	1.01	1.0E-77	AJ273014.1	EST_HUMAN	q09g04.x1 NCJ_CGAP_Kid8 Homo sapiens cDNA clone IMAGE:1881110 3'
4900	14088	23181	1.31	1.0E-77	11418424	NT	Homo sapiens collagen, type XII, alpha 1 (COL12A1), mRNA
5101	14281	23365	2.43	1.0E-77	7661849	NT	Homo sapiens KIAA0005 gene product (KIAA0005), mRNA
5101	14281	23366	2.43	1.0E-77	7661849	NT	Homo sapiens KIAA0005 gene product (KIAA0005), mRNA
5627	14851	24233	1.91	1.0E-77	AF086944.1	NT	Homo sapiens dynactin 1 (DCTN1) gene, exons 27 and 28
5627	14851	24234	1.91	1.0E-77	AF086944.1	NT	Homo sapiens dynactin 1 (DCTN1) gene, exons 27 and 28
5848	15065	24475	1.68	1.0E-77	4885182	NT	Homo sapiens diaphanous (Drosophila, homolog) 1 (DIAPH1), mRNA
6105	15199	24617	12.1	1.0E-77	5881412	NT	Homo sapiens elastin (supraaortic aortic stenosis, Williams-Beuren syndrome) (ELN), mRNA
5847	15084	24474	2.45	8.0E-78	AW947081.1	EST_HUMAN	RC2-ET0023-080500-012-e05 ET0023 Homo sapiens cDNA
85	9378	18508	1.94	8.0E-78	AW947061.1	EST_HUMAN	RC2-ET0023-080500-012-e05 ET0023 Homo sapiens cDNA
85	9378	18509	1.94	8.0E-78	AW947061.1	EST_HUMAN	AU118789 HEMBA1 Homo sapiens cDNA clone HEMBA1004354 5'
3288	12517	21648	1.45	6.0E-78	BF344101.1	EST_HUMAN	AU118789 HEMBA1 Homo sapiens cDNA clone HEMBA1004354 5'
5905	15122		2.51	6.0E-78	11432710	NT	602016926F1 NCJ_CGAP_Bm64 Homo sapiens cDNA clone IMAGE:4152511 5'
222	9501	18632	1.24	5.0E-78	11422488	NT	Homo sapiens GDNF family receptor alpha 1 (GFRAL), mRNA
2528	11716	20933	8.37	5.0E-78	AW673424.1	EST_HUMAN	Homo sapiens hypothetical protein FLJ11316 (FLJ11316), mRNA
3363	12591	21731	4.41	5.0E-78	M55588.1	NT	ba54h03.y3 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:2800405 5' similar to WP:Y48B6A.6
5401	14629	23742	2.51	5.0E-78	AF038536.1	NT	CE22121
5478	14705	24059	10.31	5.0E-78	11418585	NT	Human collagenase type IV (CLG4) gene, exon 6
6143	15327	24763	2.23	5.0E-78	AW953120.1	EST_HUMAN	Homo sapiens Best's macular dystrophy related protein mRNA, partial cds
6787	15992	25450	8.12	5.0E-78	U60889.1	NT	Homo sapiens transforming growth factor, beta-induced, 68kD (TGFB1), mRNA
6788	15993	25451	5.58	5.0E-78	BE908036.1	EST_HUMAN	EST365190 MAGE resequences, MAGB Homo sapiens cDNA
1145	10368	19519	1.2	4.0E-78	AL043314.2	EST_HUMAN	Human lysosomal alpha-mannosidase (manB) gene, exon 7
1506	10719	19891	1.36	4.0E-78	AL355941.1	NT	Human lysosomal alpha-mannosidase (manB) gene, exon 7
2284	11479	20701	19.91	4.0E-78	AF107405.1	NT	601648061F1 NIH_MGC_62 Homo sapiens cDNA clone IMAGE:3931887 5'
4313	13514	22607	1.61	4.0E-78	7856878	NT	DKFZp434N0323_r1 434 (synonym: hies3) Homo sapiens cDNA clone IMAGE:3931887 5'
7184	16371	25851	2.19	4.0E-78	11560151	NT	Novel human gene mapping to chromosome 22
							Homo sapiens pre-mRNA splicing factor (SFRS3) mRNA, complete cds
							Homo sapiens syncytin (LOC30816), mRNA
							Homo sapiens hypothetical C2H2 zinc finger protein FLJ22504 (FLJ22504), mRNA



Table 4

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7194	16371	25852	2.19	4.0E-78	11560151	NT	Homo sapiens hypothetical C2H2 zinc finger protein FLJ22504 (FLJ22504), mRNA
7346	16562	26051	1.92	4.0E-78	11426610	NT	Homo sapiens regulatory factor X-associated ankyrin-containing protein (RFXANK), mRNA
7857	17096	26626	2.18	4.0E-78	AF169148.1	NT	Homo sapiens s-CaBP1 (CABP1) mRNA, complete cds
8092	17226	26763	3.42	4.0E-78	X05844.1	NT	Human transforming growth factor-beta precursor gene exons 4-5 (and joined mature peptide)
8961	17833	23910	3.24	4.0E-78	AB011388.1	NT	Homo sapiens gene for AF-6, complete cds
184	8446	18576	2.52	3.0E-78	AF095801.1	NT	Homo sapiens gRF1 gene, complete cds
184	8446	18577	2.52	3.0E-78	AF095801.1	NT	Homo sapiens aRF1 gene, complete cds
2288	11463	20683	2.07	3.0E-78	4502142	NT	Homo sapiens apoptosis inhibitor 3 (API3) mRNA
2380	11573	20792	1.23	3.0E-78	7708705	NT	Homo sapiens SH3 and PX domain-containing protein SH3PX1 (SH3PX1), mRNA
3746	12666		1.62	3.0E-78	AU140604.1	EST_HUMAN	AU140604 PLAGE3 Homo sapiens cDNA clone PLACE3000373 5'
3805	13023	22134	0.77	3.0E-78	4507334	NT	Homo sapiens synaptobrevin 1 (SYNJ1), mRNA
4082	13023	22134	0.69	3.0E-78	4507334	NT	Homo sapiens synaptobrevin 1 (SYNJ1), mRNA
5082	14262	23347	1.05	3.0E-78	AF069810.1	NT	Homo sapiens neuritin III-alpha gene, partial cds
7166	16343		6.59	3.0E-78	BE144758.1	EST_HUMAN	CMO-HT0180-041098-065-c07 HT0180 Homo sapiens cDNA
7554	16759	26253	6.1	3.0E-78	BE156318.1	EST_HUMAN	QV0-HT0367-150200-114-g09 HT0367 Homo sapiens cDNA
3085	12321		5.97	2.0E-78	U04489.1	NT	Homo sapiens type IV collagen alpha 5 chain (COL4A5) gene, exon 20
3990	13204		2.23	2.0E-78	AA311872.1	EST_HUMAN	EST182583 Jurkat T-cells VI Homo sapiens cDNA 5' and
6389	15569	25026	3.78	2.0E-78	BF689800.1	EST_HUMAN	602186526F1 NIH_MGC_49 Homo sapiens cDNA clone IMAGE:4298569 5'
6478	15875	25146	2.79	2.0E-78	AV714177.1	EST_HUMAN	AV714177 DCB Homo sapiens cDNA clone DCBAWF09 5'
6615	15811	25267	2.8	2.0E-78	AI557509.1	EST_HUMAN	P2.1_16_B07.r tumor2 Homo sapiens cDNA 3'
6615	15811	25268	2.8	2.0E-78	AI557509.1	EST_HUMAN	P2.1_16_B07.r tumor2 Homo sapiens cDNA 3'
7646	16846	26344	3.63	2.0E-78	AI197837.1	EST_HUMAN	q150M05.x1 NCI_CGAP_Brn25 Homo sapiens cDNA clone IMAGE:1855961 3' similar to WP.R90.1
7684	16863	26391	6.13	2.0E-78	N66951.1	EST_HUMAN	CE06325 PROTEIN KINASE ;
5229	14403	23486	1.73	1.0E-78	4758843	NT	ZB48T12.s1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:285823 3'
5333	14584	23638	3.18	1.0E-78	11417304	NT	Homo sapiens nucleoporin 155KD (NUP155) mRNA
8452	17510	24019	1.3	1.0E-78	11430460	NT	Homo sapiens GAP-like protein (LOC51306), mRNA
							Homo sapiens low density lipoprotein-related protein 2 (LRP2), mRNA
8556	17578	23998	1.28	1.0E-78		NT	Homo sapiens similar to lymphocyte activation-associated protein (H. sapiens) (LOC63140), mRNA
8920	18203	23692	1.72	1.0E-78	AI650919.1	EST_HUMAN	wa20b08.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2298615 3'
4709	13900	22899	4.24	9.0E-78	11525891	NT	Homo sapiens peptide YY (PYY), mRNA
4880	14088	23164	3.22	9.0E-78	BE000837.1	EST_HUMAN	RC2-BN0074-090300-014-c12 BN0074 Homo sapiens cDNA
5408	14638	23764	15.25	9.0E-78	AB028070.1	NT	Homo sapiens mRNA for activator of S phase Kinase, complete cds

Table 4

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5807	15024	24424	2.48	9.0E-79	5454145	NT	Homo sapiens ubiquitin-conjugating enzyme E2E 3 (homologous to yeast UBC4/5) (UBE2E3) mRNA
6792	15987	25447	4.89	9.0E-79	J02853.1	NT	Homo sapiens casein kinase II alpha subunit mRNA, complete cds
6792	15987	25448	4.89	9.0E-79	J02853.1	NT	Homo sapiens casein kinase II alpha subunit mRNA, complete cds
7635	16838	26332	1.73	9.0E-79	AY008273.1	NT	Homo sapiens TRAF8-regulated IKK activator 1 beta Uev1A mRNA, complete cds
8045	17181	26720	3.28	9.0E-79	11423827	NT	Homo sapiens suppressor of white apricot homolog 2 (SWAP2), mRNA
8045	17181	26721	3.28	9.0E-79	11423827	NT	Homo sapiens suppressor of white apricot homolog 2 (SWAP2), mRNA
8093	17227	26764	3.83	9.0E-79	11417260	NT	Homo sapiens threonyl-tRNA synthetase (TARS), mRNA
8093	17227	26765	3.83	9.0E-79	11417260	NT	Homo sapiens threonyl-tRNA synthetase (TARS), mRNA
9170	17985	23885	1.48	9.0E-79	11417877	NT	Homo sapiens gamma-glutamyltransferase 1 (GGT1), mRNA
3723	12943	22060	0.82	8.0E-79	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C010
4492	13680	22782	1.36	8.0E-79	D28476.1	NT	Human mRNA for KIAA0045 gene, complete cds
4492	13680	22783	1.36	8.0E-79	D28476.1	NT	Human mRNA for KIAA0045 gene, complete cds
3219	12453	21598	20.38	7.0E-79	BE619648.1	EST_HUMAN	601472768T1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3875657 3'
8301	17409		5.63	6.0E-79	AA699828.1	EST_HUMAN	494604.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:462558 3' similar to
8028	17166	26704	4.48	5.0E-79	AL163282.2	NT	TR:Q15408 Q15408 NEUTRAL PROTEASE LARGE SUBUNIT ;
3141	12376		1.06	4.0E-79	8922325	NT	Homo sapiens chromosome 21 segment HS21C082
318	9589	18720	1.21	3.0E-79	AF114488.1	NT	Homo sapiens hypothetical protein FLJ10283 (FLJ10283), mRNA
985	10216	19372	3.68	3.0E-79	AF232708.1	NT	Homo sapiens intersectin short isoform (ITSN), complete cds
3084	12300	21424	2.34	3.0E-79	U08410.1	NT	Homo sapiens cell-line tsA201a chloride ion current inducer protein (Cln) gene, complete cds
5149	14328	23417	0.78	3.0E-79	AF114488.1	NT	Human zinc finger protein ZNF131 mRNA, partial cds
5149	14328	23418	0.78	3.0E-79	AF114488.1	NT	Homo sapiens intersectin short isoform (ITSN) mRNA, complete cds
5374	14603	23712	4.61	3.0E-79	AF110322.1	NT	Homo sapiens intersectin short isoform (ITSN) mRNA, complete cds
5544	14768	24134	1.75	3.0E-79	AB020869.1	NT	Homo sapiens MSTP016 (MST016) mRNA, complete cds
5560	14783	24152	3.47	3.0E-79	11426770	NT	Homo sapiens mRNA for KIAA0892 protein, partial cds
5560	14783	24153	3.47	3.0E-79	11426770	NT	Homo sapiens netrin 1 (NTN1), mRNA
6108	15202	24619	3.01	3.0E-79	AB014520.1	NT	Homo sapiens netrin 1 (NTN1), mRNA
6108	15202	24620	3.01	3.0E-79	AB014520.1	NT	Homo sapiens mRNA for KIAA0620 protein, partial cds
7437	16646	26138	1.89	3.0E-79	AF249273.1	NT	Homo sapiens Bcl-2-associated transcription factor short form mRNA, complete cds
7437	16646	26139	1.89	3.0E-79	AF249273.1	NT	Homo sapiens Bcl-2-associated transcription factor short form mRNA, complete cds
292	9566		0.81	2.0E-79	H63129.1	EST_HUMAN	yr4803.s1 Soares_fetal_liver_spleen_1NFLS Homo sapiens cDNA clone IMAGE:208541 3'
640	9886	19011	1.14	2.0E-79	BE378926.1	EST_HUMAN	601159415F2 NIH_MGC_53 Homo sapiens cDNA clone IMAGE:3511107 5'
936	10169	19326	1.04	2.0E-79	4757841	NT	Homo sapiens BCL2-like 2 (BCL2L2) mRNA

Table 4

## Single Exon Probes Expressed in HELA Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1042	10268		1.68	2.0E-79	AI523747.1	EST_HUMAN	h18h07.x1 NCI CGAP P128 Homo sapiens cDNA clone IMAGE:2118685 3'
2116	11315	20531	5.52	2.0E-79	4585863	NT	Homo sapiens phosphodiesterase 6A, cGMP-specific, rod, alpha (PDE6A), mRNA
2116	11315	20532	5.52	2.0E-79	4585863	NT	Homo sapiens phosphodiesterase 6A, cGMP-specific, rod, alpha (PDE6A), mRNA
2159	11357	20575	3.99	2.0E-79	AJ271408.1	NT	Homo sapiens mRNA for Fas-associated factor, FAF1 (Faf1 gene)
2279	11474	20697	3.2	2.0E-79	AF244138.1	NT	Homo sapiens hepatocellular carcinoma-associated antigen 88 (HCA88) mRNA, complete cds
4051	13281	22364	1.07	2.0E-79	AA341536.1	EST_HUMAN	EST146988 Fetal kidney II Homo sapiens cDNA 5' end
4147	13353	22455	1.24	2.0E-79	AJ271408.1	NT	Homo sapiens mRNA for Fas-associated factor, FAF1 (Faf1 gene)
4697	13888	22988	0.66	2.0E-79	AL163206.2	NT	Homo sapiens chromosome 21 segment HS21C008
6149	15333	24770	2.41	2.0E-79	7382479	NT	Homo sapiens Rho GTPase activating protein 6 (ARHGAP6), transcript variant 4, mRNA
6149	15333	24771	2.41	2.0E-79	7382479	NT	Homo sapiens Rho GTPase activating protein 6 (ARHGAP6), transcript variant 4, mRNA
6627	15823	25285	3.2	2.0E-79	11427428	NT	Homo sapiens hypothetical protein FLJ11006 (FLJ11006), mRNA
7598	16801	26293	4.64	2.0E-79	BE064386.1	EST_HUMAN	RC4-BT0310-110300-015-f10 BT0310 Homo sapiens cDNA
7598	16801	26294	4.64	2.0E-79	BE064386.1	EST_HUMAN	RC4-BT0310-110300-015-f10 BT0310 Homo sapiens cDNA
8339	14501	23586	2.95	2.0E-79	7662357	NT	Homo sapiens KIAA0879 protein (KIAA0879), mRNA
8425	17494	24011	4.83	2.0E-79	AB020640.1	NT	Homo sapiens mRNA for KIAA0833 protein, partial cds
8668	17644	23978	3.11	2.0E-79	11418322	NT	Homo sapiens cadherin EGF LAG seven-pass G-type receptor 1 (CELSR1), mRNA
5925	18068		3.21	1.0E-79	BF363071.1	EST_HUMAN	MRO-NN0087-260600-017-b10 NN0087 Homo sapiens cDNA
8143	17275	26819	4.11	1.0E-79	BF087405.1	EST_HUMAN	QV2-HT0540-120800-358-a05 HT0540 Homo sapiens cDNA
8454	18289		1.35	1.0E-79	AI460115.1	EST_HUMAN	ea78a04.x1 Barstead colon HPLRB7 Homo sapiens cDNA clone IMAGE:2151438 3'
3111	12346	21473	15.25	9.0E-80	AA725848.1	EST_HUMAN	a23a05.s1 Soares_testis_NHT Homo sapiens cDNA clone 1343648 3'
3111	12346	21474	15.25	9.0E-80	AA725848.1	EST_HUMAN	a23a05.s1 Soares_testis_NHT Homo sapiens cDNA clone 1343648 3'
7615	16818		1.66	9.0E-80	AI498668.1	EST_HUMAN	tm47d08.x1 NCI CGAP Kid11 Homo sapiens cDNA clone IMAGE:2161263 3'
7825	17017	26532	12.17	9.0E-80		NT	Homo sapiens solute carrier family 7 (cationic amino acid transporter, y+ system), member 8 (SLC7A8), mRNA
7825	17017	26533	12.17	9.0E-80	11433924	NT	Homo sapiens solute carrier family 7 (cationic amino acid transporter, y+ system), member 8 (SLC7A8), mRNA
3580	12802		4.51	8.0E-80	U94387.1	NT	Homo sapiens Y chromosome spermatogenesis candidate protein (RBM) pseudogene mRNA, partial cds
6337	15517	24964	2.95	8.0E-80	11422647	NT	Homo sapiens KIAA0724 gene product (KIAA0724), mRNA
6337	15517	24965	2.95	8.0E-80	11422647	NT	Homo sapiens KIAA0724 gene product (KIAA0724), mRNA
4974	14161	23252	0.82	7.0E-80	H04618.1	EST_HUMAN	y49d02.11 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:152067 5'
910	10145	19308	2.28	6.0E-80	AI422197.1	EST_HUMAN	tf58d02.x1 NCI CGAP_Bm23 Homo sapiens cDNA clone IMAGE:2103459 3' similar to SW-NUEM_HUMAN Q16795 NADH-UBIQUINONE OXIDOREDUCTASE 39 KD SUBUNIT PRECURSOR;

Page 263 of 382  
Table 4  
Single Exon Probes Expressed in HELA Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1620	10833	20008	3.71	6.0E-80	U64898.1	NT	Homo sapiens NRD convertase mRNA, complete cds
2261	11456	20673	6.76	6.0E-80	6631094	NT	Homo sapiens minichromosome maintenance deficient (S. cerevisiae) 3 (MCM3), mRNA
2261	11456	20674	6.76	6.0E-80	6631094	NT	Homo sapiens minichromosome maintenance deficient (S. cerevisiae) 3 (MCM3), mRNA
4270	13473	22568	2.1	6.0E-80	AB032881.1	NT	Homo sapiens mRNA for KIAA1155 protein, partial cds
4270	13473	22569	2.1	6.0E-80	AB032881.1	NT	Homo sapiens mRNA for KIAA1155 protein, partial cds
6701	14920	24314	3.22	6.0E-80	AJ404468.1	NT	Homo sapiens mRNA for dynamin heavy chain (DNABH gene)
5764	14983	24382	3.97	6.0E-80	11436736	NT	Homo sapiens tubby like protein 3 (TULP3), mRNA
7515	16720	28210	2.93	6.0E-80	11427366	NT	Homo sapiens brefeldin A-inhibited guanine nucleotide-exchange protein 1 (BIG1), mRNA
7777	16972	28485	21.54	6.0E-80	AF226730.1	NT	Homo sapiens Cyt19 mRNA, complete cds
8232	17361	26899	2.16	6.0E-80	AF102265.1	NT	Homo sapiens N-acetylglucosamine-phosphate mutase mRNA, complete cds
8308	10145	19308	1.46	6.0E-80	AI42197.1	EST_HUMAN	t59d02.x1 NCL CGAP_Bm23 Homo sapiens cDNA clone IMAGE:2103459 3' similar to SW:NUEM_HUMAN Q16795 NADH-UBIQUINONE OXIDOREDUCTASE 39 KD SUBUNIT PRECURSOR ;
8436	18173		2.28	6.0E-80	AF240786.1	NT	Homo sapiens glutathione S-transferase theta 2 (GSTT2) and glutathione S-transferase theta 1 (GSTT1) genes, complete cds
8848	17631		6.14	6.0E-80	AB028900.1	NT	Homo sapiens CST gene for carboside sulfotransferase, exon 1, 2, 3, 4, 5
9165	18307		1.69	6.0E-80	AJ133127.1	NT	Homo sapiens mRNA for sodium-glucose cotransporter (SGLT2 gene)
595	9842	18962	2.27	5.0E-80	4508228	NT	Homo sapiens proteasome (prosome, macropain) 26S subunit, non-ATPase, 3 (PSMD3) mRNA
845	10082	19241	1.45	5.0E-80	AF108830.1	NT	Homo sapiens serine-threonine protein kinase (MNBH) mRNA, complete cds
845	10082	19242	1.45	5.0E-80	AF108830.1	NT	Homo sapiens serine-threonine protein kinase (MNBH) mRNA, complete cds
1197	10417		5.59	5.0E-80	X91647.1	NT	H. sapiens next gene (exon 12)
1455	10668		2.61	5.0E-80	AL163283.2	NT	Homo sapiens chromosome 21 segment HS21C083
2329	11522	20744	1	5.0E-80	U89358.1	NT	Human I(3)mb1 protein homolog mRNA, complete cds
2394	11587	20805	7.09	5.0E-80	AB037855.1	NT	Homo sapiens mRNA for KIAA1434 protein, partial cds
2747	11928	21140	2.06	5.0E-80	4504282	NT	Homo sapiens H3 histone family, member J (H3FJ) mRNA
4016	13228	22330	1.08	5.0E-80	AB019038.1	NT	Homo sapiens HMT-1 mRNA for beta-1,4-mannosyltransferase, complete cds
4016	13228	22331	1.08	5.0E-80	AB019038.1	NT	Homo sapiens HMT-1 mRNA for beta-1,4-mannosyltransferase, complete cds
4973	14160	23251	1.16	5.0E-80	AL163288.2	NT	Homo sapiens chromosome 21 segment HS21C088
5237	14411	23491	2.76	5.0E-80	AL163285.2	NT	Homo sapiens chromosome 21 segment HS21C085
6841	16046	25511	8.8	4.0E-80	F25915.1	EST_HUMAN	HSPD13155 HM3 Homo sapiens cDNA clone s4000045F03
221	9500		17.47	3.0E-80	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C010
4718	13910	23012	1.02	3.0E-80	BF085009.1	EST_HUMAN	PMO-GN0018-040800-002-E03 GN0018 Homo sapiens cDNA
4929	14117		12.26	3.0E-80	BE817485.1	EST_HUMAN	QV4-BN0263-040800-241-g10 BN0263 Homo sapiens cDNA

Page 264 of 382  
Table 4  
Single Exon Probes Expressed in HELA Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5579	14803	24178		2	3.0E-80	AI091675.1	cc23e12.x1 Soares_NSF_F8_QW_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:1567054 3' similar to TR:O35780 O35780 PIG-L;
1767	10977	20168	6.28	2.0E-80	R35321.1	EST_HUMAN	yg85a08.r1 Soares infant brain 1N1B Homo sapiens cDNA clone IMAGE:38080 5'
1828	11036	20232	1.53	2.0E-80	AI444821.1	EST_HUMAN	RET487 subtracted retina cDNA library Homo sapiens cDNA clone RET487
2022	11223	20431	5.67	2.0E-80	AL043116.2	EST_HUMAN	DKFZp434D1323_r1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434D1323 5'
6818	16012	25478	2.2	2.0E-80	AW984270.1	EST_HUMAN	EST376343 MAGE resequences, MAGH Homo sapiens cDNA
7448	18654	26145	6.59	2.0E-80	AA383382.1	EST_HUMAN	z170f12.r1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:72727 5' similar to TR:G191315
345	9613		2.45	1.0E-80	AL163303.2	NT	G191315 ANDROGEN-DEPENDENT EXPRESSED PROTEIN.;
809	10048	19189	1.37	1.0E-80	AF231920.1	NT	Homo sapiens chromosome 21 segment HS21C103 Homo sapiens chromosome 21 unknown mRNA
1924	11128		2.64	1.0E-80	AI732656.1	EST_HUMAN	nm011f12.x5 NCI_CGAP_Co6 Homo sapiens cDNA clone IMAGE:1076495 3' similar to contains OFR.11 OFR repetitive element;
4458	13854	22748	1.38	1.0E-80	AF077188.1	NT	Homo sapiens cullin 4A (CUL4A) mRNA, complete cds
4835	14024	23118	0.6	1.0E-80	N69520.1	EST_HUMAN	za39g07.r1 Soares fetal liver spleen 1N1FLS Homo sapiens cDNA clone IMAGE:284972 5' similar to contains Alu repetitive element
5350	14580		3.73	1.0E-80	BE386615.1	EST_HUMAN	601274305F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3815433 5'
5641	14865	24248	5.71	1.0E-80	L10347.1	NT	Human pro-alpha1 type II collagen (COL2A1) gene exons 1-54, complete cds
6323	15504	24950	2.87	1.0E-80	AI948731.1	EST_HUMAN	wq25c05.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2472286 3'
6323	15504	24951	2.87	1.0E-80	AI948731.1	EST_HUMAN	wq25c05.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2472286 3'
7245	19465	25955	2.04	1.0E-80	11641276	NT	Homo sapiens similar to rat myonegallin (LOC64182), mRNA
7245	19465	25956	2.04	1.0E-80	11641276	NT	Homo sapiens similar to rat myonegallin (LOC64182), mRNA
8724	17676	23950	2.02	1.0E-80	11417801	NT	Homo sapiens meningioma (disrupted in balanced translocation) 1 (MN1), mRNA
7278	18495	25986	3.34	8.0E-81	AI251752.1	EST_HUMAN	qh90g05.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1854288 3'
7278	18495	25987	3.34	8.0E-81	AI251752.1	EST_HUMAN	qh90g05.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1854288 3'
7713	18912	26420	6.93	8.0E-81	BE394525.1	EST_HUMAN	601310631F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3632070 5'
2173	11370	20591	1.83	7.0E-81	AA011080.1	EST_HUMAN	za21d10.r1 Soares_fetal_heart_NbHH19W Homo sapiens cDNA clone IMAGE:359835 5' similar to SW_KRHA_RABIT_Q02957 KERATIN, GLYCINE/TYROSINE-RICH OF HAIR. [1], contains element MER22 repetitive element;
6188	15368	24808	2.88	7.0E-81	AI822115.1	EST_HUMAN	za81c08.x5 Soares_fetal_lung_NbHL19W Homo sapiens cDNA clone IMAGE:289918 3'
4381	13582	22683	5.13	6.0E-81	BE256829.1	EST_HUMAN	601111970F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3352840 5'
4381	13582	22684	5.13	6.0E-81	BE256829.1	EST_HUMAN	601111970F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3352840 5'
5316	14548	23617	1.74	6.0E-81	4501848	NT	Homo sapiens ATP-binding cassette, sub-family A (ABC1), member 3 (ABCA3), mRNA
5316	14548	23618	1.74	6.0E-81	4501848	NT	Homo sapiens ATP-binding cassette, sub-family A (ABC1), member 3 (ABCA3), mRNA
8887	17767	23937	1.88	6.0E-81	BF679022.1	EST_HUMAN	602153668F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4294601 5'

Page 265 of 382  
Table 4  
Single Exon Probes Expressed in HELA Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8887	17167	23938	1.88	6.0E-81	BF679022.1	EST_HUMAN	602153666F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4294601 5'
2183	11380	20804	4.15	5.0E-81	BE268042.1	EST_HUMAN	601126505F1 NIH_MGC_8 Homo sapiens cDNA clone IMAGE:3345480 5'
8113	17247	28787	2.92	5.0E-81	8506634	NT	Homo sapiens hypothetical protein (FLJ11045), mRNA
225	9504	18634	0.89	4.0E-81	AF252257.1	NT	Homo sapiens CRP2 binding protein mRNA, partial cds.
709	9951	19090	0.86	4.0E-81	AI521435.1	EST_HUMAN	th60e12.x1 NCL_CGAP_Ov23 Homo sapiens cDNA clone IMAGE:2122702 3' similar to TR:Q85560 Q85560
3135	12370	21501	4.19	4.0E-81	AB037766.1	NT	Homo sapiens mRNA for KIAA1345 protein, partial cds
4142	13348	22447	2.53	4.0E-81	AF263306.1	NT	Homo sapiens rab3 interacting protein variant 2 mRNA, partial cds
4142	13348	22448	2.53	4.0E-81	AF263308.1	NT	Homo sapiens rab3 interacting protein variant 2 mRNA, partial cds
6554	15750	25211	2.38	4.0E-81	X08989.1	NT	Human mRNA for amyloid A4(751) protein
6638	15833	25294	3.01	4.0E-81	U20197.1	NT	Human cone photoreceptor cGMP-phosphodiesterase alpha' subunit gene, exons 2 and 3
6638	15833	25295	3.01	4.0E-81	U20197.1	NT	Human cone photoreceptor cGMP-phosphodiesterase alpha' subunit gene, exons 2 and 3
6635	16029	25494	3.59	4.0E-81	AB018001.1	NT	Homo sapiens mRNA for Death-associated protein kinase 2, complete cds
7740	16938	26444	3.01	4.0E-81	4759085	NT	Homo sapiens vesicle trafficking protein sec22b (SEC22B) mRNA
7740	16938	26445	3.01	4.0E-81	4759085	NT	Homo sapiens vesicle trafficking protein sec22b (SEC22B) mRNA
8331	18239	23706	4.54	4.0E-81	11417862	NT	Homo sapiens calcineurin binding protein 1 (KIAA0330), mRNA
8331	18239	23707	4.54	4.0E-81	11417862	NT	Homo sapiens calcineurin binding protein 1 (KIAA0330), mRNA
9055	17887	23897	4.02	4.0E-81	11417974	NT	Homo sapiens transcobalamin II; macrocytic anemia (TCN2), mRNA
1274	10489	19648	12.21	3.0E-81	Y18000.1	NT	Homo sapiens NF2 gene
1274	10489	19647	12.21	3.0E-81	Y18000.1	NT	Homo sapiens NF2 gene
2339	11532	20755	11.44	3.0E-81	AF077188.1	NT	Homo sapiens cullin 4A (CUL4A) mRNA, complete cds
2848	12186	21318	6.63	3.0E-81	4506280	NT	Homo sapiens pleiotrophin (heparin binding growth factor 8, neurite growth-promoting factor 1) (PTN) mRNA
2848	12186	21319	6.63	3.0E-81	4506280	NT	Homo sapiens pleiotrophin (heparin binding growth factor 8, neurite growth-promoting factor 1) (PTN) mRNA
2786	12026	21152	2.43	2.0E-81	BE784836.1	EST_HUMAN	601474072F1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3877121 5'
2786	12026	21153	2.43	2.0E-81	BE784836.1	EST_HUMAN	601474072F1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3877121 5'
3755	12874	22090	0.83	2.0E-81	AW611542.1	EST_HUMAN	hg85c01.x1 NCL_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2852384 3'
4882	13874	22874	1.91	2.0E-81	5453871	NT	Homo sapiens platelet-derived growth factor receptor-like (PDGFR) mRNA
9207	12874	22090	2.67	2.0E-81	AW611542.1	EST_HUMAN	hg85c01.x1 NCL_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2852384 3'
3632	12853	21972	1.31	1.0E-81	AW680658.1	EST_HUMAN	EST372729 IMAGE resequences, MAGF Homo sapiens cDNA
4516	13712	22805	2.89	1.0E-81	AA040370.1	EST_HUMAN	z445f09.r1 Soares_pregnant_uterus_NbhPU Homo sapiens cDNA clone IMAGE:485825 5' similar to PIR:S52437 S52437 CDP-diacylglycerol synthase - fruit fly
4648	13840	22830	7.9	1.0E-81	BE047998.1	EST_HUMAN	t245c04.y1 NCL_CGAP_Bm52 Homo sapiens cDNA clone IMAGE:2291528 5'

Page 266 of 382  
Table 4  
Single Exon Probes Expressed in HELA Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5164	14343	23432	3.88	1.0E-81	9966844	NT	Homo sapiens chromosome 12 open reading frame 3 (C12ORF3), mRNA
5283	14492	26925	3.55	1.0E-81	U87928.1	NT	Human acetylcholinesterase (ACO2) gene, exon 3
5367	14597	23674	3.93	1.0E-81	11432968	NT	Homo sapiens polymerase (DNA directed), gamma (POLG), mRNA
5387	14597	23675	3.93	1.0E-81	11432968	NT	Homo sapiens polymerase (DNA directed), gamma (POLG), mRNA
5511	14736	24099	3.39	1.0E-81	U52351.1	NT	Homo sapiens arm-repeat protein NPRAP/neurojuncin (CTNND2) mRNA, partial cds
5511	14736	24100	3.39	1.0E-81	U52351.1	NT	Homo sapiens arm-repeat protein NPRAP/neurojuncin (CTNND2) mRNA, partial cds
6403	15584	25041	7.33	1.0E-81	11432968	NT	Homo sapiens polymerase (DNA directed), gamma (POLG), mRNA
7008	16186	25659	2.87	1.0E-81	BE958278.1	EST_HUMAN	601845051F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:3930228 5'
7008	16186	25660	2.87	1.0E-81	BE958278.1	EST_HUMAN	601845051F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:3930228 5'
7081	16238	25711	6.11	1.0E-81	BE564387.1	EST_HUMAN	601343180F1 NIH_MGC_53 Homo sapiens cDNA clone IMAGE:3685483 5'
							act14008.a1 Stratagene HeLa cell s3 937216 Homo sapiens cDNA clone IMAGE:856427 3' similar to SW:YB36_YEAST P38128 HYPOTHETICAL 60.5 KD PROTEIN IN RPS101-RPS13 INTERGENIC REGION.
7114	16281	25772	2.9	1.0E-81	AA630784.1	EST_HUMAN	
7514	16719	26209	2.12	1.0E-81	8923698	NT	Homo sapiens golgin-like protein (GLP), mRNA
7655	18655	26354	2.19	1.0E-81	AW844986.1	EST_HUMAN	MRO-CT0006-250598-019 CT0006 Homo sapiens cDNA
7655	18655	26355	2.19	1.0E-81	AW844986.1	EST_HUMAN	MRO-CT0006-250598-019 CT0006 Homo sapiens cDNA
7821	12853	21972	3.15	1.0E-81	AW860658.1	EST_HUMAN	EST372729 IMAGE resequences, MAGF Homo sapiens cDNA
8054	17190	26730	2.23	1.0E-81	BF204253.1	EST_HUMAN	601887714F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4110459 5'
8550	17573	23994	3.86	1.0E-81	11418138	NT	Homo sapiens photobolin (similar to apolipoprotein B mRNA editing protein) (DJ742C19.2), mRNA
12	9308	18410	4.82	8.0E-82	AF161408.1	NT	Homo sapiens HSPC288 mRNA, partial cds
106	9308	18410	3.64	8.0E-82	AF161408.1	NT	Homo sapiens HSPC288 mRNA, partial cds
268	9543	18673	1.81	8.0E-82	U08988.1	NT	Human CRFB4 gene, partial cds
824	10082	19214	2.49	8.0E-82	U08988.1	NT	Human CRFB4 gene, partial cds
897	10132	19284	0.74	8.0E-82	U08988.1	NT	Human CRFB4 gene, partial cds
1482	10695	19870	1.58	8.0E-82	AB037748.1	NT	Homo sapiens mRNA for KIAA1327 protein, partial cds
1633	10847	20028	1.59	8.0E-82	6715601	NT	Homo sapiens glutathione peroxidase 5 (epididymal androgen-related protein) (GPX5), transcript variant 2, mRNA
4229	13432	22526	0.76	8.0E-82	8923432	NT	Homo sapiens hypothetical protein FLJ20461 (FLJ20461), mRNA
1451	10684		1.61	7.0E-82	BF035327.1	EST_HUMAN	601458531F1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3862086 5'
2722	11901	21117	1.57	7.0E-82	AU144050.1	EST_HUMAN	AU144050 HEMBA1 Homo sapiens cDNA clone HEMBA1000752 3'
4105	13312	22410	0.71	5.0E-82	AA515512.1	EST_HUMAN	nf89911.s1 NCI CGAP_C03 Homo sapiens cDNA clone IMAGE:925186 3'
1648	10860	20041	59.84	4.0E-82	AF081484.1	NT	Homo sapiens alpha-tubulin isoform 1 mRNA, complete cds
8207	17338	26878	5.01	4.0E-82	A1837300.1	EST_HUMAN	wp75609.x1 NCI CGAP_Bm25 Homo sapiens cDNA clone IMAGE:2467624 3' similar to TR:075276 O75276 PKD1

Table 4

## Single Exon Probes Expressed in HELA Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8807	17729		6.52	4.0E-82	AF028701.2	NT	Homo sapiens presenilin-1 gene, exons 1 and 2
282	9557	18990	20.38	3.0E-82	4502166	NT	Homo sapiens amyloid beta (A4) precursor protein (protease nexin-II, Alzheimer disease) (APP), mRNA
710	9952	19091	2.58	3.0E-82	BE005705.1	EST_HUMAN	RC2-BN0120-010400-013-102 BN0120 Homo sapiens cDNA
797	10036	18187	4.71	3.0E-82	5174702	NT	Homo sapiens transforming growth factor beta-activated kinase-binding protein 1 (TAB1), mRNA
880	10116	19278	4.98	3.0E-82	4502166	NT	Homo sapiens amyloid beta (A4) precursor protein (protease nexin-II, Alzheimer disease) (APP), mRNA
1088	10294		38.43	3.0E-82	AA725948.1	EST_HUMAN	al23a05.s1 Soares_testis_NHT Homo sapiens cDNA clone 1343648 3'
1363	10578	18745	0.98	3.0E-82	AW875073.1	EST_HUMAN	RC8-PT0001-180100-021-B02 PT0001 Homo sapiens cDNA
1462	10875	19848	2.85	3.0E-82	AL163285.2	NT	Homo sapiens chromosome 21 segment HS21C085
1865	11072	20283	1.69	3.0E-82	BE813232.1	EST_HUMAN	RC1-BN0005-260700-018-g04 BN0005 Homo sapiens cDNA
3238	12473		2.36	3.0E-82	5453811	NT	Homo sapiens neurotrophic tyrosine kinase, receptor, type 2 (NTRK2) mRNA
6508	15704	25170	2.69	3.0E-82	11425206	NT	Homo sapiens ankyrin-like with transmembrane domains 1 (ANKTM1), mRNA
604	8851	18969	1.37	2.0E-82	AB023216.1	NT	Homo sapiens mRNA for KIAA0999 protein, partial cds
604	8851	18970	1.37	2.0E-82	AB023216.1	NT	Homo sapiens mRNA for KIAA0999 protein, partial cds
1661	10874	20058	1.4	2.0E-82	AL046390.1	EST_HUMAN	DKFZp434M117_r1 434 (synonym: hies3) Homo sapiens cDNA clone DKFZp434M117 5'
2835	12173	21307	0.79	2.0E-82	AL163201.2	NT	Homo sapiens chromosome 21 segment HS21C001
3831	13048	22158	1.43	2.0E-82	D87675.1	NT	Homo sapiens DNA for amyloid precursor protein, complete cds
3999	13212	22316	0.87	2.0E-82	U76833.1	NT	Human integral membrane serine protease Seprease mRNA, complete cds
4218	13421	22516	0.89	2.0E-82	4504116	NT	Homo sapiens glutamate receptor, ionotropic, kainate 1 (GRIK1) mRNA
4555	13750	22849	1.56	2.0E-82	AB029019.1	NT	Homo sapiens mRNA for KIAA1096 protein, partial cds
4555	13750	22850	1.56	2.0E-82	AB029019.1	NT	Homo sapiens mRNA for KIAA1096 protein, partial cds
4886	14074	23172	2.13	2.0E-82	AF045555.1	NT	Homo sapiens wbscr1 (WBSOR1) and wbscr5 (WBSOR5) genes, complete cds, alternatively spliced and replication factor C subunit 2 (RFC2) gene, complete cds
5110	14290	23376	1.23	2.0E-82	4507580	NT	Homo sapiens tumor necrosis factor receptor superfamily, member 5 (TNFRSF5) mRNA
5110	14290	23377	1.23	2.0E-82	4507580	NT	Homo sapiens tumor necrosis factor receptor superfamily, member 5 (TNFRSF5) mRNA
5427	14654	23781	2.59	2.0E-82	AB018270.1	NT	Homo sapiens mRNA for KIAA0727 protein, partial cds
5741	14980	24360	5.35	2.0E-82	AF234882.1	NT	Homo sapiens FAM4A1 splice variant a (FAM4A1) mRNA, complete cds
7824	17016	26531	1.74	2.0E-82	11417106	NT	Homo sapiens 3-hydroxy-3-methylglutaryl-Coenzyme A reductase (HMGCR), mRNA
7856	17046	26564	5.19	2.0E-82	U80736.1	NT	Homo sapiens CAGF9 mRNA, partial cds
7856	17046	26565	5.19	2.0E-82	U80736.1	NT	Homo sapiens CAGF9 mRNA, partial cds
8381	17452		2.21	2.0E-82	N94950.1	EST_HUMAN	z831d10.s1 Soares_parathyroid_tumor_NbHPA Homo sapiens cDNA clone IMAGE:305203 3'
8927	17810		3.89	2.0E-82	AA011278.1	EST_HUMAN	z101q09.r1 Soares_fetal_liver_spleen_INFLS_S1 Homo sapiens cDNA clone IMAGE:428568 5'
9241	18012		1.86	2.0E-82	11418097	NT	Homo sapiens SRY (sex determining region Y-box 10 (SOX10), mRNA



Page 268 of 382  
Table 4  
Single Exon Probes Expressed in HELA Cells

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
599	9846	18964	1.53	1.0E-82	11546921	NT	Homo sapiens melanoma differentiation associated protein-5 (MDA5), mRNA
1216	10434		1.61	1.0E-82	BE885106.1	EST_HUMAN	601510859F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3912207 5'
1292	10507	19668	1.54	1.0E-82	BE084396.1	EST_HUMAN	RC4-BT0310-110300-015-f10 BT0310 Homo sapiens cDNA
1293	10508	19667	1.26	1.0E-82	AB011110.2	NT	Homo sapiens mRNA for KIAA0538 protein, partial cds
7331	16547	26037	2.65	1.0E-82	AL163209.2	NT	Homo sapiens chromosome 21 segment HS21C009
7578	16783	26276	1.95	1.0E-82	AL163246.2	NT	Homo sapiens chromosome 21 segment HS21C046
6885	15880	25339	4.85	9.0E-83	BF672220.1	EST_HUMAN	602150403F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4291561 5'
1418	10631	19799	8.92	8.0E-83	BE383973.1	EST_HUMAN	601273346F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3614362 5'
1656	11947	20052	10.45	8.0E-83	N66951.1	EST_HUMAN	z48f12.s1 Soares fetal liver spleen INFLS Homo sapiens cDNA clone IMAGE:286823 3'
1365	10580	19746	1.65	7.0E-83	AW385529.1	EST_HUMAN	QV4-LT0016-271289-068-h11 LT0016 Homo sapiens cDNA
2817	12056		1.46	7.0E-83	AA584655.1	EST_HUMAN	no12h01.s1 NCI_CGAP_Phet1 Homo sapiens cDNA clone IMAGE:1100497 3' similar to contains Alu repetitive element;
4830	14019		7.39	7.0E-83	BF221813.1	EST_HUMAN	7p37e07.x1 NCI_CGAP_P28 Homo sapiens cDNA clone IMAGE:3647893 3' similar to TR:Q9Y316 Q9Y316
409	9962	18801	1.41	6.0E-83	M33320.1	NT	DJ207H1.1 ; Human platelet Glycoprotein IIb (GPIIb) gene, exons 2-29
1767	10688	20163	2.7	6.0E-83	AW573088.1	EST_HUMAN	hf31h03.x1 Soares NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2833525 3' similar to SW:YBEB_HAEIN P44471 HYPOTHETICAL PROTEIN H10034. ;
2882	12218	21354	0.72	6.0E-83	AW816405.1	EST_HUMAN	QV4-ST0234-181199-037-05 ST0234 Homo sapiens cDNA
3016	12252		1.47	6.0E-83	AF231919.1	NT	Homo sapiens chromosome 21 unknown mRNA
3537	12760	21891	0.91	6.0E-83	11430241	NT	Homo sapiens hypothetical protein FLJ10379 (FLJ10379), mRNA
5323	14555	23825	1.89	6.0E-83	4507866	NT	Homo sapiens VAMP (vesicle-associated membrane protein)-associated protein A (33kD) (VAPA) mRNA, and translated products
6291	15472	24913	1.99	6.0E-83	11422024	NT	Homo sapiens met proto-oncogene (hepatocyte growth factor receptor) (MET), mRNA
6984	16162	25633	3.82	6.0E-83	4505314	NT	Homo sapiens myomesin (M-protein) 2 (165kD) (MYOM2), mRNA
7007	16185	25657	3.15	6.0E-83	11430647	NT	Homo sapiens pre-mRNA splicing factor similar to S. cerevisiae Prp18 (PRP18), mRNA
7007	16185	25658	3.15	6.0E-83	11430647	NT	Homo sapiens pre-mRNA splicing factor similar to S. cerevisiae Prp18 (PRP18), mRNA
8062	17197		6.3	6.0E-83	AA486105.1	EST_HUMAN	ab14e10.s1 Stratagene lung (4837210) Homo sapiens cDNA clone IMAGE:840810 3' similar to contains THR12 THR repetitive element ;
8311	17416		4.29	6.0E-83	AF240786.1	NT	Homo sapiens glutathione S-transferase theta 2 (GSTT2) and glutathione S-transferase theta 1 (GSTT1) genes, complete cds
954	10187		2.23	5.0E-83	U17883.1	NT	Human succinate dehydrogenase iron-protein subunit (sdhB) gene, exon 5
2017	11950		19.94	5.0E-83	AF006305.1	NT	Homo sapiens 26S proteasome regulatory subunit (SUG2) mRNA, complete cds
3617	12838	21957	1.19	5.0E-83	AL133207.2	NT	Novel human gene mapping to chromosome X
3884	13100	22217	0.67	5.0E-83	4885180	NT	Homo sapiens deoxyribonuclease 1 (DNASE1), mRNA

Page 269 of 382  
Table 4  
Single Exon Probes Expressed in HELA Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4425	13625	22720	0.69	5.0E-83	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C010
5109	14289	23374	12.48	5.0E-83	4557013	NT	Homo sapiens catalase (CAT) mRNA
5109	14289	23375	12.48	5.0E-83	4557013	NT	Homo sapiens catalase (CAT) mRNA
5177	14355	23442	1.07	5.0E-83	AB037832.1	NT	Homo sapiens mRNA for KIAA1411 protein, partial cds
646	9892	19017	3.73	4.0E-83	AF224669.1	NT	Homo sapiens mannosidase, beta A, lysosomal (MANBA) gene, and ubiquitin-conjugating enzyme E2D 3
1005	10236		4.72	3.0E-83	AA368311.1	EST_HUMAN	(UBE2D3) genes, complete cds
2732	11911		1.22	3.0E-83	AA632654.1	EST_HUMAN	EST179542 Placenta [Homo sapiens cDNA similar to similar to endogenous retrovirus ERV9
1769	10679	20168	1.36	2.0E-83	AA983482.1	EST_HUMAN	np87c07.s1 NCI_CGAP_Thy1 Homo sapiens cDNA clone IMAGE:1133292 similar to contains THR.L2 THR repetitive element;
1769	10679	20168	1.36	2.0E-83	AA983482.1	EST_HUMAN	Q92614 MYELOBLAST KIAA0216. ;
1893	11100	20291	7.4	2.0E-83	N66951.1	EST_HUMAN	Q92614 MYELOBLAST KIAA0216. ;
2803	12043	21164	1.24	2.0E-83	BE828694.1	EST_HUMAN	Q92614 MYELOBLAST KIAA0216. ;
3236	12470		2.65	2.0E-83	11430834	NT	z44812.s1 Soares fetal liver spleen INF15 Homo sapiens cDNA clone IMAGE:295823 3'
3756	12975		0.63	2.0E-83	AL163202.2	NT	RC8-ET0046-280600-013-H12 ET0046 Homo sapiens cDNA
4329	13530	22624	4.29	2.0E-83	AF202879.1	NT	Homo sapiens sal (Drosophila)-like 1 (SALL1), mRNA
4653	13847	22838	5.89	2.0E-83	7706398	NT	Homo sapiens chromosome 21 segment HS21C002
4653	13847	22839	5.89	2.0E-83	7706398	NT	Homo sapiens hematopoietic progenitor cell antigen CD34 precursor (CD34) mRNA, partial cds
6268	15447	24886	5.44	2.0E-83	AF129533.1	NT	Homo sapiens ankyrin repeat-containing protein ASB-2 (LOC51676), mRNA
6565	15761	25223	3.51	2.0E-83	AF011920.1	NT	Homo sapiens ankyrin repeat-containing protein ASB-2 (LOC51676), mRNA
6565	15761	25224	3.51	2.0E-83	AF011920.1	NT	Homo sapiens F-box protein Fbx3b (FBL3B) mRNA, partial cds
7426	16636	26129	4.43	2.0E-83	11438448	NT	Homo sapiens protein kinase CK2 catalytic subunit alpha gene, exon 1
7500	16707	26193	2.3	2.0E-83	AL134452.1	EST_HUMAN	Homo sapiens protein kinase CK2 catalytic subunit alpha gene, exon 1
7500	16707	26194	2.3	2.0E-83	AL134452.1	EST_HUMAN	Homo sapiens KIAA0985 protein (KIAA0985), mRNA
8966	17836		4.39	2.0E-83	AB011399.1	NT	DKFZp547J135_r1 547 (synonym: hibr1) Homo sapiens cDNA clone DKFZp547J135 5'
1416	10629	19796	2.16	1.0E-83	4504328	NT	DKFZp547J135_r1 547 (synonym: hibr1) Homo sapiens cDNA clone DKFZp547J135 5'
1416	10629	19797	2.16	1.0E-83	4504328	NT	Homo sapiens gene for AF-4, complete cds
1987	11180	20400	1.81	1.0E-83	4503652	NT	Homo sapiens hydroxycarboxyl-Coenzyme A dehydrogenase3-ketocacyl-Coenzyme A thidase/enoyl-Coenzyme A hydratase (trifunctional protein), beta subunit (HADHB) mRNA
2818	11802	21019	1.72	1.0E-83	BE883890.1	EST_HUMAN	Homo sapiens hydroxycarboxyl-Coenzyme A dehydrogenase3-ketocacyl-Coenzyme A thidase/enoyl-Coenzyme A hydratase (trifunctional protein), beta subunit (HADHB) mRNA
3850	13066	22180	5.44	1.0E-83	AF053768.1	NT	Homo sapiens fatty-acid-Coenzyme A ligase, very long-chain 1 (FACVL1) mRNA

Table 4

## Single Exon Probes Expressed in HELA Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4230	13433	22527	3.15	1.0E-83	Z25822.1	NT	H. sapiens gene for mitochondrial dodecenoyl-CoA delta-isomerase, exon 3
4908	14096	23189	2.7	1.0E-83	4502166	NT	Homo sapiens amyloid beta (A4) precursor protein (protease nexin-II, Alzheimer disease) (APP), mRNA
5963	15178	24595	1.87	1.0E-83	A027614.1	EST_HUMAN	ov88b08.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1645431 3' similar to gb:M64241 QM PROTEIN (HUMAN);
3779	12897	22113	4.49	7.0E-84	BE901209.1	EST_HUMAN	601676023F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3958853 5'
1302	10517	19674	3.88	6.0E-84	BE838864.1	EST_HUMAN	RC2-FN0119-200600-011-g05 FN0119 Homo sapiens cDNA
1302	10517	19675	3.88	6.0E-84	BE838864.1	EST_HUMAN	RC2-FN0119-200600-011-g05 FN0119 Homo sapiens cDNA
2362	11555	20777	3.64	6.0E-84	AA776574.1	EST_HUMAN	aa86a03.s1 Stratagene schizo brain S11 Homo sapiens cDNA clone IMAGE:971020 3'
5296	14484		3.16	6.0E-84	AL042863.2	EST_HUMAN	DKFZp434H0322_1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434H0322 5'
5449	14675	23834	1.65	6.0E-84	AA897339.1	EST_HUMAN	al47g03.s1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1460500 3' similar to gb:M14338 VITAMIN K-DEPENDENT PROTEIN S PRECURSOR (HUMAN);
6282	15463	24905	3.1	6.0E-84	BE810371.1	EST_HUMAN	PMO-LT0019-190800-004-F02 LT0019 Homo sapiens cDNA
6460	15687	26153	2.42	6.0E-84	BE770189.1	EST_HUMAN	PM4-FT0054-160800-004-e10 FT0054 Homo sapiens cDNA
8087	17202		2.15	6.0E-84	AW369812.1	EST_HUMAN	IL0-BT0168-091189-139-g06 BT0168 Homo sapiens cDNA
721	9863	19102	3.3	5.0E-84	AA382811.1	EST_HUMAN	EST86094 Testis I Homo sapiens cDNA 5' and
2976	12213		2.48	5.0E-84	AF109718.1	NT	Homo sapiens chromosome 3 subtelomeric region
8078	17213	26745	2.34	5.0E-84	11428740	NT	Homo sapiens regulatory factor X, 3 (influences HLA class II expression) (RFX3), mRNA
1415	10628	19795	3.31	4.0E-84	AI686321.1	EST_HUMAN	wa76c04.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2302086 3' similar to
4969	14156	23248	1.1	4.0E-84	4505928	NT	SW:NRDC_HUMAN O43847 NARDILYSIN PRECURSOR;
4970	14157	23249	1.59	4.0E-84	AF069601.2	NT	Homo sapiens polymerase (DNA-directed), alpha (70kD) (POLA2), mRNA
5775	14993	24393	2.02	4.0E-84	AF059650.1	NT	Homo sapiens myosin light chain kinase isoform 2 (MLCK) mRNA, complete cds
5355	15535	24989	14.25	4.0E-84	11421326	NT	Homo sapiens histone deacetylase 3 (HDAC3) gene, complete cds
7492	16699	26184	5.84	4.0E-84	AB032956.1	NT	Homo sapiens KIAA0783 gene product (KIAA0783), mRNA
321	9592	18723	1.54	3.0E-84	AF026200.1	NT	Homo sapiens KIAA0783 gene product (KIAA0783), mRNA
1030	11134	20326	1.3	3.0E-84	5453855	NT	Homo sapiens Bech1 protein homolog mRNA, partial cds
1975	11178	20386	2.89	3.0E-84	AL096880.1	NT	Homo sapiens pericentridar material 1 (PCM1) mRNA
3568	12791	21917	1.11	3.0E-84	AB026898.1	NT	Novel human mRNA containing Zinc finger C2H2 type domains
3730	12849	22067	5.34	3.0E-84	AF014459.1	NT	Homo sapiens DNA, DLEC1 to ORCTL4 gene region, section 1/2 (DLEC1, ORCTL3, ORCTL4 genes, complete cds)
7455	16663		11.6	3.0E-84	AI983801.1	EST_HUMAN	Homo sapiens X-linked juvenile retinoschisis precursor protein (XLR51) mRNA, complete cds
2075	11275	20491	7.28	2.0E-84	BE68397.1	EST_HUMAN	wu20405.x1 Soares_Dieckgraebe_colon_NHCD Homo sapiens cDNA clone IMAGE:2520585 3' similar to gb:L05093 80S RIBOSOMAL PROTEIN L18A (HUMAN);

Page 271 of 382  
Table 4  
Single Exon Probes Expressed in HELA Cells

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2076	11275	20492	7.28	2.0E-84	BE68597.1	EST_HUMAN	CM1-BT0795-190800-272-608 BT0795 Homo sapiens cDNA
2894	12132	21268	10.41	2.0E-84	AF036943.1	NT	Homo sapiens myelin transcription factor 1-like (MYT1L) mRNA, complete cds
2916	12154	21289	1.58	2.0E-84	X89211.1	NT	H. sapiens DNA for endogenous retroviral like element
8593	17595	24003	3.31	2.0E-84	BF448000.1	EST_HUMAN	nae30a02.x1 Lupski_sympathetic_trunk Homo sapiens cDNA clone IMAGE:4090251 3' similar to TR:Q8UGS3 Q8UGS3 DJ756G23.1 ;
8583	17595	24004	3.31	2.0E-84	BF448000.1	EST_HUMAN	nae30a02.x1 Lupski_sympathetic_trunk Homo sapiens cDNA clone IMAGE:4090251 3' similar to TR:Q8UGS3 Q8UGS3 DJ756G23.1 ;
317	9588	18719	1.58	1.0E-84	AF114488.1	NT	Homo sapiens tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, zeta polypeptide (YWHAZ) mRNA
556	9806	18831	12.69	1.0E-84	4507852	NT	Homo sapiens complement component 5 (C5), mRNA
727	9869		1.24	1.0E-84	11427631	NT	am85b11.s1 Stratiogene schizo brain S11 Homo sapiens cDNA clone IMAGE:1628885 3'
1300	10515	19872	2.6	1.0E-84	AA884379.1	EST_HUMAN	601308008F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3626257 5'
2021	11222	20430	2.87	1.0E-84	BE392137.1	EST_HUMAN	Homo sapiens pericentriolar material 1 (PCM1), mRNA
2190	11387	20609	2.2	1.0E-84	11427197	NT	nm12606.s1 NCI_CGAP_SS1 Homo sapiens cDNA clone IMAGE:1239106 3'
3732	12852	22089	3.02	1.0E-84	AA720851.1	EST_HUMAN	Homo sapiens 959 kb contig between AML1 and CBR1 on chromosome 21q22; segment 1/3
4410	13810	22707	5.57	1.0E-84	AJ228041.1	NT	DKFZp434N0323_r1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434N0323 5'
4710	13901	23000	3.61	1.0E-84	AL043314.2	EST_HUMAN	DKFZp434N0323_r1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434N0323 5'
4710	13901	23001	3.61	1.0E-84	AL043314.2	EST_HUMAN	DKFZp434N0323_r1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434N0323 5'
4833	13610	22707	3.37	1.0E-84	AJ228041.1	NT	Homo sapiens 959 kb contig between AML1 and CBR1 on chromosome 21q22; segment 1/3
6124	15308	24741	2.57	1.0E-84	AL049784.1	NT	Novel human gene mapping to chromosome 13
6334	15500	24945	2.39	1.0E-84	11430848	NT	Homo sapiens NGFI-A binding protein 1 (ERG1 binding protein 1) (NAB1), mRNA
6931	16124		4.77	1.0E-84	5031884	NT	Homo sapiens nuclear transport factor 2 (placental protein 15) (PP15) mRNA
7013	14492	23581	2.88	1.0E-84	4507848	NT	Homo sapiens ubiquitin specific protease 13 (isopeptidase T-3) (USP13) mRNA
7013	14492	23582	2.88	1.0E-84	4507848	NT	Homo sapiens ubiquitin specific protease 13 (isopeptidase T-3) (USP13) mRNA
8453	17511		2.18	1.0E-84	11417812	NT	Homo sapiens purinergic receptor P2X-like 1, orphan receptor (P2RXL1), mRNA
8573	17590	23999	4.24	1.0E-84	11418185	NT	Homo sapiens aconitase 2, mitochondrial (ACO2), mRNA
874	10206		1.55	9.0E-85	AL163209.2	NT	Homo sapiens chromosome 21 segment HS21O009
1080	10305	19455	2.99	9.0E-85	U51432.1	NT	Homo sapiens nuclear protein Skip mRNA, complete cds
1080	10305	19456	2.99	9.0E-85	U51432.1	NT	Homo sapiens nuclear protein Skip mRNA, complete cds
1557	10771	19943	8.68	9.0E-85	M33282.1	NT	Human plasminogen gene, exon 7
1557	10771	19944	8.68	9.0E-85	M33282.1	NT	Human plasminogen gene, exon 7
1649	10863	20045	2.34	9.0E-85	7657020	NT	Homo sapiens DKFZp434P211 protein (DKFZP434P211), mRNA
3785	13003	22118	1.05	9.0E-85	7018418	NT	Homo sapiens nucleolar GTPase (HUMALANTIG), mRNA
4298	13441	22533	1.04	9.0E-85	AL163280.2	NT	Homo sapiens chromosome 21 segment HS21C080

Page 272 of 382  
Table 4  
Single Exon Probes Expressed in HELA Cells

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4794	13983	23087	1.89	9.0E-85	M33784.1	NT	Human ornithine decarboxylase gene, complete cds
4794	13983	23088	1.89	9.0E-85	M33784.1	NT	Human ornithine decarboxylase gene, complete cds
4897	14085	23178	1.12	9.0E-85	5901879	NT	Homo sapiens heat shock transcription factor 2 binding protein (HSF2BP), mRNA
4834	14121	23216	1.2	9.0E-85	AL163268.2	NT	Homo sapiens chromosome 21 segment HS21C088
1144	10397	19518	10.12	7.0E-85	L05094.1	NT	Homo sapiens ribosomal protein L27 mRNA, complete cds
8156	17288		11.61	7.0E-85	AF113210.1	NT	Homo sapiens MSTP030 mRNA, complete cds
7854	17093	26823	3.24	9.0E-85	11438573	NT	Homo sapiens DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 10 (RNA helicase) (DDX10), mRNA
7954	17093	26824	3.24	9.0E-85	11438573	NT	Homo sapiens DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 10 (RNA helicase) (DDX10), mRNA
2301	11495	20715	5.3	5.0E-85	AL163284.2	NT	Homo sapiens chromosome 21 segment HS21C084
5419	14647	23780	2.28	5.0E-85	BF035674.1	EST_HUMAN	601458846F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3862402 5'
5419	14647	23781	2.28	5.0E-85	BF035674.1	EST_HUMAN	601458846F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3862402 5'
7879	16878	26384	2.18	5.0E-85	AF224669.1	NT	Homo sapiens mannosidase, beta A, lysosomal (MANBA) gene, and ubiquitin-conjugating enzyme E2D 3 (UBE2D3) genes, complete cds
9205	14497		3.22	6.0E-86	AF211189.1	NT	Homo sapiens T-type calcium channel alpha1 subunit Alpha1I-a isoform (CACNA1I) mRNA, complete cds
7220	16397		2.61	4.0E-85	BE079263.1	EST_HUMAN	RC1-BT0823-120200-011-007 BT0823 Homo sapiens cDNA
1308	10522	19681	0.77	3.0E-85	AF096157.1	NT	Homo sapiens protein phosphatase 2A BR gamma subunit gene, exon 6
1750	10962	20144	35.52	3.0E-85	T97495.1	EST_HUMAN	yec3g09.1 Soares fetal liver spleen 1NPLS Homo sapiens cDNA clone IMAGE:121504 5'
4305	13506	22602	1.15	3.0E-85	BE267189.1	EST_HUMAN	601189704F2 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3533616 5'
4920	14108	23203	1.43	3.0E-85	11024695	NT	Homo sapiens F-box only protein 24 (FBXO24), mRNA
4920	14108	23204	1.43	3.0E-85	11024695	NT	Homo sapiens F-box only protein 24 (FBXO24), mRNA
4987	14174	23264	1.03	3.0E-85	7363442	NT	Homo sapiens effector receptor, family 12, subfamily D, member 2 (OR12D2), mRNA
5727	14945	24341	5.2	3.0E-85	7662309	NT	Homo sapiens KIAA0793 gene product (KIAA0793), mRNA
5727	14945	24342	5.2	3.0E-85	7662309	NT	Homo sapiens KIAA0793 gene product (KIAA0793), mRNA
6065	15255		7.81	3.0E-86	AJ404483.1	NT	Homo sapiens mRNA for dynein heavy chain (DNAH9 gene)
6758	15953	25411	5.03	3.0E-85	11430889	NT	Homo sapiens phospholipase C, epsilon (PLCE), mRNA
8039	17175	26715	2.38	3.0E-85	5031660	NT	Homo sapiens EGF-like repeats and discoidin-like domains 3 (EDIL3), mRNA
9064	17910		3.81	3.0E-85	11418177	NT	Homo sapiens Ran GTPase activating protein 1 (RANGAP1), mRNA
970	10202	19358	0.64	2.0E-85	7657266	NT	Homo sapiens KIAA0929 protein Msc2 interacting nuclear target (MINT) homolog (KIAA0929), mRNA
1047	10273	19425	2.37	2.0E-85	AF248540.1	NT	Homo sapiens Intersectin 2 (SH3D1B) mRNA, complete cds
1408	10621	19785	1.02	2.0E-85	7702025	NT	Homo sapiens CGI-201 protein (LOC51340), mRNA

Page 273 of 382  
Table 4  
Single Exon Probes Expressed in HELA Cells

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1424	10637	19806	10.87	2.0E-85	5174775	NT	Homo sapiens apolipoprotein C-II (APOC2) mRNA
1424	10637	19807	10.87	2.0E-85	5174775	NT	Homo sapiens apolipoprotein C-II (APOC2) mRNA
2197	11394	20616	1.78	2.0E-85	U10525.1	NT	Human DNA polymerase beta gene, exons 12 and 13
2775	10560		7.76	2.0E-85	7657468	NT	Human sapiens similar to rat integral membrane glycoprotein POM121 (POM121L1), mRNA
2987	12224	21357	2.02	2.0E-85	M30838.1	NT	Human Ku (p70/p80) subunit mRNA, complete cds
4326	13527	22621	6.55	2.0E-85	4505880	NT	Homo sapiens plasminogen (PLG) mRNA
4932	14120	23215	1.04	2.0E-85	AL163284.2	NT	Homo sapiens chromosome 21 segment HS21C084
6845	16034	25498	2.59	2.0E-85	A1760820.1	EST_HUMAN	w167h08.x1 NCI_CGAP_K1d12 Homo sapiens cDNA clone IMAGE:2398431 3' similar to contains element
2251	11448		2.28	1.0E-85	BE794306.1	EST_HUMAN	MSR1 repetitive element;
2357	11550	20771	8.25	1.0E-85	BE818392.1	EST_HUMAN	601462817F1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3866021 5'
2357	11550	20772	8.25	1.0E-85	BE818392.1	EST_HUMAN	601462817F1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3866021 5'
7009	16187	25661	3.36	1.0E-85	BE257917.1	EST_HUMAN	601109738F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3350553 5'
7498	16705	26190	2.91	1.0E-85	AA778785.1	EST_HUMAN	Z45f03.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:453245 3'
7498	16705	26191	2.91	1.0E-85	AA778785.1	EST_HUMAN	Z45f03.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:453245 3'
7568	16773	26265	2.74	1.0E-85	BF311552.1	EST_HUMAN	601897003F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4126440 5'
7568	16773	26266	2.74	1.0E-85	BF311552.1	EST_HUMAN	601897003F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4126440 5'
7631	16832	26329	2.84	1.0E-85	Y00052.1	NT	Human mRNA for T-cell cyclophilin
8458	17679	23951	3.47	1.0E-85	11417862	NT	Homo sapiens calcineurin binding protein 1 (KIAA0330), mRNA
8730	17679	23951	4.77	1.0E-85	11417862	NT	Homo sapiens calcineurin binding protein 1 (KIAA0330), mRNA
1432	10645		36.13	9.0E-86	BE274217.1	EST_HUMAN	601120778F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:2967860 5'
5722	14940	24336	2.69	8.0E-86	11424140	NT	Homo sapiens similar to CDC28 protein kinase 1 (H. sapiens) (LOC63041), mRNA
945	10178	19332	1.29	7.0E-86	AA860801.1	EST_HUMAN	aj88f08.s1 Soares_parathyroid_tumor_NbHPA Homo sapiens cDNA clone IMAGE:1403559 3'
945	10178	19333	1.29	7.0E-86	AA860801.1	EST_HUMAN	aj88f08.s1 Soares_parathyroid_tumor_NbHPA Homo sapiens cDNA clone IMAGE:1403559 3'
6076	14522	23565	6.39	7.0E-86	11421737	NT	Homo sapiens Tax1 (human T-cell leukemia virus type I) binding protein 1 (TAX1BP1), mRNA
6698	15893	25354	3.63	7.0E-86	L38557.1	NT	Homo sapiens galactose oxidase (GALC) gene, exon 15
7533	16738	26228	2.69	7.0E-86	11417012	NT	Homo sapiens similar to transcription factor CA150 (H. sapiens) (LOC63170), mRNA
7533	16738	26229	2.69	7.0E-86	11417012	NT	Homo sapiens similar to transcription factor CA150 (H. sapiens) (LOC63170), mRNA
1301	10516	18673	3.14	6.0E-86	4505492	NT	Homo sapiens coagulate dehydrogenase (liponamide) (OGDH) mRNA
216	9495	18629	1.96	4.0E-86	BE547173.1	EST_HUMAN	601072594F1 NIH_MGC_12 Homo sapiens cDNA clone IMAGE:3458830 5'
5675	14895	24287	11.54	4.0E-86	BE295943.1	EST_HUMAN	601176885F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3531853 5'
7783	9495	18629	1.88	4.0E-86	BE547173.1	EST_HUMAN	601072594F1 NIH_MGC_12 Homo sapiens cDNA clone IMAGE:3458830 5'
4276	13479	22577	1.06	3.0E-86	BE867703.1	EST_HUMAN	601443262F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3847455 5'
5487	14713	24070	7.08	3.0E-86	AW340846.1	EST_HUMAN	x282h12.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:2871719 3'

Page 274 of 382  
Table 4  
Single Exon Probes Expressed in HELA Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7141	16318	25800	2.86	3.0E-86	BE886478.1	EST_HUMAN	601509868F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3911303 5'
7141	16318	25801	2.86	3.0E-86	BE886479.1	EST_HUMAN	601509868F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3911303 5'
7073	16408	25883	10.4	3.0E-86	AI659240.1	EST_HUMAN	U18602.x1 NCI_CGAP_P128 Homo sapiens cDNA clone IMAGE:2251371 3'
8427	18171		2.01	3.0E-86	BE410354.1	EST_HUMAN	601302333F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3636753 5'
271	8546	18875	2.25	2.0E-86	AA306264.1	EST_HUMAN	EST177232 Jurkat T-cells VI Homo sapiens cDNA 5' end
420	9673		2.72	2.0E-86	AL163203.2	NT	Homo sapiens chromosome 21 segment HS21C003
1198	10418	19571	2.57	2.0E-86	N58977.1	EST_HUMAN	yz19a08.r1 Scores_multiple_sclerosis_2NbHMSP Homo sapiens cDNA clone IMAGE:283478 5'
2158	11356	20574	18.73	2.0E-86	9835487	NT	Human endogenous retrovirus, complete genome
3363	12620	21751	1.49	2.0E-86	AW968142.1	EST_HUMAN	EST178215 MAGI Homo sapiens cDNA
3727	12946	22063	3.14	2.0E-86	AF156776.1	NT	Homo sapiens lysophosphatidic acid acyltransferase-delta (LPAAT-delta) mRNA, complete cds
3727	12946	22064	3.14	2.0E-86	AF156776.1	NT	Homo sapiens lysophosphatidic acid acyltransferase-delta (LPAAT-delta) mRNA, complete cds
4017	13228		2.83	2.0E-86	AW515742.1	EST_HUMAN	U687g08.x1 NCI_CGAP_GC8 Homo sapiens cDNA clone IMAGE:2816542 3'
4799	13088	23096	4.21	2.0E-86	AF056490.1	NT	Homo sapiens cAMP-specific phosphodiesterase 8A (PDE8A) mRNA, partial cds
5083	14273	23356	0.94	2.0E-86	4505778	NT	Homo sapiens phosphatase kinase, alpha 1 (muscle) (PHKA1), mRNA
6646	15841	25301	3.57	2.0E-86	11437135	NT	Homo sapiens butyrobetaine (gamma), 2-oxoglutarate dioxygenase (gamma-butyrobetaine hydroxylase) (BBOX), mRNA
6646	15841	25302	3.57	2.0E-86	11437135	NT	Homo sapiens butyrobetaine (gamma), 2-oxoglutarate dioxygenase (gamma-butyrobetaine hydroxylase) (BBOX), mRNA
7196	16373	25854	3.67	2.0E-86	11545846	NT	Homo sapiens basic-helix-loop-helix-PAS protein (NPAS3), mRNA
7196	16373	25855	3.67	2.0E-86	11545846	NT	Homo sapiens basic-helix-loop-helix-PAS protein (NPAS3), mRNA
7479	16687	26169	1.82	2.0E-86	4758051	NT	Homo sapiens ribosomal protein S6 kinase, 60kD, polypeptide 5 (RPS6KA5) mRNA
8900	17793	23924	4.33	2.0E-86	11418189	NT	Homo sapiens thyroid autoantigen 70kD (Ku antigen) (G22P1), mRNA
9077	17902		2.64	2.0E-86	AB011399.1	NT	Homo sapiens gene for AF-6, complete cds
1577	10790	19868	2.82	1.0E-86	4828855	NT	Homo sapiens NADH dehydrogenase (ubiquinone) Fe-S protein 1 (75kD) (NADH-coenzyme Q reductase) (NDUFS1) mRNA
3126	12361	21490	1.41	1.0E-86	5453649	NT	Homo sapiens fibulin 5 (FBLN5) mRNA
3201	12436	21571	2.53	1.0E-86	L20492.1	NT	Human gamma-glutamyl transpeptidase mRNA, complete cds
3265	12498	21628	1.13	1.0E-86	AL163209.2	NT	Homo sapiens chromosome 21 segment HS21C009
3265	12498	21629	1.13	1.0E-86	AL163209.2	NT	Homo sapiens chromosome 21 segment HS21C009
3921	13137	22255	0.97	1.0E-86	7706161	NT	Homo sapiens hypothetical protein (LOC51318), mRNA
3921	13137	22256	0.97	1.0E-86	7706161	NT	Homo sapiens hypothetical protein (LOC51318), mRNA
4251	13454	22546	6.26	1.0E-86	AL163300.2	NT	Homo sapiens chromosome 21 segment HS21C100
4823	13817	22807	0.82	1.0E-86	4507334	NT	Homo sapiens synaptobrevin 1 (SYNJ1), mRNA
4937	14124	23219	1.42	1.0E-86	AF100781.1	NT	Homo sapiens FK506-binding protein FKBP23 isoform mRNA, complete cds

Table 4

## Single Exon Probes Expressed in HELA Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5468	14694	24047	3.81	1.0E-98	AL163284.2	NT	Homo sapiens chromosome 21 segment HS21C084
8132	14694	24047	2.91	1.0E-98	AL163284.2	NT	Homo sapiens chromosome 21 segment HS21C084
5370	14600		1.74	9.0E-87	AI150703.1	EST_HUMAN	qb77c09.x1 Soares_fetal_heart_NBHH18W Homo sapiens cDNA clone IMAGE:1706128 3' similar to SW:K1CJ_MOUSE P02535 KERA1N, TYPE I CYTOSKELETAL 10;
6272	15452	24891	2.05	9.0E-87	4757721	NT	Homo sapiens a disintegrin and metalloproteinase domain 22 (ADAM22), mRNA
6272	15452	24892	2.05	9.0E-87	4757721	NT	Homo sapiens a disintegrin and metalloproteinase domain 22 (ADAM22), mRNA
486	9738	19871	78.74	8.0E-87	X62245.1	NT	O cuticulus mRNA for elongation factor 1 alpha
2258	11453	20871	2.01	7.0E-87	BF08321.1	EST_HUMAN	7h85f02.x1 NCI_CGAP_C016 Homo sapiens cDNA clone IMAGE:3322779 3'
2258	11453	20872	2.01	7.0E-87	BF08321.1	EST_HUMAN	7h85f02.x1 NCI_CGAP_C016 Homo sapiens cDNA clone IMAGE:3322779 3'
7098	16273	25750	3.8	7.0E-87	AL043314.2	EST_HUMAN	DKFZp434N0323_r1 434 (synonym: hbs3) Homo sapiens cDNA clone DKFZp434N0323 5'
7098	16273	25751	3.8	7.0E-87	AL043314.2	EST_HUMAN	DKFZp434N0323_r1 434 (synonym: hbs3) Homo sapiens cDNA clone DKFZp434N0323 5'
7466	16674	26168	11.33	7.0E-87	K03002.1	NT	Human mRNA from chromosome 15 gene with homology to MHC-HLA-SB-1 intron A
7468	16674	26157	11.33	7.0E-87	K03002.1	NT	Human mRNA from chromosome 15 gene with homology to MHC-HLA-SB-1 intron A
3500	12724	21860	0.67	6.0E-87	7657213	NT	Homo sapiens hormonally upregulated neu tumor-associated kinase (HUNK), mRNA
7312	16530					NT	Homo sapiens similar to SET translocation (myeloid leukemia-associated) (H. sapiens) (LOC63102), mRNA
1166	10388	19539	6.71	5.0E-87	AA38281.1	EST_HUMAN	EST86094 Testis   Homo sapiens cDNA 5' end
8732	10388	19539	2.59	5.0E-87	AA38281.1	EST_HUMAN	EST86094 Testis   Homo sapiens cDNA 5' end
973	10205	19360	1.04	4.0E-87	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C010
1180	10401	19554	18.34	4.0E-87	AB037835.1	NT	Homo sapiens mRNA for KIAA1414 protein, partial cds
1989	11202	20413	2.08	4.0E-87	AB007925.1	NT	Homo sapiens mRNA for KIAA0456 protein, partial cds
2049	11250	20461	0.99	4.0E-87	R78133.1	EST_HUMAN	y80f10.r1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:145579 5' similar to contains Alu repetitive element;
2049	11250	20462	0.99	4.0E-87	R78133.1	EST_HUMAN	y80f10.r1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:145579 5' similar to contains Alu repetitive element;
2386	11579	20795	1.87	4.0E-87	7706289	NT	Homo sapiens CGI-60 protein (LOC51626), mRNA
2386	11579	20786	1.87	4.0E-87	7706289	NT	Homo sapiens CGI-60 protein (LOC51626), mRNA
3441	12686	21800	1.43	4.0E-87		NT	Homo sapiens myeloid/lymphoid or mixed-lineage leukemia (trithorax (Drosophila) homolog), translocated to, 4 (MLLT4) mRNA
5416	14844	23776	6.4	4.0E-87	O00321	SWISSPROT	ETS-RELATED PROTEIN 71 (ETS TRANSLLOCATION VARIANT 2)
5685	14905	24298	4.8	4.0E-87	BE247284.1	EST_HUMAN	TCBAP1E4051 Pediatric pre-B cell acute lymphoblastic leukemia Baylor-HGSC project=TCBA Homo sapiens cDNA clone TCBAP4051
7724	16923	26432	3.91	4.0E-87	M60876.1	NT	Human von Willebrand factor pseudogene corresponding to exons 23 through 34
8258	17385	26918	3.1	4.0E-87	11417339	NT	Homo sapiens similar to heat shock 70kD protein 9B (mortalin-2) (H. sapiens) (LOC63184), mRNA



Table 4

## Single Exon Probes Expressed in HELA Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8831	18223	23695	1.46	4.0E-87	11417862	NT	Homo sapiens calcineurin binding protein 1 (KIAA0330), mRNA
8831	18223	23696	1.46	4.0E-87	11417862	NT	Homo sapiens calcineurin binding protein 1 (KIAA0330), mRNA
8994	17855		21.93	4.0E-87	11417812	NT	Homo sapiens purinergic receptor P2X-like 1, orphan receptor (P2RXL1), mRNA
2731	11910	21124	5.33	2.0E-87	4885420	NT	Homo sapiens high-mobility group (nonhistone chromosome) protein 4 (HMG4), mRNA
2800	12138		1.12	2.0E-87	BF327820.1	EST_HUMAN	QV0-BN0148-050600-254-a03 BN0148 Homo sapiens cDNA
3767	12985	22101	0.7	2.0E-87	AU118935.1	EST_HUMAN	AU118935 HEMBA1 Homo sapiens cDNA clone HEMBA1000307 5'
5517	14742	24108	10.95	2.0E-87	BE734190.1	EST_HUMAN	601569041F1 NIH_MGC 21 Homo sapiens cDNA clone IMAGE:3843730 5'
5517	14742	24109	10.95	2.0E-87	BE734190.1	EST_HUMAN	601569041F1 NIH_MGC 21 Homo sapiens cDNA clone IMAGE:3843730 5'
5800	15017		5.29	2.0E-87	BE567193.1	EST_HUMAN	601341383F1 NIH_MGC 53 Homo sapiens cDNA clone IMAGE:3883348 5'
6276	15456	24897	30.73	2.0E-87	N48128.1	EST_HUMAN	W21e07.11 Soares fetal liver spleen TNF1LS Homo sapiens cDNA clone IMAGE:2433398 5'
6370	15550	25006	34.06	2.0E-87	N48128.1	EST_HUMAN	W21e07.11 Soares fetal liver spleen TNF1LS Homo sapiens cDNA clone IMAGE:2433398 5'
6598	15794	25252	14.69	2.0E-87	X52851.1	NT	Human cyclophilin gene for cyclophilin (EC 5.2.1.8)
1190	11945		2.22	1.0E-87	7705683	NT	Homo sapiens putative glycolipid transfer protein (LOC51054), mRNA
1434	10647	19819	2.01	1.0E-87	AW361977.1	EST_HUMAN	PM2-CT0265-141099-001-g04 CT0265 Homo sapiens cDNA
1434	10647	19820	2.01	1.0E-87	AW361977.1	EST_HUMAN	PM2-CT0265-141099-001-g04 CT0265 Homo sapiens cDNA
3680	12911	22030	16.53	1.0E-87	Y00052.1	NT	Human mRNA for T-cell cyclophilin
3714	12934	22052	2.67	1.0E-87	4758827	NT	Homo sapiens neuroxin III (NRXN3), mRNA
5762	14981	24379	2	1.0E-87	AF073371.1	NT	Homo sapiens growth factor receptor-bound protein 10 (GRB10) gene, exon 8
5762	14981	24380	2	1.0E-87	AF073371.1	NT	Homo sapiens growth factor receptor-bound protein 10 (GRB10) gene, exon 8
6498	15696	25160	12.4	1.0E-87	AF214562.1	NT	Homo sapiens tracheal epithelium enriched protein (PLUNC) gene, complete cds
6874	16152	25623	2.81	1.0E-87	BE818183.1	EST_HUMAN	RC6-BN0276-050700-012-E02 BN0276 Homo sapiens cDNA
6974	16152	25624	2.81	1.0E-87	BE818183.1	EST_HUMAN	RC6-BN0276-050700-012-E02 BN0276 Homo sapiens cDNA
7570	16775		1.86	1.0E-87	D10083.1	NT	Homo sapiens RGH1 gene, retrovirus-like element
7608	16811	26306	1.86	1.0E-87	5031660	NT	Homo sapiens EGF-like repeats and discoidin-like domains 3 (EDIL3), mRNA
7608	16811	26307	1.86	1.0E-87	5031660	NT	Homo sapiens EGF-like repeats and discoidin-like domains 3 (EDIL3), mRNA
8827	18371		1.67	1.0E-87	7657632	NT	Homo sapiens sulfotransferase-related protein (SULTX3), mRNA
1114	10338	19489	7.21	9.0E-88	AF167465.1	NT	Homo sapiens double stranded RNA activated protein kinase (PKR) gene, exon 12
1357	10572	19737	2.4	9.0E-88	AB037620.1	NT	Homo sapiens mRNA for KIAA1399 protein, partial cds
1357	10572	19738	2.4	9.0E-88	AB037620.1	NT	Homo sapiens mRNA for KIAA1399 protein, partial cds
2091	11291	20503	2.43	9.0E-88	AB037620.1	NT	Homo sapiens DKFZP586P1522 protein (DKFZP586P1522), mRNA
3608	12827	21947	1.22	9.0E-88	AL163209.2	NT	Homo sapiens chromosome 21 segment HS21C009
4255	13458	22550	3.4	9.0E-88	X91929.1	NT	H. sapiens ECE-1 gene (exon 9)
4255	13458	22551	3.4	9.0E-88	X91929.1	NT	H. sapiens ECE-1 gene (exon 9)

Table 4

## Single Exon Probes Expressed in HELA Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5028	14213	23287	1.01	9.0E-88	AB026888.1	NT	Homo sapiens DNA, DLEC1 to ORCTL4 gene region, section 1/2 (DLEC1, ORCTL3, ORCTL4 genes, complete cds)
1786	11005		3.42	5.0E-88	7661887	NT	Homo sapiens KIAA00063 gene product (KIAA00063), mRNA
2603	11787	21008	6.14	5.0E-88	N89399.1	EST_HUMAN	K9719F Human fetal heart, Lambda ZAP Express Homo sapiens cDNA clone K9719 5' similar to ZINC FINGER PROTEIN HZF1
2858	12186	21330	0.76	5.0E-88	AF114488.1	NT	Homo sapiens Intersectin short isoform (ITSN), complete cds
2872	12209	21348	1.02	5.0E-88	AF114488.1	NT	Homo sapiens Intersectin short isoform (ITSN), complete cds
2872	12209	21347	1.02	5.0E-88	AF114488.1	NT	Homo sapiens Intersectin short isoform (ITSN), complete cds
3367	12595		2.76	5.0E-88	AI693217.1	EST_HUMAN	wd88h08.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:2336799 3' similar to contains Alu repetitive element; contains element MER22 MER22 repetitive element ;
3509	12733	21871	0.96	5.0E-88	AF114488.1	NT	Homo sapiens Intersectin short isoform (ITSN), complete cds
4748	13839	23043	0.74	5.0E-88	AF114488.1	NT	Homo sapiens Intersectin short isoform (ITSN), complete cds
5987	15269	24696	2.41	5.0E-88	H10932.1	EST_HUMAN	ym06b10.r1 Soares infant brain 1N1B Homo sapiens cDNA clone IMAGE:47129 5'
8572	11005		1.59	5.0E-88	7661887	NT	Homo sapiens KIAA00063 gene product (KIAA00063), mRNA
9214	11005		1.4	5.0E-88	7661887	NT	Homo sapiens KIAA00063 gene product (KIAA00063), mRNA
1337	10552	19717	1.15	4.0E-88	BF091229.1	EST_HUMAN	PM1-TN0028-050900-004-f10 TN0028 Homo sapiens cDNA
1337	10552	19718	1.15	4.0E-88	BF091229.1	EST_HUMAN	PM1-TN0028-050900-004-f10 TN0028 Homo sapiens cDNA
6181	15363	24803	1.71	4.0E-88	11416585	NT	Homo sapiens transforming growth factor, beta-induced, 68kD (TGFB1), mRNA
7484	16691	26174	1.8	4.0E-88	4502694	NT	Homo sapiens cell division cycle 10 (homologous to CDC10 of S. cerevisiae) (CDC10), mRNA
8023	17160	26696	2.52	4.0E-88	7661947	NT	Homo sapiens KIAA0152 gene product (KIAA0152), mRNA
8023	17160	26697	2.52	4.0E-88	7661947	NT	Homo sapiens KIAA0152 gene product (KIAA0152), mRNA
739	9880	18121	0.91	3.0E-88	11545800	NT	Homo sapiens hypothetical protein FLJ21634 (FLJ21634), mRNA
1781	10991		2.73	3.0E-88	4508020	NT	Homo sapiens zinc finger protein 259 (ZNF259) mRNA
2899	12137	21275	6.07	3.0E-88	N6951.1	EST_HUMAN	z848f12.s1 Soares fetal liver spleen 1N1FLS Homo sapiens cDNA clone IMAGE:285823 3'
4226	13428	22520	0.91	3.0E-88	4501912	NT	Homo sapiens a disintegrin and metalloproteinase domain 23 (ADAM23) mRNA
4226	13428	22521	0.91	3.0E-88	4501912	NT	Homo sapiens a disintegrin and metalloproteinase domain 23 (ADAM23) mRNA
4474	13672		4.18	3.0E-88	11428300	NT	Homo sapiens hypothetical protein FLJ20220 (FLJ20220), mRNA
5328	14560	23632	2.81	3.0E-88	11428567	NT	Homo sapiens velsin-containing protein (VCP), mRNA
5483	14709	24065	3.48	3.0E-88	9958888	NT	Homo sapiens polycythemia rubra vera 1; cell surface receptor (PRV1), mRNA
5538	14782	24129	3.92	3.0E-88	11420697	NT	Homo sapiens v-r1 simian leukemia viral oncogene homolog A (res related) (RALA), mRNA
6111	15205	24624	14.23	3.0E-88	AF279265.1	NT	Homo sapiens putative anion transporter 1 mRNA, complete cds
6308	15489	24934	6.98	3.0E-88	11438400	NT	Homo sapiens retinoblastoma-binding protein 2 (RBBP2), mRNA
8432	15628	25094	15.11	3.0E-88	11421726	NT	Homo sapiens growth differentiation factor 5 (cartilage-derived morphogenetic protein-1) (GDF5), mRNA

Page 278 of 382  
Table 4  
Single Exon Probes Expressed in HELA Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8558	17580		3.87	3.0E-98	11417874	NT	Homo sapiens transcobalamin II; macrocytic anemia (TCN2), mRNA
1043	10269	19419	1.37	2.0E-98	7305198	NT	Homo sapiens Calsenilin, presenilin-binding protein, EF hand transcription factor (CSEN), mRNA
1601	10815	19991	1.96	2.0E-98	AF246219.1	NT	Homo sapiens SNARE protein kinase SNAK mRNA, complete cds
1722	10834	20117	5.7	2.0E-98	AF246219.1	NT	Homo sapiens SNARE protein kinase SNAK mRNA, complete cds
4417	13617	22713	2.06	2.0E-98	5031666	NT	Homo sapiens dynein, axonemal, light polypeptide 4 (DNAL4), mRNA
5621	14844	24223	5.34	1.0E-98	AW139565.1	EST_HUMAN	U1H-B11-aaa-d-04-0-U1.s1 NCI_CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2718750 3'
5621	14844	24224	5.34	1.0E-98	AW139565.1	EST_HUMAN	U1H-B11-aaa-d-04-0-U1.s1 NCI_CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2718750 3'
5953	15169	24582	23.77	1.0E-98	AB007877.1	NT	Homo sapiens KIAA0417 mRNA, complete cds
5953	15169	24583	23.77	1.0E-98	AB007877.1	NT	Homo sapiens KIAA0417 mRNA, complete cds
6158	16341	24778	4.02	1.0E-98	AA488981.1	EST_HUMAN	aa54a11.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:824732 3' similar to WP:B0272.2
6950	16128	25596	2.94	1.0E-98	AL043314.2	EST_HUMAN	CE00851;
7981	16416	25903	3.87	1.0E-98	AA891479.1	EST_HUMAN	DKFZp434N0323_r1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434N0323 5'
8780	17717		5.85	1.0E-98	AL163246.2	NT	os91g03.s1 NCI_CGAP_GC3 Homo sapiens cDNA clone IMAGE:1612756 3' similar to gb:M16342
7525	16730	28220	8.72	9.0E-99	11421238	NT	Heterogeneous nuclear ribonucleoproteins C1/C2 (HUMAN);
2692	11872	21087	0.96	8.0E-99	BE311557.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C046
439	9693	18831	1.05	7.0E-99	7657213	NT	Homo sapiens transgelin 2 (TAGLN2), mRNA
439	9693	18832	1.05	7.0E-99	7657213	NT	Homo sapiens transgelin 2 (TAGLN2), mRNA
4904	14092	23185	2.94	7.0E-99	4557390	NT	601142409F1 NIH_MGC_14 Homo sapiens cDNA clone IMAGE:3508186 5'
4951	14138	23232	6.21	7.0E-99	AL045748.1	EST_HUMAN	Homo sapiens hormonally upregulated neu tumor-associated kinase (HUNK), mRNA
7791	16985	26500	2.86	7.0E-99	M59783.1	NT	Homo sapiens complement component 8, beta polypeptide (C8B) mRNA
9240	18011		1.76	7.0E-99	U87927.1	NT	DKFZp434E246_r1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434E246 5'
1030	10258	19407	1.83	6.0E-99	5803114	NT	Human aldose reductase (AR) gene, segment 2
2180	11377	20599	4.97	6.0E-99	4506124	NT	Homo aconitase hydratase (ACO2) gene, exon 2
2397	11590	20807	7.83	6.0E-99	4507788	NT	Homo sapiens inner membrane protein, mitochondrial (mitofilin) (IMMT), mRNA
2397	11590	20808	7.83	6.0E-99	4507788	NT	Homo sapiens serine/threonine-protein kinase PRP4 homolog (PRP4) mRNA
3498	12722	21858	0.95	6.0E-99	7661817	NT	Homo sapiens ubiquitin-conjugating enzyme E2L 3 (UBE2L3) mRNA
4478	13676	22765	1.37	6.0E-99	7661737	NT	Homo sapiens ubiquitin-conjugating enzyme E2L 3 (UBE2L3) mRNA
4638	13633	22921	3.22	6.0E-99	AB007866.2	NT	Homo sapiens HSPC019 protein (HSPC019), mRNA
4639	13633	22922	3.22	6.0E-99	AB007866.2	NT	Homo sapiens HSPC019 protein (HSPC019), mRNA
5214	14389	23474	1.53	6.0E-99	6806918	NT	Homo sapiens mRNA for KIAA0408 protein, partial cds
5214	14389	23475	1.53	6.0E-99	6806918	NT	Homo sapiens low density lipoprotein-related protein 2 (LRP2), mRNA
5214	14389	23475	1.53	6.0E-99	6806918	NT	Homo sapiens low density lipoprotein-related protein 2 (LRP2), mRNA

Page 279 of 382  
Table 4  
Single Exon Probes Expressed in HELA Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5105	14285	23369	2.93	5.0E-99	BE244323.1	EST_HUMAN	TCBAP2E0383 Pediatric pre-B cell acute lymphoblastic leukemia Baylor-HGSC project=TCBA Homo sapiens cDNA clone TCBAP0383
5105	14285	23370	2.93	5.0E-99	BE244323.1	EST_HUMAN	TCBAP2E0383 Pediatric pre-B cell acute lymphoblastic leukemia Baylor-HGSC project=TCBA Homo sapiens cDNA clone TCBAP0383
7700	18899	28408	1.84	4.0E-98	AI799872.1	EST_HUMAN	we9Tc03.x1 Scores_NFL_T_GBC S1 Homo sapiens cDNA clone IMAGE:2348452 3'
2830	12069	21191	2.07	3.0E-99	AW976181.1	EST_HUMAN	EST388280 MAGE resequences, MAGN Homo sapiens cDNA
8985	17849	23986	2.42	3.0E-99	AV705749.1	EST_HUMAN	AV705749 ADB Homo sapiens cDNA clone ADBBGA01 5'
125	9687	18807	1.11	2.0E-99	7706670	NT	Homo sapiens PXR2b protein (PXR2b), mRNA
125	9687	18808	1.11	2.0E-99	7706670	NT	Homo sapiens PXR2b protein (PXR2b), mRNA
414	9687	18807	0.69	2.0E-99	7706670	NT	Homo sapiens PXR2b protein (PXR2b), mRNA
414	9687	18808	0.69	2.0E-99	7706670	NT	Homo sapiens PXR2b protein (PXR2b), mRNA
536	9787	18910	0.78	2.0E-99	AB037763.1	NT	Homo sapiens mRNA for KIAA1342 protein, partial cds
2834	12073	21195	1.58	2.0E-99	AI222095.1	EST_HUMAN	qg96c08.x1 Scores_NFL_T_GBC S1 Homo sapiens cDNA clone IMAGE:1843022 3' similar to gb:J04131 GAMMA-GLUTAMYLTRANSFERASE 1 PRECURSOR (HUMAN); contains Alu repetitive element
3527	12751	21883	0.64	2.0E-99	AA759149.1	EST_HUMAN	sh70e03.s1 Scores_testis NHT Homo sapiens cDNA clone 1320988 3'
3527	12751	21884	0.64	2.0E-99	AA759149.1	EST_HUMAN	sh70e03.s1 Scores_testis NHT Homo sapiens cDNA clone 1320988 3'
4127	13333	22431	1.26	2.0E-99	AF089897.1	NT	Homo sapiens topoisomerase-related function protein (TRF4-2) mRNA, partial cds
4135	13341	22441	5.58	2.0E-99	X58742.1	NT	H.sapiens HCK gene for tyrosine kinase (PTK), exons 10-11
4135	13341	22442	5.58	2.0E-99	X58742.1	NT	H.sapiens HCK gene for tyrosine kinase (PTK), exons 10-11
4342	13544	22635	1.7	2.0E-99	AL163203.2	NT	Homo sapiens chromosome 21 segment HS21C003
4500	13688	22782	1.06	2.0E-99	AJ007378.1	NT	Homo sapiens GGT gene, exon 5
5040	14224	23308	0.95	2.0E-99	AJ007378.1	NT	Homo sapiens GGT gene, exon 5
5361	14591	23798	56	2.0E-99	BE541744.1	EST_HUMAN	Homo sapiens melanoma differentiation associated protein-5 (MDA5), mRNA
5432	14659	23798	2.85	2.0E-99	AB007546.1	NT	601065998F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3452423 5'
6364	15544	24999	4.77	2.0E-99	U81004.1	NT	Homo sapiens gene for LECT2, complete cds
6436	15633	25098	2.36	2.0E-99	11428801	NT	Human GT24 (GT24) mRNA, partial cds
7913	17128	26658	3.35	2.0E-99	11434411	NT	Homo sapiens solute carrier family 24 (sodium/potassium/calcium exchanger), member 2 (SLC24A2), mRNA
8104	17238	26776	5.65	2.0E-99	11433673	NT	Homo sapiens integrin, alpha 3 (antigen CD49C, alpha 3 subunit of VLA-3 receptor) (ITGA3), mRNA
8208	17339	26879	2.84	2.0E-99	U10682.1	NT	Homo sapiens cell adhesion molecule with homology to L1 CAM (close homologue of L1) (CHL1), mRNA
8259	17388		2.22	2.0E-99	11417260	NT	Human MAGE-7 antigen (MAGE7) pseudogene, complete cds
							Homo sapiens threonyl-tRNA synthetase (TARS), mRNA

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Single Exon Probes Expressed in HELA Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8107	17241	28780	6.09	1.0E-89	BF196052.1	EST_HUMAN	h81d09.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:3134897 3' similar to TR:O54778 O54778 SOLUTE CARRIER FAMILY 22 -LIKE 2 PROTEIN;
8107	17241	28781	6.09	1.0E-89	BF196052.1	EST_HUMAN	h81d09.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:3134897 3' similar to TR:O54778 O54778 SOLUTE CARRIER FAMILY 22 -LIKE 2 PROTEIN;
1070	10296	19445	2.31	8.0E-90	AL163246.2	NT	Homo sapiens chromosome 21 segment HS21C046
1071	10296	19445	2.97	8.0E-90	AL163246.2	NT	Homo sapiens chromosome 21 segment HS21C046
1338	11991	19719	3.38	8.0E-90	BE670561.1	EST_HUMAN	7e36f08.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3284583 3'
1338	11991	19720	3.38	8.0E-90	BE670561.1	EST_HUMAN	7e36f08.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3284583 3'
846	10083		2.87	7.0E-90	AF223391.1	NT	Homo sapiens cadmium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced
3032	12688	21395	1.22	6.0E-90	X91926.1	NT	H. sapiens ECE-1 gene (exon 6)
3032	12688	21398	1.22	6.0E-90	X91926.1	NT	H. sapiens ECE-1 gene (exon 6)
4212	13415	22510	8.66	6.0E-90	8922398	NT	Homo sapiens hypothetical protein FLJ10388 (FLJ10388), mRNA
4212	13415	22511	8.66	6.0E-90	8922398	NT	Homo sapiens hypothetical protein FLJ10388 (FLJ10388), mRNA
5847	14870	24256	3.59	6.0E-90	U77700.1	NT	Homo sapiens HsGON1 mRNA, partial cds
5847	14870	24257	3.59	6.0E-90	U77700.1	NT	Homo sapiens HsGON1 mRNA, partial cds
6570	15768	25227	6.84	6.0E-90	4504784	NT	Homo sapiens inositol 1,4,5-trisphosphate receptor, type 3 (ITPR3) mRNA
6570	15768	25228	6.84	6.0E-90	4504784	NT	Homo sapiens inositol 1,4,5-trisphosphate receptor, type 3 (ITPR3) mRNA
158	8440		24.41	5.0E-90	AB035344.1	NT	Homo sapiens TCEB gene, exon 1-10b
1200	10420	19573	1.75	5.0E-90	U80226.1	NT	Human gamma-aminobutyric acid transaminase mRNA, partial cds
2521	11709	20925	1.83	5.0E-90	AF114487.1	NT	Homo sapiens intersecin long isoform (ITSN) mRNA, complete cds
4537	13732	22830	2.47	5.0E-90	4506354	NT	Homo sapiens pregnancy-zone protein (PZP) mRNA
4612	13808	22897	1.1	5.0E-90	AA705222.1	EST_HUMAN	282g10.s1 Soares_fetal_liver_spleen_INFLS_S1 Homo sapiens cDNA clone IMAGE:461442 3'
4612	13808	22898	1.1	5.0E-90	AA705222.1	EST_HUMAN	282g10.s1 Soares_fetal_liver_spleen_INFLS_S1 Homo sapiens cDNA clone IMAGE:461442 3'
5486	14712	24069	3.24	5.0E-90	Z16411.1	NT	H. sapiens mRNA encoding phospholipase c
5558	14712	24069	2.51	5.0E-90	Z16411.1	NT	H. sapiens mRNA encoding phospholipase c
6171	15353	24791	2.22	5.0E-90	AF113708.1	NT	Homo sapiens angiotensin 4 (ANG4) mRNA, partial cds
6171	15353	24792	2.22	5.0E-90	AF113708.1	NT	Homo sapiens angiotensin 4 (ANG4) mRNA, partial cds
6318	15489	24844	7.67	5.0E-90	4557258	NT	Homo sapiens adenylate cyclase 9 (ADCY9) mRNA
6557	15753	25216	4.76	5.0E-90	11345483	NT	Homo sapiens hypothetical protein FLJ13222 (FLJ13222), mRNA
7195	16372	25853	4.96	5.0E-90	11433721	NT	Homo sapiens ATPase, aminophospholipid transporter-like, Class I, type 8A, member 2 (ATP8A2), mRNA
9048	17921		1.36	5.0E-90	AB011399.1	NT	Homo sapiens gene for AF-6, complete cds
9095	17911		1.72	5.0E-90	AI523388.1	EST_HUMAN	ar78h05.x1 Barstead aorta HPLRB6 Homo sapiens cDNA clone IMAGE:2128761 3'

Page 281 of 382  
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Single Exon Probes Expressed in HELA Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
307	9580	18712	1.78	4.0E-90	AF231920.1	NT	Homo sapiens chromosome 21 unknown mRNA
307	9580	18713	1.78	4.0E-90	AF231920.1	NT	Homo sapiens chromosome 21 unknown mRNA
1094	10318	19470	2.85	4.0E-90	4505316	NT	Homo sapiens myosin phosphatase, target subunit 1 (MYPT1), mRNA
1684	10877	20082	8.83	4.0E-90	X99033.1	NT	H. sapiens gene encoding discoidin receptor tyrosine kinase, exon 18
2813	12053	21175	1.1	4.0E-90		NT	Homo sapiens low density lipoprotein-related protein 2 (LRP2), mRNA
2813	12053	21176	1.1	4.0E-90	6806918	NT	Homo sapiens low density lipoprotein-related protein 2 (LRP2), mRNA
2888	12225	21358	1.5	4.0E-90	6806918	NT	Homo sapiens low density lipoprotein-related protein 2 (LRP2), mRNA
2888	12225	21359	1.5	4.0E-90	6806918	NT	Homo sapiens low density lipoprotein-related protein 2 (LRP2), mRNA
4859	13853	22950	4.47	4.0E-90	D87875.1	NT	Homo sapiens DNA for amyloid precursor protein, complete cds
4809	13998	23104	1.63	4.0E-90	AB033070.1	NT	Homo sapiens mRNA for KIAA1244 protein, partial cds
4833	14022	23116	1.9	4.0E-90	M85867.1	NT	Human prohormone converting enzyme (NEC2) gene, exon 8
5231	14005	23488	1.03	4.0E-90	5728777	NT	Homo sapiens collagen, type XII, alpha 1 (COL12A1), mRNA
8984	12053	21176	1.35	4.0E-90	6806918	NT	Homo sapiens low density lipoprotein-related protein 2 (LRP2), mRNA
8148	17280	26825	52.24	3.0E-90	BE663833.1	EST_HUMAN	Homo sapiens low density lipoprotein-related protein 2 (LRP2), mRNA
218	9497	18831	3.74	2.0E-90	BE637913.1	EST_HUMAN	601335244F1 NIH_MGC_39 Homo sapiens cDNA clone IMAGE:3688147 5'
1181	10402	19555	8.41	2.0E-90	5031748	NT	601067378F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3453834 5'
1181	10402	19556	8.41	2.0E-90	5031748	NT	Homo sapiens high-mobility group (nonhistone chromosomal) protein 17 (HMG17), mRNA
3830	13047	22157	2.29	2.0E-90	A1138213.1	EST_HUMAN	Homo sapiens high-mobility group (nonhistone chromosomal) protein 17 (HMG17), mRNA
4694	13885	22886	1.12	2.0E-90	AB006827.1	NT	qc54c02.x1 Soares_placenta_86c6weeks_2NbpHP8t9W Homo sapiens cDNA clone IMAGE:1713410 3'
4931	14119	23214	9.77	2.0E-90	5729855	NT	similar to SW-OLF3_MOUSE P23275 OLFATORY RECEPTOR OR3. ;
5566	14791	24163	4.95	2.0E-90	AW872688.1	EST_HUMAN	Homo sapiens GRB2-related adaptor protein (GRAP) mRNA
7012	16190	25663	6.27	2.0E-90	11427320	NT	HYPOTHETICAL 35.5 KD PROTEIN. ;
7012	16190	25664	6.27	2.0E-90	11427320	NT	Homo sapiens similar to laminin receptor 1 (67kD, ribosomal protein SA) (H. sapiens) (LOC83484), mRNA
8008	16441	25929	3.86	2.0E-90	11024711	NT	Homo sapiens similar to laminin receptor 1 (67kD, ribosomal protein SA) (H. sapiens) (LOC83484), mRNA
281	9556	18689	4.74	1.0E-90	4502166	NT	Homo sapiens myosin, heavy polypeptide 4, skeletal muscle (MYH4), mRNA
379	11939	18779	1.31	1.0E-90	AF231920.1	NT	Homo sapiens amyloid beta (A4) precursor protein (protease nexin-II, Alzheimer disease) (APP), mRNA
380	11939	18779	1.24	1.0E-90	AF231920.1	NT	Homo sapiens chromosome 21 unknown mRNA
702	9644	18079	1.92	1.0E-90	AJ237589.1	NT	Homo sapiens chromosome 21 unknown mRNA

Table 4

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
702	9844	19080	1.92	1.0E-90	AJ237589.1	NT	Homo sapiens mRNA for T-box transcription factor (TBX20 gene), partial
737	9978	19118	11.4	1.0E-90	AF264750.1	NT	Homo sapiens ALR-like protein mRNA, partial cds
737	9978	19119	11.4	1.0E-90	AF264750.1	NT	Homo sapiens ALR-like protein mRNA, partial cds
1118	10342		1.49	1.0E-90	4507828	NT	Homo sapiens Kruppel-like factor 7 (ubiquitous) (KLIF7), mRNA
1313	10529	19690	3.36	1.0E-90	AF098154.1	NT	Homo sapiens protein phosphatase 2A BR gamma subunit gene, exon 3
1313	10529	19691	3.36	1.0E-90	AF098154.1	NT	Homo sapiens protein phosphatase 2A BR gamma subunit gene, exon 3
1643	10857		3.08	1.0E-90	BE378884.1	EST_HUMAN	601159563F2 NIH_MGC_53 Homo sapiens cDNA clone IMAGE:3611118 5'
1866	11073	20284	2.95	1.0E-90	11420514	NT	Homo sapiens similar to SALL1 (sal (Drosophila)-like (LOC57167), mRNA
2805	12045	21167	6.75	1.0E-90	6005720	NT	Homo sapiens chromosome 8 open reading frame 2 (C8ORF2), mRNA
3835	13052	22163	1.47	1.0E-90	AB020710.1	NT	Homo sapiens mRNA for KIAA0903 protein, partial cds
3835	13052	22164	1.47	1.0E-90	AB020710.1	NT	Homo sapiens mRNA for KIAA0903 protein, partial cds
4415	13615	22711	1.76	1.0E-90	AF167340.1	NT	Homo sapiens soluble interleukin 1 receptor accessory protein (IL1RAP) gene, exon 8, alternative exons 9 and complete cds, alternatively spliced
5262	14435	23509	1.28	1.0E-90	AB037820.1	NT	Homo sapiens mRNA for KIAA1399 protein, partial cds
5262	14435	23510	1.28	1.0E-90	AB037820.1	NT	Homo sapiens mRNA for KIAA1399 protein, partial cds
5523	14748	24115	2.09	1.0E-90	AB014533.1	NT	Homo sapiens mRNA for KIAA0633 protein, partial cds
6395	15545	25000	2.56	1.0E-90	11426758	NT	Homo sapiens solute carrier family 1 (high affinity aspartate/glutamate transporter), member 6 (SLC1A6), mRNA
6725	15920	25379	3.54	1.0E-90	114222086	NT	Homo sapiens brefeldin A-inhibited guanine nucleotide-exchange protein 2 (BIG2), mRNA
6859	16049	25514	2.42	1.0E-90	11422109	NT	Homo sapiens CGI-15 protein (LOC51006), mRNA
6859	16049	25515	2.42	1.0E-90	11422109	NT	Homo sapiens CGI-15 protein (LOC51006), mRNA
9036	17860	23894	1.51	1.0E-90	AB002059.1	NT	Homo sapiens DNA for Human P2XM, complete cds
9036	17860	23895	1.51	1.0E-90	AB002059.1	NT	Homo sapiens DNA for Human P2XM, complete cds
4178	13382	22483	5.53	8.0E-91	D12234.1	EST_HUMAN	HUM0005381 Liver HepG2 cell line. Homo sapiens cDNA clone s381 3'
3451	12876	21811	1.9	5.0E-91	AA702794.1	EST_HUMAN	280604.s1 Soares_fetal_liver_spleen_TNFS_S1 Homo sapiens cDNA clone IMAGE:448015 3'
4822	14011	23109	1.46	5.0E-91	7110634	NT	Homo sapiens chromosome 22 open reading frame 5 (C22ORF5), mRNA
4822	14011	23110	1.46	5.0E-91	7110634	NT	Homo sapiens chromosome 22 open reading frame 5 (C22ORF5), mRNA
9088	17895		1.23	6.0E-91	AI193588.1	EST_HUMAN	q97011.x1 Soares_fetal_lung_NbHL19W Homo sapiens cDNA clone IMAGE:1744385 3' similar to contains MIR_b2 MIR repetitive element:
3168	12401	21535	1.56	4.0E-91	AF156776.1	NT	Homo sapiens lysophosphatidic acid acyltransferase-delta (LPAAT-delta) mRNA, complete cds
3168	12401	21536	1.56	4.0E-91	AF156776.1	NT	Homo sapiens lysophosphatidic acid acyltransferase-delta (LPAAT-delta) mRNA, complete cds
7504	16711	26199	6.21	4.0E-91	AL163284.2	NT	Homo sapiens chromosome 21 segment HS21C084
8508	17545	23983	2.28	4.0E-91	M77994.1	EST_HUMAN	EST01579 Hippocampus, Striatum (cat. #836205) Homo sapiens cDNA clone HHC60 similar to Retrovirus-related gag polyprotein

Page 283 of 382  
Table 4  
Single Exon Probes Expressed in HELA Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8509	17545	24031	2.28	4.0E-91	M77894.1	EST_HUMAN	EST01579 Hippocampus, Striatum (cat. #936205) Homo sapiens cDNA clone HHCMS0 similar to
1595	10809	19885	1.4	3.0E-91	11430193	NT	Retrovirus-related gag polyprotein
1595	10809	19888	1.4	3.0E-91	11430193	NT	Homo sapiens solute carrier family 4, anion exchanger, member 3 (SLC4A3), mRNA
3313	12543	21677	1.41	3.0E-91	AL163283.2	NT	Homo sapiens solute carrier family 4, anion exchanger, member 3 (SLC4A3), mRNA
3439	12684	21787	3.24	3.0E-91	AB033104.1	NT	Homo sapiens chromosome 21 segment HS21C083
3439	12684	21798	3.24	3.0E-91	AB033104.1	NT	Homo sapiens mRNA for KIAA1278 protein, partial cds
3770	12988	22104	0.97	3.0E-91	AF084530.1	NT	Homo sapiens mRNA for KIAA1278 protein, partial cds
4590	13784	22875	5.52	3.0E-91	M30938.1	NT	Homo sapiens cyclin-D binding Myb-like protein mRNA, complete cds
4899	14186	23275	3.31	3.0E-91	AL163285.2	NT	Human Ku (p70/p80) subunit mRNA, complete cds
4899	14186	23278	3.31	3.0E-91	AL163285.2	NT	Homo sapiens chromosome 21 segment HS21C085
5789	15008		3.05	3.0E-91	4502740	NT	Homo sapiens chromosome 21 segment HS21C085
5921	15138	24549	3.58	3.0E-91	11497611	NT	Homo sapiens cyclin-dependent kinase 8 (CDK8) mRNA
5921	15138	24550	3.58	3.0E-91	11497611	NT	Homo sapiens gamma-aminobutyric acid (GABA) B receptor, 1 (GABBR1), transcript variant 2, mRNA
6351	15531	24882	4.48	3.0E-91	U86959.1	NT	Homo sapiens gamma-aminobutyric acid (GABA) B receptor, 1 (GABBR1), transcript variant 2, mRNA
6351	15531	24983	4.48	3.0E-91	U86959.1	NT	Human L-type calcium channel beta-1 subunit (CACNLB1) gene, exons 10 and 11
8768	17704	23955	1.33	3.0E-91	AF240786.1	NT	Human L-type calcium channel beta-1 subunit (CACNLB1) gene, exons 10 and 11
9124	14490	23535	4.48	3.0E-91	AF169555.1	NT	Homo sapiens glutathione S-transferase theta 2 (GSTT2) and glutathione S-transferase theta 1 (GSTT1) genes, complete cds
9124	14490	23538	4.48	3.0E-91	AF169555.1	NT	Homo sapiens beta-ureidopropionase (BUP1) gene, exon 8
50	9347	18460	2.75	1.0E-91	AL163284.2	NT	Homo sapiens beta-ureidopropionase (BUP1) gene, exon 8
1252	10488	19832	9.01	1.0E-91	AW449748.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C084
6015	15285	24889	1.89	1.0E-91	BF348182.1	EST_HUMAN	UI-H-B13-eks-d01-0-U1.s1 NCI_CGAP_Sub5 Homo sapiens cDNA clone IMAGE:2735280 3'
6015	15285	24890	1.89	1.0E-91	BF348182.1	EST_HUMAN	602022088F1 NCI_CGAP_Bim67 Homo sapiens cDNA clone IMAGE:4157804 5'
8675	18308		1.69	1.0E-91	H15212.1	EST_HUMAN	602022088F1 NCI_CGAP_Bim67 Homo sapiens cDNA clone IMAGE:4157804 5'
1248	10465	19828	19.2	9.0E-92	AJ001689.1	NT	Yn30e03.r1 Soares infant brain 1N1B Homo sapiens cDNA clone IMAGE:49587 5'
1248	10465	19827	19.2	9.0E-92	AJ001689.1	NT	Homo sapiens NKX2D gene, exon 10
5428	14653	23780	3.81	9.0E-92	J03007.1	NT	Homo sapiens NKX2D gene, exon 10
5483	14718	24078	1.9	9.0E-92	11427149	NT	Human Nar K+ ATPase alpha-subunit mRNA, partial cds
5850	15088	24478	3.95	9.0E-92	AF310105.1	NT	Homo sapiens hypothetical protein FLJ20260 (FLJ20260), mRNA
6846	16035	25499	2.27	9.0E-92	11422086	NT	Homo sapiens NALP1 mRNA, complete cds
92	8085	18514	3.46	8.0E-92	W28367.1	EST_HUMAN	Homo sapiens brefeldin A-inhibited guanine nucleotide-exchange protein 2 (BIG2), mRNA
							2673 Human retina cDNA randomly primed sublibrary Homo sapiens cDNA



Table 4

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
290	9584	18897	6.09	8.0E-92	BE386383.1	EST_HUMAN	601273513F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3614667 5'
1790	11000	20195	1.06	8.0E-92	11434722	NT	Homo sapiens diacylglycerol kinase, gamma (80kD) (DGKG), mRNA
1790	11000	20196	1.06	8.0E-92	11434722	NT	Homo sapiens diacylglycerol kinase, gamma (80kD) (DGKG), mRNA
4207	13410	22504	0.94	8.0E-92	AA909157.1	EST_HUMAN	om13602 s1 Soares_NFL_T_GBC_ST Homo sapiens cDNA clone IMAGE:1540922 3' similar to contains L1.b2 L1 repetitive element;
5132	14310	23401	0.77	8.0E-92	AW157571.1	EST_HUMAN	au83h08.x1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2782811 3' similar to
6808	15804	25260	4.9	8.0E-92	L04183.1	NT	TR-O60302 O60302 KIAA0555 PROTEIN, contains element MIER22 repetitive element;
6808	15804	25261	4.9	8.0E-92	L04183.1	NT	Human lens membrane protein (mp19) gene, exon 11
6781	15886	25446	3.26	8.0E-92	AB014511.1	NT	Human lens membrane protein (mp19) gene, exon 11
7382	16597	26085	5.33	8.0E-92	AF074393.1	NT	Homo sapiens mRNA for KIAA0811 protein, partial cds
7900	17116	26648	2.27	8.0E-92	4503340	NT	Homo sapiens nuclear mitogen- and stress-activated protein kinase-1 (MSK1) mRNA, complete cds
8859	17792	23835	1.7	8.0E-92	11434704	NT	Homo sapiens dihydrofolamide S-succinyltransferase (E2 component of 2-oxo-glutarate complex) (DLST) mRNA
26	8322	18425	1.35	7.0E-92	AB031007.1	NT	Homo sapiens fragile X mental retardation, autosomal homolog 1 (FXR1), mRNA
241	11963	18649	0.97	7.0E-92	AB018301.1	NT	Homo sapiens DNA, MHC class I region, 7.1 ancestral haplotype
241	11963	18650	0.97	7.0E-92	AB018301.1	NT	Homo sapiens mRNA for KIAA0758 protein, partial cds
588	9845		1.47	7.0E-92	AF007822.1	NT	Homo sapiens mRNA for KIAA0758 protein, partial cds
1287	10502	19663	1.21	7.0E-92	4502384	NT	Homo sapiens cytoplasmic Sepsase truncated isoform mRNA, complete cds
2153	11351	20567	6.03	7.0E-92	5031570	NT	Homo sapiens B-cell CLL/lymphoma 7b (BCL7B) mRNA
2153	11351	20568	6.03	7.0E-92	5031570	NT	Homo sapiens ARP2 (actin-related protein 2, yeast) homolog (ACTR2), mRNA
2530	11718	20935	9.05	7.0E-92	AF167706.1	NT	Homo sapiens ARP2 (actin-related protein 2, yeast) homolog (ACTR2), mRNA
2684	11866	21076	6.58	7.0E-92	6005738	NT	Homo sapiens cyclase-rich repeat-containing protein S52 precursor, mRNA, complete cds
2708	11888	21105	2.57	7.0E-92	AB031007.1	NT	Homo sapiens NRAS-related gene (D1S155E), mRNA
3319	14467	21681	0.74	7.0E-92	4507500	NT	Homo sapiens DNA, MHC class I region, 7.1 ancestral haplotype
3319	14467	21682	0.74	7.0E-92	4507500	NT	Homo sapiens T-cell lymphoma invasion and metastasis 1 (TIAM1) mRNA
4586	13780	22872	1.34	7.0E-92	S71824.1	NT	Homo sapiens T-cell lymphoma invasion and metastasis 1 (TIAM1) mRNA
4586	13780	22873	1.34	7.0E-92	S71824.1	NT	Homo sapiens T-cell lymphoma invasion and metastasis 1 (TIAM1) mRNA
5104	14370	23457	0.95	7.0E-92	4506118	NT	N-CAM=145 kDa neural cell adhesion molecule [human, small cell lung cancer cell line OS2-R, mRNA, 2960 nt]
5305	14537	23541	5.59	7.0E-92	AA446203.1	EST_HUMAN	N-CAM=145 kDa neural cell adhesion molecule [human, small cell lung cancer cell line OS2-R, mRNA, 2960 nt]
1587	10780		1.21	5.0E-92	BE380882.1	EST_HUMAN	Homo sapiens prospero-related homeobox 1 (PROX1) mRNA
							zw66d12.11 Soares testis_NHT Homo sapiens cDNA clone IMAGE:781175 5'
							601283012F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3605018 5'

Page 285 of 382  
Table 4  
Single Exon Probes Expressed in HELA Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2721	11900	21118	2.78	3.0E-92	BE609714.1	EST_HUMAN	601501242F1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3902939 5'
5603	14827	24203	5.34	3.0E-92	AA378338.1	EST_HUMAN	EST191020 Synovial sarcoma Homo sapiens cDNA 5' end similar to ribosomal protein S13
7349	16585	28054	4.3	3.0E-92	X15804.1	NT	Human mRNA for alpha-actinin
7349	16585	28055	4.3	3.0E-92	X15804.1	NT	Human mRNA for alpha-actinin
27	9323	18426	1.34	2.0E-92	4501898	NT	Homo sapiens actinin A receptor, type IIB (ACVR2B) mRNA
144	9426	18560	13.1	2.0E-92	AF154830.1	NT	Homo sapiens carbamyl phosphatase synthetase 1 mRNA, complete cds
183	9462	18592	3.22	2.0E-92	11422846	NT	Homo sapiens hypothetical protein DJ462023.2 (DJ462023.2), mRNA
183	9462	18593	3.22	2.0E-92	11422846	NT	Homo sapiens hypothetical protein DJ462023.2 (DJ462023.2), mRNA
757	9898	18144	3.85	2.0E-92	BE289180.1	EST_HUMAN	601118337F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3028304 5'
757	9898	18145	3.85	2.0E-92	BE289180.1	EST_HUMAN	601118337F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3028304 5'
1889	10901		1.47	2.0E-92	S78653.1	NT	mrg-mas-related [human, Genomic, 2416 nt]
1905	11111	20305	1.45	2.0E-92	A1818119.1	EST_HUMAN	wk27d07.x1 NCI CGAP_Bm25 Homo sapiens cDNA clone IMAGE:2413549 3' similar to TR:Q12844
1905	11111	20308	1.45	2.0E-92	A1818119.1	EST_HUMAN	Q12844 BREAKPOINT CLUSTER REGION PROTEIN ;
2015	11217	20426	6.59	2.0E-92	4508880	NT	wk27d07.x1 NCI CGAP_Bm25 Homo sapiens cDNA clone IMAGE:2413549 3' similar to TR:Q12844
2621	11805	21022	24.63	2.0E-92	6912457	NT	Homo sapiens syndecan 4 (amphiglycan, ryudocan) (SDC4) mRNA
2782	10844	20022	2.37	2.0E-92	11418424	NT	Homo sapiens calcineurin binding protein 1 (KIAA0330), mRNA
2782	10844	20023	2.37	2.0E-92	11418424	NT	Homo sapiens collagen, type XII, alpha 1 (COL12A1), mRNA
3591	12812	21832	1.29	2.0E-92	AF231919.1	NT	Homo sapiens collagen, type XII, alpha 1 (COL12A1), mRNA
3591	12812	21933	1.29	2.0E-92	AF231919.1	NT	Homo sapiens chromosome 21 unknown mRNA
3686	12887	22008	5.14	2.0E-92	5803180	NT	Homo sapiens stress-induced-phosphoprotein 1 (Hsp70/Hsp80-organizing protein) (STIP1), mRNA
4274	13477	22574	1.37	2.0E-92	M10976.1	NT	Human endogenous retroviral DNA (4-1), complete retroviral segment
4766	13955	23056	0.84	2.0E-92	AF136523.1	NT	Homo sapiens bile salt export pump (BSEP) mRNA, complete cds
5017	14204		3.73	2.0E-92	AL040437.1	EST_HUMAN	DKFZp334C0414_1 434 (synonym: hies3) Homo sapiens cDNA clone DKFZp334C0414 5'
5248	14421		0.95	2.0E-92	4759169	NT	Homo sapiens sterol regulatory element binding transcription factor 2 (SREBF2) mRNA
5941	15157	24569	2.81	2.0E-92	AB028991.1	NT	Homo sapiens mRNA for KIAA1088 protein, partial cds
7344	16580	26048	7.05	2.0E-92	11434900	NT	Homo sapiens thyroid stimulating hormone receptor (TSHR), mRNA
7703	16802	26410	1.75	2.0E-92	AW836280.1	EST_HUMAN	CM4-L T0026-161299-062-g06 LT0026 Homo sapiens cDNA
7703	16802	26411	1.75	2.0E-92	AW836280.1	EST_HUMAN	CM4-L T0026-161299-062-g08 LT0026 Homo sapiens cDNA
8878	17774	23943	2.73	2.0E-92	AB028016.1	NT	Homo sapiens mRNA for KIAA1093 protein, partial cds
8897	17791	23923	1.35	2.0E-92	AF106656.1	NT	Homo sapiens adenylosuccinate lyase gene, complete cds
9163	11805	21022	29.98	2.0E-92	6912457	NT	Homo sapiens calcineurin binding protein 1 (KIAA0330), mRNA

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9269	18312	23600	1.48	2.0E-92	AF106656.1	NT	Homo sapiens adenylosuccinate lyase gene, complete cds
1817	11025	20219	1.36	1.0E-92	R78078.1	EST_HUMAN	y80e08.r1 Soares placenta N62-IP Homo sapiens cDNA clone IMAGE:145574 5'
1817	11025	20220	1.36	1.0E-92	R78078.1	EST_HUMAN	y80e08.r1 Soares placenta N62-IP Homo sapiens cDNA clone IMAGE:145574 5'
2041	11242	20451	66.35	1.0E-92	4506668	NT	Homo sapiens ribosomal protein, large, P1 (RPLP1), mRNA
1998	11201	20412	3.07	9.0E-93	AU121681.1	EST_HUMAN	AU121681 MAMMA1 Homo sapiens cDNA clone MAMMA1000738 5'
							EST188414 HCC cell line (metastasis to liver in mouse) II Homo sapiens cDNA 5' end similar to ribosomal protein L28
2009	11212		43.7	9.0E-93	AA316723.1	EST_HUMAN	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced
2609	11783		1.25	9.0E-93	AF223391.1	NT	601281867F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3003832 5'
3583	12814	21835	1.06	9.0E-93	BE388571.1	EST_HUMAN	AU121681 MAMMA1 Homo sapiens cDNA clone MAMMA1000738 5'
4328	13529	22623	1.11	9.0E-93	AU121681.1	EST_HUMAN	Homo sapiens ribosomal protein L10a (RPL10A), mRNA
8157	17289		18.88	9.0E-93	11418526	NT	601460521F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3863908 5'
5929	15145	24556	2.46	8.0E-93	BF036384.1	EST_HUMAN	Homo sapiens chromosome 21 unknown mRNA
250	9526	18658	7.52	7.0E-93	AF231819.1	NT	Homo sapiens T-cell lymphoma invasion and metastasis 1 (TIAM1), mRNA
3041	12278	21406	0.85	6.0E-93	11528178	NT	Homo sapiens mRNA for KIAA0811 protein, partial cds
1388	10602	19767	1.49	5.0E-93	AB014511.1	NT	Homo sapiens mRNA for KIAA0811 protein, partial cds
1411	10824	19789	11.61	5.0E-93	AI874184.1	EST_HUMAN	wc09c08.x1 NCI_CGAP_P128 Homo sapiens cDNA clone IMAGE:2314870 3'
1411	10824	19790	11.61	5.0E-93	AI874184.1	EST_HUMAN	wc09c08.x1 NCI_CGAP_P128 Homo sapiens cDNA clone IMAGE:2314870 3'
3189	12434	21569	5.83	5.0E-93	X04201.1	NT	Human skeletal muscle 1.3 kb mRNA for tropomyosin
							Homo sapiens protein phosphatase-1 regulatory subunit 7 (PPP1R7) gene, exon 11, complete cds and alternatively spliced product
8382	15562	25018	3.42	5.0E-93	AF087136.1	NT	Homo sapiens secretory pathway component Sec31B-1 mRNA, alternatively spliced, complete cds
8971	16149	25620	2.22	5.0E-93	AF274863.1	NT	Homo sapiens nucleobindin 2 (NUCB2), mRNA
7402	16615	28105	2.18	5.0E-93	11439599	NT	Homo sapiens gamma-glutamyltransferase 1 (GGT1), mRNA
8774	18037	23844	2.01	5.0E-93	11417877	NT	Homo sapiens gamma-glutamyltransferase 1 (GGT1), mRNA
87	9380		5.23	4.0E-93	AA459833.1	EST_HUMAN	z50e08.s1 Soares testis_NHT Homo sapiens cDNA clone IMAGE:795688 3' similar to SW:CLPA_RAT
451	9704	18841	0.84	4.0E-93	4557879	NT	P37397 CALPONIN, ACIDIC ISOFORM;
451	9704	18842	0.84	4.0E-93	4557879	NT	Homo sapiens interferon gamma receptor 1 (IFNGR1) mRNA
781	10020	19169	3.31	4.0E-93	7657454	NT	Homo sapiens interferon gamma receptor 1 (IFNGR1) mRNA
781	10020	19170	3.31	4.0E-93	7657454	NT	Homo sapiens pascadillo (zabrafish) homolog 1, containing BRCT domain (PES1), mRNA
1191	10411	19565	2.02	4.0E-93	8923658	NT	Homo sapiens pascadillo (zabrafish) homolog 1, containing BRCT domain (PES1), mRNA
1948	11150	20352	4.6	4.0E-93	AF047877.1	NT	Homo sapiens hypothetical protein FLJ20731 (FLJ20731), mRNA
2208	11406	20630	1.21	4.0E-93	AF157476.1	NT	Homo sapiens dytrophin (DMD) gene, deletion breakpoints 1-3 in intron 5
							Homo sapiens DNA polymerase zeta catalytic subunit (REV3) mRNA, complete cds

Table 4

## Single Exon Probes Expressed in HELA Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3542	12765	21898	0.92	4.0E-93	7705398	NT	Homo sapiens tumor antigen SLP-8p (HCC8), mRNA
4025	13236	22341	1.62	4.0E-93	4504654	NT	Homo sapiens interleukin 18 receptor 1 (IL18R1), mRNA
5047	12765	21898	0.65	4.0E-93	7705398	NT	Homo sapiens tumor antigen SLP-8p (HCC8), mRNA
5508	14733	24095	4.77	4.0E-93	T46884.1	EST_HUMAN	y894c12.11 Stratagene liver (#837224) Homo sapiens cDNA clone IMAGE:78838 5' similar to similar to SP-A44391 A44391 SERUM RESPONSE ELEMENT-BINDING PROTEIN SRE-ZBP - HUMAN,
7693	18882	26401	18.41	4.0E-93	AV692051.1	EST_HUMAN	AV692051 GKC Homo sapiens cDNA clone GKDRF07 5'
3631	12852	21970	15.64	3.0E-93	BF690630.1	EST_HUMAN	602246554F1 NIH_MGC_62 Homo sapiens cDNA clone IMAGE:4332036 5'
3631	12852	21971	15.64	3.0E-93	BF690630.1	EST_HUMAN	602246554F1 NIH_MGC_62 Homo sapiens cDNA clone IMAGE:4332036 5'
4220	13423		1.43	3.0E-93	AF225896.1	NT	Homo sapiens tensin mRNA, complete cds
5103	14283		1.05	3.0E-93	AF231981.1	NT	Homo sapiens long chain polyunsaturated fatty acid elongation enzyme (HELO1) mRNA, complete cds
7379	16595	26082	5.39	3.0E-93	AI824826.1	EST_HUMAN	wb02d05.x1 NCJ_CGAP_G06 Homo sapiens cDNA clone IMAGE:2304489 3'
195	9475	18608	50.31	2.0E-93	AB015610.1	NT	Chlorococcus eethiops mRNA for ribosomal protein S4X, complete cds
195	9475	18607	50.31	2.0E-93	AB015610.1	NT	Chlorococcus eethiops mRNA for ribosomal protein S4X, complete cds
328	9599	18729	9.28	2.0E-93	AL163285.2	NT	Homo sapiens chromosome 21 segment HS21C085
329	9599	18729	8.05	2.0E-93	AL163285.2	NT	Homo sapiens chromosome 21 segment HS21C085
2100	11300	20514	2.1	2.0E-93	U40763.1	NT	Human Cdk-associated RS cyclophilin CARS-Cyp mRNA, complete cds
2449	11640	20861	3.05	2.0E-93	BE252982.1	EST_HUMAN	601117588F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3358220 5'
5175	14353	23441	0.97	2.0E-93	BE253201.1	EST_HUMAN	601116810F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3357243 5'
5403	14631	23743	4.28	2.0E-93	AW994385.1	EST_HUMAN	EST378458 IMAGE resequences, MAGH Homo sapiens cDNA
8683	17640		1.69	2.0E-93	AA126735.1	EST_HUMAN	z29c10.s1 Soares_pregnant uterus_NbHPU Homo sapiens cDNA clone IMAGE:503346 3'
8749	17692		1.73	2.0E-93	L41825.1	NT	Homo sapiens CYP17 gene, 5' end
9025	17875		4.17	2.0E-93	BF035327.1	EST_HUMAN	601458531F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3862086 5'
103	9396	18525	2.46	1.0E-93	AF238997.1	NT	Homo sapiens CTR1 pseudogene
103	9396	18526	2.46	1.0E-93	AF238997.1	NT	Homo sapiens CTR1 pseudogene
524	9775	18900	11.32	1.0E-93	7657016	NT	Homo sapiens hypothetical protein (DJ328E19.C1.1), mRNA
607	9854	18873	4.39	1.0E-93	AI146755.1	EST_HUMAN	cy64b08.x1 NCJ_CGAP_CLL1 Homo sapiens cDNA clone IMAGE:1672503 3' similar to TR:Q62384 Q62384 ZINC FINGER PROTEIN ;
882	10118	19280	10.07	1.0E-93	D81675.1	NT	Homo sapiens DNA for amyloid precursor protein, complete cds
1244	10460	19619	8.18	1.0E-93	8923270	NT	Homo sapiens hypothetical protein FLJ20291 (FLJ20291), mRNA
1244	10460	19820	8.18	1.0E-93	8923270	NT	Homo sapiens hypothetical protein FLJ20291 (FLJ20291), mRNA
1353	10568	19732	2.25	1.0E-93	AF167708.1	NT	Homo sapiens cysteine-rich repeat-containing protein S52 precursor, mRNA, complete cds

Page 288 of 382  
Table 4  
Single Exon Probes Expressed in HELA Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2308	11500	20721	5.96	1.0E-93	AF231981.1	NT	Homo sapiens long chain polyunsaturated fatty acid elongation enzyme (HELO1) mRNA, complete cds
2426	11617	20839	12.19	1.0E-93	AF050086.1	NT	Homo sapiens MHC class 1 region
2472	11683		2.57	1.0E-93	AL137200.1	NT	Novel human gene mapping to chromosome 1
2774	10518	19678	2.75	1.0E-93	BE287369.1	EST_HUMAN	601177686F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3532965 5'
2774	10518	19677	2.75	1.0E-93	BE297369.1	EST_HUMAN	601177686F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3532965 5'
2884	12122	21255	3.73	1.0E-93	D87675.1	NT	Homo sapiens DNA for amyloid precursor protein, complete cds
3182	12417		2.24	1.0E-93	AF231981.1	NT	Homo sapiens long chain polyunsaturated fatty acid elongation enzyme (HELO1) mRNA, complete cds
4421	13821	22716	3.49	1.0E-93	AL163284.2	NT	Homo sapiens chromosome 21 segment HS21C084
5474	14701	24055	1.97	1.0E-93	U78509.1	NT	Homo sapiens glucocorticoid receptor (GRL) gene, intron D, exon 5, and intron E
5474	14701	24056	1.97	1.0E-93	U78509.1	NT	Homo sapiens glucocorticoid receptor (GRL) gene, intron D, exon 5, and intron E
5624	14848	24230	10.31	1.0E-93	4557792	NT	Homo sapiens neurofibronin 1 (neurofibromatosis, von Recklinghausen disease, Watson disease) (NF1) mRNA
5994	15277	24707	2.01	1.0E-93	11431590	NT	Homo sapiens protein kinase C, beta 1 (PRKCB1), mRNA
6185	15367	24807	3.71	1.0E-93	D42072.1	NT	Human mRNA for NF1 N-isoform-exon11, complete cds
6547	15743	25204	2.45	1.0E-93	AB037832.1	NT	Homo sapiens mRNA for KIAA1411 protein, partial cds
6894	15600	25068	2.82	1.0E-93	AB040918.1	NT	Homo sapiens mRNA for KIAA1485 protein, partial cds
6954	16132	25600	4.68	1.0E-93	X13474.1	NT	Human PreA4 gene for Alzheimer's disease A4 amyloid protein precursor (exon 8)
6954	16132	25601	4.68	1.0E-93	X13474.1	NT	Human PreA4 gene for Alzheimer's disease A4 amyloid protein precursor (exon 9)
8312	18101	23807	2.74	1.0E-93	A1298292.1	EST_HUMAN	qm03c12.x1 NCL_CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1880758 3' similar to WP.T19B4.4 CE13742
8930	17812		1.28	1.0E-93	AJ230125.1	NT	Homo sapiens GGT1 gene, exon 1
9018	17870		3.25	1.0E-93	11417856	NT	Homo sapiens glutathione S-transferase theta 2 (GSTT2), mRNA
9200	18353		1.46	1.0E-93	AF240786.1	NT	Homo sapiens glutathione S-transferase theta 2 (GSTT2) and glutathione S-transferase theta 1 (GSTT1) genes, complete cds
9339	13155	22272	2.41	6.0E-94	AF142482.1	NT	Homo sapiens transcription enhancer factor-5 mRNA, complete cds
9143	17949		1.5	6.0E-94	11418351	NT	Homo sapiens mitogen-activated protein kinase 12 (MAPK12), mRNA
5379	14608	23719	4.05	5.0E-94	AB014512.1	NT	Homo sapiens mRNA for KIAA0612 protein, partial cds
5379	14608	23720	4.05	5.0E-94	AB014512.1	NT	Homo sapiens mRNA for KIAA0612 protein, partial cds
5687	14807	24300	4.88	5.0E-94	AA722434.1	EST_HUMAN	zg87g06.s1 Soares fetal heart_Nb-H19W Homo sapiens cDNA clone IMAGE:408594 3'
6092	15283	24725	1.76	5.0E-94	A015800.1	EST_HUMAN	083405.s1 Soares total_fetus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:1623369 3'
7544	18749	26242	2.23	5.0E-94	11423962	NT	Homo sapiens adenylylate kinase 2 (AK2), mRNA
7544	18749	26243	2.23	5.0E-94	11423962	NT	Homo sapiens adenylylate kinase 2 (AK2), mRNA

Table 4

## Single Exon Probes Expressed in HELA Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8638	18358	23608	6.17	5.0E-94	T89398.1	EST_HUMAN	yd98b04.s1 Soares fetal liver spleen INFLS Homo sapiens cDNA clone IMAGE:116239 3'
9227	18005		1.86	5.0E-94	9558724	NT	Homo sapiens cleavage and polyadenylation specific factor 1, 160kD subunit (CPSF1), mRNA
1809	11018		17.14	4.0E-94	L05094.1	NT	Homo sapiens ribosomal protein L27 mRNA, complete cds
2619	11803	21020	1.96	4.0E-94	4506008	NT	Homo sapiens protein phosphatase 1, regulatory subunit 10 (PPP1R10) mRNA
3652	12873	21991	1.02	4.0E-94	AW197851.1	EST_HUMAN	xn89f12.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2701679 3'
3652	12873	21992	1.02	4.0E-94	AW197851.1	EST_HUMAN	xn89f12.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2701679 3'
4729	13920	23023	4.08	4.0E-94	AI591312.1	EST_HUMAN	hw11f10.x1 NCL_CGAP_Bm52 Homo sapiens cDNA clone IMAGE:2259403 3' similar to TR:Q15265 Q15285 PROTEIN TYROSINE PHOSPHATASE
5856	15074	24486	1.89	4.0E-94	11440670	NT	Homo sapiens solute carrier family 22 (organic cation transporter), member 1-like (SLC22A1L), mRNA
5856	15074	24487	1.89	4.0E-94	11440670	NT	Homo sapiens solute carrier family 22 (organic cation transporter), member 1-like (SLC22A1L), mRNA
7989	18424	25911	1.88	4.0E-94	11545792	NT	Homo sapiens hypothetical protein FLJ12455 (FLJ12455), mRNA
617	9862	18982	1.1	3.0E-94	AB022785.1	NT	Homo sapiens ASH2L gene, complete cds, similar to Drosophila ash2 gene
728	9970	19108	0.9	3.0E-94	4502506	NT	Homo sapiens complement component 5 (C5) mRNA
1713	10925	20109	2.41	3.0E-94	AF167708.1	NT	Homo sapiens cysteine-rich repeat-containing protein S52 precursor, mRNA, complete cds
1713	10925	20110	2.41	3.0E-94	AF167706.1	NT	Homo sapiens cysteine-rich repeat-containing protein S52 precursor, mRNA, complete cds
1742	10954	20137	3.37	3.0E-94	4557558	NT	Homo sapiens E1A binding protein p300 (EP300) mRNA
4171	13375	22474	0.66	3.0E-94	AA464805.1	EST_HUMAN	zw63g08.r1 Soares_tetral_fetus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:774782 5'
4308	13509	22604	1.2	3.0E-94	AA781836.1	EST_HUMAN	ai59h06.s1 Soares_testis_NHT Homo sapiens cDNA clone 1375163 3'
5528	14750	24117	3.33	3.0E-94	11496268	NT	Homo sapiens zinc finger protein 277 (ZNF277), mRNA
5849	15066	24478	5.57	3.0E-94	11526228	NT	Homo sapiens chromosome 21 open reading frame 18 (C21ORF18), mRNA
6849	15844	25305	5.17	3.0E-94	AB014579.1	NT	Homo sapiens mRNA for KIAA0879 protein, partial cds
6958	16136	25607	3.97	3.0E-94	AF087942.1	NT	Homo sapiens glycogenin-1L mRNA, complete cds
7665	16864	26366	1.79	3.0E-94	4757821	NT	Homo sapiens axonal transport of synaptic vesicles (ATSV) mRNA
151	9433	18967	1.68	1.0E-94	BE295714.1	EST_HUMAN	601175792F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3351038 5'
3054	12290	21415	2.17	1.0E-94	BE253433.1	EST_HUMAN	601111696F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3352559 5'
3054	12290	21416	2.17	1.0E-94	BE253433.1	EST_HUMAN	601111696F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3352559 5'
4352	13554	22650	1.54	1.0E-94	9506692	NT	Homo sapiens hypothetical protein (FLJ20746), mRNA
7010	16188	25662	2.51	1.0E-94	BE780478.1	EST_HUMAN	601468748F1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3872099 5'
7634	16835	26331	3.18	1.0E-94	U65590.1	NT	Homo sapiens IL-1 receptor antagonist IL-1Ra (IL-1RN) gene, alternatively spliced forms, complete cds
7884	17054	26575	2.47	1.0E-94	AI272244.1	EST_HUMAN	ap22e02.x1 Schiller diglondrogiloma Homo sapiens cDNA clone IMAGE:1956122 3' similar to TR:Q62845 Q62845 NEURAL CELL ADHESION PROTEIN BIG-2 PRECURSOR

Page 290 of 382  
Table 4  
Single Exon Probes Expressed in HELA Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8763	9433	18567	1.42	1.0E-94	BE205714.1	EST_HUMAN	601175762F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3531038 5'
9064	9433	18567	1.69	1.0E-94	BE205714.1	EST_HUMAN	601175762F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3531038 5'
1471	10684	19859	8.53	9.0E-95	AF027302.1	NT	Homo sapiens TNF-alpha stimulated ABC protein (ABC50) mRNA, complete cds
3119	12354	21482	1.11	9.0E-95	7662027	NT	Homo sapiens KIAA0255 gene product (KIAA0255), mRNA
3119	12354	21483	1.11	9.0E-95	7662027	NT	Homo sapiens KIAA0255 gene product (KIAA0255), mRNA
6344	15740	25201	2.86	9.0E-95	AF274753.1	NT	Homo sapiens progressive ankylosis-like protein (ANK) mRNA, complete cds
146	9428	18562	8.86	8.0E-95	AF154830.1	NT	Homo sapiens carbamyl phosphate synthetase 1 mRNA, complete cds
4533	13729	22825	1.87	8.0E-95	AI700888.1	EST_HUMAN	we09e04.x1 NCI CGAP Lu24 Homo sapiens cDNA clone IMAGE:2340606 3' similar to gb:K00558
4533	13729	22826	1.97	8.0E-95	AI700998.1	EST_HUMAN	TUBULIN ALPHA-1 CHAIN (HUMAN); we09e04.x1 NCI CGAP Lu24 Homo sapiens cDNA clone IMAGE:2340606 3' similar to gb:K00558
6180	15362	24801	1.66	8.0E-95	11426529	NT	Homo sapiens proteasome (prosome, macropain) 26S subunit, non-ATPase, 11 (PSMD11), mRNA
6180	15362	24802	1.66	8.0E-95	11426529	NT	Homo sapiens proteasome (prosome, macropain) 26S subunit, non-ATPase, 11 (PSMD11), mRNA
6528	15724	25189	2.69	8.0E-95	AF032897.1	NT	Homo sapiens potassium channel subunit (HERG-3) mRNA, complete cds
6669	16091	25558	2.63	8.0E-95	11420944	NT	Homo sapiens KIAA0255 gene product (KIAA0255), mRNA
6669	16091	25559	2.63	8.0E-95	11420944	NT	Homo sapiens KIAA0255 gene product (KIAA0255), mRNA
7024	16201	25679	2.45	8.0E-95	5174644	NT	Homo sapiens KIAA0255 gene product (KIAA0255), mRNA
7033	16210		3.18	8.0E-95	AB037816.1	NT	Homo sapiens proline dehydrogenase (proline oxidase) (PRODH) mRNA
7302	16521	26012	1.85	8.0E-95	AF112152.1	NT	Homo sapiens developmental arteries and neural crest EGF-like protein mRNA, complete cds
8018	17157	26693	2.51	8.0E-95	10864024	NT	Homo sapiens HCF-binding transcription factor Zhangfai (ZF), mRNA
8986	17850		15.84	8.0E-95	AA628056.1	EST_HUMAN	zu84b01.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:744849 3' similar to contains L1.1 L1 repetitive element
280	9555	18887	9.96	7.0E-95	D87675.1	NT	Homo sapiens DNA for amyloid precursor protein, complete cds
280	9555	18888	9.96	7.0E-95	D87675.1	NT	Homo sapiens DNA for amyloid precursor protein, complete cds
4360	13562	22658	7.94	7.0E-95	M95708.1	NT	Homo sapiens Ly-6-like protein (CD59) mRNA, complete cds
4407	13607		1.32	7.0E-95	AL163246.2	NT	Homo sapiens chromosome 21 segment HS21C046
7456	16684	26163	1.9	3.0E-95	R83190.1	EST_HUMAN	yp87g11.1 Soares fetal liver spleen 1NLS Homo sapiens cDNA clone IMAGE:194468 5'
1621	10834	20009	3.28	2.0E-95	7662027	NT	Homo sapiens KIAA0255 gene product (KIAA0255), mRNA
1621	10834	20010	3.28	2.0E-95	7662027	NT	Homo sapiens KIAA0255 gene product (KIAA0255), mRNA
1910	11115	20311	3.87	2.0E-95	4507512	NT	Homo sapiens tissue inhibitor of metalloproteinase 3 (Sorbyfundus dystrophy, pseudoinflammatory) (TIMP3) mRNA
1913	11118	20315	1.83	2.0E-95	BE383873.1	EST_HUMAN	601312161F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3658862 5'
2360	11583	20800	1.13	2.0E-95	5453665	NT	Homo sapiens G protein-coupled receptor 19 (GPR19) mRNA
2360	11583	20801	1.13	2.0E-95	5453665	NT	Homo sapiens G protein-coupled receptor 19 (GPR19) mRNA

Table 4

## Single Exon Probes Expressed in HELA Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2428	11619	20840	3.71	2.0E-95	AF240786.1	NT	Homo sapiens glutathione S-transferase theta 2 (GSTT2) and glutathione S-transferase theta 1 (GSTT1) genes, complete cds
2479	11699	20887	11.4	2.0E-95	4789423	NT	Homo sapiens glycine cleavage system protein H (aminomethyl carrier) (GCSH) mRNA
3121	12356	21485	3.34	2.0E-95	AF015452.1	NT	Homo sapiens Usurpin-gamma mRNA, complete cds
3539	12762	21892	2.88	2.0E-95	7705900	NT	Homo sapiens unconventional myosin-15 (LOC51168), mRNA
3539	12762	21893	2.98	2.0E-95	7705900	NT	Homo sapiens unconventional myosin-15 (LOC51168), mRNA
3595	12816	21938	1.25	2.0E-95	AB037807.1	NT	Homo sapiens mRNA for KIAA1398 protein, partial cds
3731	12951	22068	0.85	2.0E-95	AI290264.1	EST_HUMAN	qm01c02.x1 Soares_NIHMPu_S1 Homo sapiens cDNA clone IMAGE:1880546 3' similar to WP.T23G7.4
4355	13557	22652	1.79	2.0E-95	7857185	NT	CE03705 ;
5084	14244	23331	3.37	2.0E-95	7861979	NT	Homo sapiens hypothetical protein (HS322B1A), mRNA
5121	14300	23388	1.7	2.0E-95	AA447831.1	EST_HUMAN	Homo sapiens KIAA0187 gene product (KIAA0187), mRNA
5121	14300	23389	1.7	2.0E-95	AA447831.1	EST_HUMAN	zr11d07.r1 Soares_total_Tetus Nb2HF8_9w Homo sapiens cDNA clone IMAGE:786157 5'
5431	14558	23798	4.23	2.0E-95	7705764	NT	zr11d07.r1 Soares_total_Tetus Nb2HF8_9w Homo sapiens cDNA clone IMAGE:786157 5'
5431	14558	23797	4.23	2.0E-95	7705764	NT	Homo sapiens CGI-48 protein (LOC51086), mRNA
5731	14950	24349	4.34	2.0E-95	M59724.1	NT	Homo sapiens CGI-48 protein (LOC51086), mRNA
5910	15127	24536	2.53	2.0E-95	AF237737.1	NT	Human muscle-type phosphofructokinase (PFK-M) gene, exon 7
6815	18010	25473	3.61	2.0E-95	11421795	NT	Homo sapiens ciliary dynein heavy chain 9 (DNAH9) mRNA, complete cds
7311	16528	26020	2.34	2.0E-95	4757853	NT	Homo sapiens ribophorin II (RPN2), mRNA
8735	17681	23953	2.2	2.0E-95	AF240786.1	NT	Homo sapiens bone morphogenetic protein receptor, type IA (BMPRI1A) mRNA
9154	17698	23884	5.88	2.0E-95	11418164	NT	Homo sapiens glutathione S-transferase theta 2 (GSTT2) and glutathione S-transferase theta 1 (GSTT1) genes, complete cds
5498	14724	24082	7.75	1.0E-95	AA284651.1	EST_HUMAN	Homo sapiens adenylosuccinate lyase (ADSL), mRNA
5498	14724	24083	7.75	1.0E-95	AA284651.1	EST_HUMAN	Homo sapiens ovary tumor NbHOT Homo sapiens cDNA clone IMAGE:714007 6' similar to
6298	15477	24919	3.3	1.0E-95	BF370000.1	EST_HUMAN	zr23h04.r1 Soares ovary tumor NbHOT Homo sapiens cDNA clone IMAGE:714007 5' similar to
6298	15477	24920	3.3	1.0E-95	BF370000.1	EST_HUMAN	TR:G1087084 G1087084 F55H2.6 ;
6527	15723	25188	2.63	9.0E-96	BE897259.1	EST_HUMAN	zr23h04.r1 Soares ovary tumor NbHOT Homo sapiens cDNA clone IMAGE:714007 5' similar to
448	11987	18838	1.64	8.0E-96	BE897607.1	EST_HUMAN	TR:G1087084 G1087084 F55H2.6 ;
448	11987	18839	1.64	8.0E-96	BE897607.1	EST_HUMAN	TR:G1087084 G1087084 F55H2.6 ;
5444	14870	22220	2.59	8.0E-96	AF231920.1	EST_HUMAN	RC8-FN0019-290600-011-G11 FN0019 Homo sapiens cDNA
3887	13103	20647	0.88	7.0E-96	AF231920.1	EST_HUMAN	RC8-FN0019-290600-011-G11 FN0019 Homo sapiens cDNA
2225	11421	20647	1.38	6.0E-96	BE171984.1	EST_HUMAN	RC8-FN0019-290600-011-G11 FN0019 Homo sapiens cDNA



Page 292 of 382  
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Single Exon Probes Expressed in HELA Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3290	12521	21652	0.88	6.0E-96	AL163201.2	NT	Homo sapiens chromosome 21 segment HS21C001
3457	12682	21816	19.61	6.0E-96	M26873.1	NT	Human glyceraldehyde-3-phosphate dehydrogenase pseudogene 3 end
8079	17214	26748	1.88	6.0E-96	7662289	NT	Homo sapiens KIAA0763 gene product (KIAA0763), mRNA
8079	17214	26747	1.88	6.0E-96	7662289	NT	Homo sapiens KIAA0763 gene product (KIAA0763), mRNA
8118	17252	26763	2.29	6.0E-96	8923939	NT	Homo sapiens myosin, heavy polypeptide 2, skeletal muscle, adult (MYH2), mRNA
325	9596	18725	2.91	5.0E-96	AB032988.1	NT	Homo sapiens mRNA for KIAA1172 protein, partial cds
852	10088	19248	3.55	5.0E-96	AB032988.1	NT	Homo sapiens mRNA for KIAA1172 protein, partial cds
852	10088	19249	3.55	5.0E-96	AB032988.1	NT	Homo sapiens mRNA for KIAA1172 protein, partial cds
2581	11767	21361	6.37	5.0E-96	11410767	NT	Homo sapiens phosphodiesterase 6A, cGMP-specific, rod, alpha (PDE6A), mRNA
2892	12228	21361	0.65	5.0E-96	6912735	NT	Homo sapiens transient receptor potential channel 5 (TRPC5), mRNA
4925	14113		1.74	5.0E-96	X68012.1	NT	H. sapiens DNA for monoamine oxidase type A (7) (partial)
5992	15274	24703	3.98	5.0E-96	11424399	NT	Homo sapiens A kinase (PRKA) anchor protein 1 (AKAP1), mRNA
5992	15274	24704	3.98	5.0E-96	11424399	NT	Homo sapiens A kinase (PRKA) anchor protein 1 (AKAP1), mRNA
8495	15692	25156	2.69	5.0E-96	M68347.1	NT	Human type IV collagenase (CLG4B) gene, exon 5
8495	15692	25157	2.69	5.0E-96	M68347.1	NT	Human type IV collagenase (CLG4B) gene, exon 5
4173	13377		18.09	3.0E-96	H68856.1	EST_HUMAN	yr871121 Soares fetal liver spleen 1NFSL Homo sapiens cDNA clone IMAGE:212327 5'
421	9674		2.93	2.0E-96	4503098	NT	Homo sapiens chondroitin sulfate proteoglycan 4 (melanoma-associated) (CSPG4), mRNA
755	9998	19141	2.39	2.0E-96	AL163248.2	NT	Homo sapiens chromosome 21 segment HS21C048
4789	13958	23059	1.66	2.0E-96	BE148074.1	EST_HUMAN	RC3-HT0230-040500-110-g02 HT0230 Homo sapiens cDNA
6759	15954		6.71	2.0E-96	AV689461.1	EST_HUMAN	AV689461 GKC Homo sapiens cDNA clone GKCFMD07 5'
8416	17489		2.01	2.0E-96	AW249440.1	EST_HUMAN	2818351.5prime NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2818351 5'
677	9921	19052	2.89	1.0E-96	Y18990.1	NT	Human endogenous retrovirus type K (HERV-K), gag, pol and env genes
1751	10963	20145	3.39	1.0E-96	AW955054.1	EST_HUMAN	EST367124 MAGE resequences, MAGC Homo sapiens cDNA
1751	10963	20146	3.39	1.0E-96	AW955054.1	EST_HUMAN	EST367124 MAGE resequences, MAGC Homo sapiens cDNA
2231	11951	20653	1.03	1.0E-96	U51472.2	NT	Felis catus superfast myosin heavy chain (sMyHC) mRNA, complete cds
6686	15981	25340	28.75	1.0E-96	11419429	NT	Homo sapiens similar to actonucleotide pyrophosphatase/phosphodiesterase 3 (H. sapiens) (LOC83214), mRNA
8403	14488	23533	1.38	1.0E-96	4826863	NT	Homo sapiens neuronal cell adhesion molecule (NRCAM) mRNA
8403	14488	23534	1.38	1.0E-96	4826863	NT	Homo sapiens neuronal cell adhesion molecule (NRCAM) mRNA
6315	15495		3.65	6.0E-97	BE141849.1	EST_HUMAN	IL5-HT0117-011099-004-D07 HT0117 Homo sapiens cDNA
7944	17084	26813	2.09	6.0E-97	X15804.1	NT	Human mRNA for alpha-actinin
8487	15684	25135	2.41	5.0E-97	AL043314.2	EST_HUMAN	DKFZ434N0323_1 434 (synonym: hbs3) Homo sapiens cDNA clone DKFZp434N0323 5'
6506	15702	25168	13.07	5.0E-97	AA418026.1	EST_HUMAN	z07e12.s1 Soares_NhHMPu_S1 Homo sapiens cDNA clone IMAGE:787758 3' similar to TR:G1304125

Page 293 of 382  
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6983	16161	25632	3.44	5.0E-97	BF154912.1	EST_HUMAN	RCO-BT0812-250900-032-a09 BT0812 Homo sapiens cDNA
8080	17215	26748	2.4	5.0E-97	BE148597.1	EST_HUMAN	MRO-HT0241-150500-010-b02 HT0241 Homo sapiens cDNA
8080	17215	26749	2.4	5.0E-97	BE148597.1	EST_HUMAN	MRO-HT0241-150500-010-b02 HT0241 Homo sapiens cDNA
947	10180	18336	1.69	4.0E-97	BE004436.1	EST_HUMAN	CMO-BN0108-170300-293-a08 BN0108 Homo sapiens cDNA
1874	11081	20271	1.08	4.0E-97	5453572	NT	Homo sapiens brefeldin A-inhibited guanine nucleotide-exchange protein 2 (BIG2), mRNA
6007	15257	24681	6.08	4.0E-97	Y11339.2	NT	Homo sapiens mRNA for GalNAc alpha-2, 6-sialyltransferase 1, long form
6007	15257	24682	6.08	4.0E-97	Y11339.2	NT	Homo sapiens mRNA for GalNAc alpha-2, 6-sialyltransferase 1, long form
7722	16921	26429	1.74	4.0E-97	11863122	NT	Homo sapiens AXL receptor tyrosine kinase (AXL), transcript variant 1, mRNA
7722	16921	26430	1.74	4.0E-97	11863122	NT	Homo sapiens AXL receptor tyrosine kinase (AXL), transcript variant 1, mRNA
8608	17604		6	4.0E-97	11418318	NT	Homo sapiens G-2 and S-phase expressed 1 (GTSE1), mRNA
247	8524	18654	0.86	3.0E-97	AB032988.1	NT	Homo sapiens mRNA for KIAA1172 protein, partial cds
884	10120	19282	8.01	3.0E-97	4502168	NT	Homo sapiens amyloid beta (A4) precursor protein (protease nexin-II, Alzheimer disease) (APP), mRNA
884	10120	19283	8.01	3.0E-97	4502168	NT	Homo sapiens amyloid beta (A4) precursor protein (protease nexin-II, Alzheimer disease) (APP), mRNA
1443	11935	19832	2.27	3.0E-97	4758813	NT	Homo sapiens N-myc (and STAT) interactor (NMI), mRNA
2402	11952	20813	3.91	3.0E-97	U36255.1	NT	Human beta-primin-adaptin (BAM22) gene, exon 7
3227	12461	21593	1.34	3.0E-97	5174478	NT	Homo sapiens pericentrih (PCNT) mRNA
4769	13978	23082	31.26	1.0E-97	4503470	NT	Homo sapiens eukaryotic translation elongation factor 1 alpha 1 (EEF1A1) mRNA
5840	15057	24404	2.46	1.0E-97	BE566486.1	EST_HUMAN	601339320F1 NIH_MGC_53 Homo sapiens cDNA clone IMAGE:3881821 5'
7284	16513	26005	4.29	1.0E-97	11427757	NT	Homo sapiens KIAA0649 gene product (KIAA0649), mRNA
7284	16513	26006	4.29	1.0E-97	11427757	NT	Homo sapiens KIAA0649 gene product (KIAA0649), mRNA
7657	17047	26568	3.58	1.0E-97	AA553761.1	EST_HUMAN	hK29g02.s1 NCL CGAP_Cot11 Homo sapiens cDNA clone IMAGE:1014962 3'
8004	18439	25926	18.38	1.0E-97	11426272	NT	Homo sapiens ribosomal protein S15 (RPS15), mRNA
8004	18439	25927	18.38	1.0E-97	11426272	NT	Homo sapiens ribosomal protein S15 (RPS15), mRNA
911	10146	18307	3.5	9.0E-98	BE090973.1	EST_HUMAN	PM4-BT0724-010400-008-a12 BT0724 Homo sapiens cDNA
1283	10498	19658	0.87	9.0E-98	8393062	NT	Homo sapiens cat eye syndrome critical region gene 1 (CECR1), mRNA
5247	14420	23497	1.46	9.0E-98	11419594	NT	Homo sapiens FSH primary response (LPR1, rat) homolog 1 (FSHPRH1), mRNA
8434	15631	25096	11.48	9.0E-98	4758119	NT	Homo sapiens death-associated protein (DAP), mRNA
8434	15631	25097	11.48	9.0E-98	4758119	NT	Homo sapiens death-associated protein (DAP), mRNA
7574	16779	26273	2.66	9.0E-98	AB023222.1	NT	Homo sapiens mRNA for KIAA1005 protein, partial cds
7574	16779	26274	2.66	9.0E-98	AB023222.1	NT	Homo sapiens mRNA for KIAA1005 protein, partial cds
8621	10146	19307	2.6	9.0E-98	BE090973.1	EST_HUMAN	PM4-BT0724-010400-008-a12 BT0724 Homo sapiens cDNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
25	9321		1.5	8.0E-98	AJ251158.1	NT	Homo sapiens partial MICB gene for MHC class I chain-related protein B, exons 2-3 and joined CDS
1701	10913	20100	3.45	8.0E-98	AB017007.1	NT	Homo sapiens PMS2L16 mRNA, partial cds
1701	10913	20101	3.45	8.0E-98	AB017007.1	NT	Homo sapiens PMS2L16 mRNA, partial cds
3778	12996	22112	7.09	8.0E-98	J04469.1	NT	Human mitochondrial creatine kinase (CKMT) gene, complete cds
2144	11342	20560	1.34	3.0E-98	AJ403124.1	EST_HUMAN	AJ403124.3.4 (downregulated in larynx carcinoma) Homo sapiens cDNA clone l8
2568	11753	20973	3.5	3.0E-98	AB014607.1	NT	Homo sapiens mRNA for KIAA0707 protein, partial cds
2706	11885		6.43	3.0E-98	AA077498.1	EST_HUMAN	7B18H01 Chromosome 7 Fetal Brain cDNA Library Homo sapiens cDNA clone 7B18H01
6062	15252	24675	1.94	3.0E-98	11418210	NT	Homo sapiens activator of S phase kinase (ASK), mRNA
6062	15252	24676	1.94	3.0E-98	11418210	NT	Homo sapiens activator of S phase kinase (ASK), mRNA
7035	16212	25088	2.7	3.0E-98	AJ403124.1	EST_HUMAN	AJ403124.3.4 (downregulated in larynx carcinoma) Homo sapiens cDNA clone l8
7035	16212	25089	2.7	3.0E-98	AJ403124.1	EST_HUMAN	AJ403124.3.4 (downregulated in larynx carcinoma) Homo sapiens cDNA clone l8
7526	16731	26221	2.58	3.0E-98	U59309.1	NT	Human fumatease precursor (FH) mRNA, nuclear gene encoding mitochondrial protein, complete cds
9213	17994		3.36	3.0E-98	11418177	NT	Homo sapiens Ran GTPase activating protein 1 (RANGAP1), mRNA
743	9984	19127	0.75	2.0E-98	BE261694.1	EST_HUMAN	601149486F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3502245 5'
2047	11248	20458	3.98	2.0E-98	BE264281.1	EST_HUMAN	601172658F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3528134 5'
2204	11401	20626	2.69	2.0E-98	AL163202.2	NT	Homo sapiens chromosome 21 segment HS21C002
2342	11535	20758	0.91	2.0E-98	AF248540.1	NT	Homo sapiens Intersectin 2 (SH3D1B) mRNA, complete cds
2342	11535	20759	0.91	2.0E-98	AF248540.1	NT	Homo sapiens Intersectin 2 (SH3D1B) mRNA, complete cds
3096	12332	21458	1.3	2.0E-98	AB032377.1	NT	Homo sapiens hCHK1 gene for checkpoint kinase, exon 2
3096	12332	21459	1.3	2.0E-98	AB032377.1	NT	Homo sapiens hCHK1 gene for checkpoint kinase, exon 2
4084	13293	22392	1.45	2.0E-98	8923308	NT	Homo sapiens hypothetical protein FLJ20333 (FLJ20333), mRNA
4284	13487	22566	0.84	2.0E-98	AF032897.1	NT	Homo sapiens potassium channel subunit (HERG-3) mRNA, complete cds
4333	13534	22625	3.89	2.0E-98	4758331	NT	Homo sapiens fatty-acid-Coenzyme A ligase, long-chain 4 (FACL4) mRNA
4843	14032	23123	1.04	2.0E-98	AF218902.1	NT	Homo sapiens attractin precursor (ATRIN) gene, exon 16
4843	14032	23124	1.04	2.0E-98	AF218902.1	NT	Homo sapiens attractin precursor (ATRIN) gene, exon 16
5384	14613	23726	5.47	2.0E-98	7706512	NT	Homo sapiens PDZ domain-containing guanine nucleotide exchange factor 1 (LOC51735), mRNA
6658	15853	25312	3.8	2.0E-98	11428813	NT	Homo sapiens SH3-domain GRB2-like 2 (SH3GL2), mRNA
6658	15853	25313	3.8	2.0E-98	11428813	NT	Homo sapiens SH3-domain GRB2-like 2 (SH3GL2), mRNA
8626	17619	23971	4.63	2.0E-98	11435947	NT	Homo sapiens chromosome 12 open reading frame 3 (C12ORF3), mRNA
411	9664	18804	50.73	1.0E-98	AI862007.1	EST_HUMAN	W36804.x1 NC1_CGAP_U11 Homo sapiens cDNA clone IMAGE:2281743 3' similar to SW:RL2B_HUMAN
461	9714	18849	2.16	1.0E-98	AW998611.1	EST_HUMAN	P26316 60S RIBOSOMAL PROTEIN L23A. ;
							PMO-BN0065-100300-001-c06 BN0065 Homo sapiens cDNA

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1768	10976	20165	45.72	1.0E-98	N49818.1	EST_HUMAN	yv23f05.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:243585 5' similar to PIR:S54204 S54204 ribosomal protein L29 - human ;
5342	14572	23648	3.57	1.0E-98	AA195854.1	EST_HUMAN	z98c08.r1 Stratagene muscle 937209 Homo sapiens cDNA clone IMAGE:628240 5' similar to TR:G806562
6764	15959	25413	3.58	1.0E-98	AF141349.1	NT	G806562 NEBULIN. ;
6764	15959	25414	3.58	1.0E-98	AF141349.1	NT	Homo sapiens beta-tubulin mRNA, complete cds
5880	14900	24294	4.01	9.0E-99	AW968635.1	EST_HUMAN	Homo sapiens beta-tubulin mRNA, complete cds
7682	16881	26388	2.79	9.0E-99	A1479829.1	EST_HUMAN	EST1380711 IMAGE resequences, MAGJ Homo sapiens cDNA
7682	16881	26388	2.79	9.0E-99	A1479829.1	EST_HUMAN	EST1380711 IMAGE resequences, MAGJ Homo sapiens cDNA
7952	17091	26621	2.22	9.0E-99	AA134604.1	EST_HUMAN	EST1380711 IMAGE resequences, MAGJ Homo sapiens cDNA
5585	14809	24183	9.28	7.0E-99	AF035908.1	NT	EST1380711 IMAGE resequences, MAGJ Homo sapiens cDNA
8134	17287	26811	2.64	7.0E-99	AF001886.1	NT	EST1380711 IMAGE resequences, MAGJ Homo sapiens cDNA
478	9730	18604	0.66	6.0E-99	U10991.1	NT	EST1380711 IMAGE resequences, MAGJ Homo sapiens cDNA
2097	11297	20509	2.73	6.0E-99	11430555	NT	EST1380711 IMAGE resequences, MAGJ Homo sapiens cDNA
2097	11297	20510	2.73	6.0E-99	11430555	NT	EST1380711 IMAGE resequences, MAGJ Homo sapiens cDNA
4760	13951	23052	1.05	6.0E-99	4502660	NT	EST1380711 IMAGE resequences, MAGJ Homo sapiens cDNA
5228	14402	23485	0.95	6.0E-99	8923244	NT	EST1380711 IMAGE resequences, MAGJ Homo sapiens cDNA
6705	15900	25361	2.55	6.0E-99	AB036429.1	NT	EST1380711 IMAGE resequences, MAGJ Homo sapiens cDNA
6735	15930	25389	4.2	6.0E-99	AF080255.1	NT	EST1380711 IMAGE resequences, MAGJ Homo sapiens cDNA
6735	15930	25389	4.2	6.0E-99	AF080255.1	NT	EST1380711 IMAGE resequences, MAGJ Homo sapiens cDNA
7307	16525	26016	4.46	6.0E-99	11526289	NT	EST1380711 IMAGE resequences, MAGJ Homo sapiens cDNA
929	10163	18319	0.59	5.0E-99	U35464.1	NT	EST1380711 IMAGE resequences, MAGJ Homo sapiens cDNA
929	10163	18320	0.59	5.0E-99	U35464.1	NT	EST1380711 IMAGE resequences, MAGJ Homo sapiens cDNA
1934	11138	20334	1.39	5.0E-99	Y11365.1	NT	EST1380711 IMAGE resequences, MAGJ Homo sapiens cDNA
4582	13756	22854	1.41	5.0E-99	AF009680.1	NT	EST1380711 IMAGE resequences, MAGJ Homo sapiens cDNA
8637	17626		2.18	5.0E-99	BE890177.1	EST_HUMAN	EST1380711 IMAGE resequences, MAGJ Homo sapiens cDNA
6569	15765		6.7	3.0E-99	M85586.1	NT	EST1380711 IMAGE resequences, MAGJ Homo sapiens cDNA
1246	10463		13.38	2.0E-99	AW274792.1	EST_HUMAN	EST1380711 IMAGE resequences, MAGJ Homo sapiens cDNA
3225	12459	21592	1.58	2.0E-99	M30938.1	NT	EST1380711 IMAGE resequences, MAGJ Homo sapiens cDNA
4498	13696	22789	0.82	2.0E-99	BE612554.1	EST_HUMAN	EST1380711 IMAGE resequences, MAGJ Homo sapiens cDNA

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## Single Exon Probes Expressed in HELA Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4498	13698	22780	0.82	2.0E-99	BE612554.1	EST_HUMAN	601452087F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3855781 5'
4540	13735	22833	2.2	2.0E-99	AF095703.1	NT	Homo sapiens short chain L-3-hydroxyacyl-CoA dehydrogenase precursor (HADHSC) gene, nuclear gene encoding mitochondrial protein, complete cds
6883	15878	25337	2.24	2.0E-99	W23507.1	EST_HUMAN	zb46d08.r1 Soares, fetal lung, NBRL 19W Homo sapiens cDNA clone IMAGE:306635 5' similar to gb:M16182 BETA-GLUCURONIDASE PRECURSOR (HUMAN);
7670	16869	26372	4.48	2.0E-99	AF247457.2	NT	Homo sapiens myosin X (MYO10) mRNA, complete cds
320	9591	18722	1.48	1.0E-99	AF114487.1	NT	Homo sapiens intersectin long isoform (ITSN) mRNA, complete cds
384	9848	18783	0.88	1.0E-99	11528150	NT	Homo sapiens GA-binding protein transcription factor, alpha subunit (60kD) (GABPA), mRNA
1425	10638	19808	5	1.0E-99	M30038.1	NT	Human Ku (p70/p80) subunit mRNA, complete cds
1541	10754	19927	1.5	1.0E-99	AF192523.1	NT	Homo sapiens truncated Niemann-Pick C3 protein (NPC3) mRNA, complete cds
1541	10754	19928	1.5	1.0E-99	AF192523.1	NT	Homo sapiens truncated Niemann-Pick C3 protein (NPC3) mRNA, complete cds
1895	11102	20283	1.21	1.0E-99	4503730	NT	Homo sapiens FK506-binding protein 6 (38kD) (FKBP6) mRNA, and translated products
1895	11102	20284	1.21	1.0E-99	4503730	NT	Homo sapiens FK506-binding protein 6 (38kD) (FKBP6) mRNA, and translated products
3050	12286	21412	1.22	1.0E-99	J03171.1	NT	Human interferon-alpha receptor (HuIFN-alpha-Rec) mRNA, complete cds
4374	13576	22872	2.53	1.0E-99	AF098018.1	NT	Homo sapiens fatty acid amide hydrolase (FAAH) gene, exon 14
4374	13576	22873	2.53	1.0E-99	AF098018.1	NT	Homo sapiens fatty acid amide hydrolase (FAAH) gene, exon 14
6922	16115	25581	2.58	1.0E-99	AW340174.1	EST_HUMAN	h402h02.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2908371 3' similar to TR:002711
7741	16937	26446	1.78	1.0E-99	5801979	NT	O02711 PRO-POL-DUTPASE POLYPROTEIN;
7916	17131	26661	2.7	1.0E-99	AB023222.1	NT	Homo sapiens heat shock transcription factor 2 binding protein (HSF2BP), mRNA
8286	17393	26923	1.78	1.0E-99	AF223391.1	NT	Homo sapiens mRNA for KIAA1005 protein, partial cds
8387	17488		4.43	1.0E-99	AF240786.1	NT	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-48, and partial cds, alternatively spliced
1	9299	18401	2.49	1.0E-100	AL163247.2	NT	Homo sapiens glutathione S-transferase theta 2 (GSTT2) and glutathione S-transferase theta 1 (GSTT1) genes, complete cds
2	9299	18401	4.78	1.0E-100	AL163247.2	NT	Homo sapiens chromosome 21 segment HS21C047
96	9363	18487	1.69	1.0E-100	11418230	NT	Homo sapiens chromosome 21 segment HS21C047
88	9363	18488	1.69	1.0E-100	11418230	NT	Homo sapiens Testis-specific XK-related protein on Y (XKRY), mRNA
86	9379	18510	0.69	1.0E-100	AW275237.1	EST_HUMAN	Homo sapiens Testis-specific XK-related protein on Y (XKRY), mRNA
172	9453	18584	0.83	1.0E-100	AL163206.2	NT	xa78b11.x1 NCJ_CGAP_Brm53 Homo sapiens cDNA clone IMAGE:2824605 3'
322	9593	18724	1.06	1.0E-100	AL163249.2	NT	Homo sapiens chromosome 21 segment HS21C006
348	9616	18743	2.37	1.0E-100	T05087.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C049
443	9697		1.92	1.0E-100	AF003528.1	NT	EST02975 Fetal brain, Stralagene (cat#936208) Homo sapiens cDNA clone HFBGR32
							Homo sapiens X-linked anhidrotic ectodermal dysplasia protein gene (EDA), exon 2 and flanking repeat regions

Table 4

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
496	9749		6.33	1.0E-100	X99331.1	NT	G.gorilla DNA for ZNF80 gene homolog
516	9787	18893	1.06	1.0E-100	BE160609.1	EST_HUMAN	RC3-H10625-040500-022-b09 HT0625 Homo sapiens cDNA
1026	10252	19402	2.26	1.0E-100	7661685	NT	Homo sapiens DKFZP586M0122 protein (DKFZP586M0122), mRNA
1026	10252	19403	2.26	1.0E-100	7661685	NT	Homo sapiens DKFZP586M0122 protein (DKFZP586M0122), mRNA
1532	10746		1.36	1.0E-100	AW207555.1	EST_HUMAN	UI-H-B1-efk-c-07-U1.s1 NC1_CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2722164 3'
1536	10749	19922	1.26	1.0E-100	AI200857.1	EST_HUMAN	qf52106.x1 Scores_testis_NHT Homo sapiens cDNA clone IMAGE:1754633 3' similar to SW:CYT_COTJA
2207	11404		1.09	1.0E-100	D83349.1	NT	P81081 CYSTATIN 1
2401	11594	20812	0.99	1.0E-100	X62498.1	NT	Rat mRNA for short type PB-cadherin, complete cds
2667	11848	21063	1.09	1.0E-100	11418976	NT	H. sapiens mRNA for IFN-gamma (pKC-0)
2983	12220		5.64	1.0E-100	D11078.1	NT	Homo sapiens KIAA0957 protein (KIAA0957), mRNA
4193	13397	22487	1.68	1.0E-100	AF057354.1	NT	Homo sapiens RGH2 gene, retrovirus-like element
4221	13424	22517	2.1	1.0E-100	4503792	NT	Homo sapiens myotubularin-related protein 1a mRNA, partial cds
5123	14302	23390	3.15	1.0E-100	5032104	NT	Homo sapiens follicle stimulating hormone receptor (FSHR) mRNA
5123	14302	23391	3.15	1.0E-100	5032104	NT	Homo sapiens small optic lobes (Drosophila) homolog (SOLH) mRNA
5319	14551	23621	1.73	1.0E-100	BF244218.1	EST_HUMAN	Homo sapiens small optic lobes (Drosophila) homolog (SOLH) mRNA
5536	14760	24127	1.98	1.0E-100	AU118182.1	EST_HUMAN	Homo sapiens small optic lobes (Drosophila) homolog (SOLH) mRNA
5875	15093	24506	5.22	1.0E-100	AU140214.1	EST_HUMAN	Homo sapiens small optic lobes (Drosophila) homolog (SOLH) mRNA
6037	15245	24687	5.68	1.0E-100	X04571.1	NT	Homo sapiens small optic lobes (Drosophila) homolog (SOLH) mRNA
6831	15827	25289	10.17	1.0E-100	BF103853.1	EST_HUMAN	Homo sapiens small optic lobes (Drosophila) homolog (SOLH) mRNA
6843	15838		8.14	1.0E-100	AL163203.2	NT	Human mRNA for kidney epidermal growth factor (EGF) precursor
6837	16031	25496	2.53	1.0E-100	AB040918.1	NT	Homo sapiens chromosome 21 segment HS21C003
6952	16130	25598	2.6	1.0E-100	AB046846.1	NT	Homo sapiens mRNA for KIAA1485 protein, partial cds
6952	16130	25599	2.6	1.0E-100	AB046846.1	NT	Homo sapiens mRNA for KIAA1826 protein, partial cds
7343	16559	26047	6.66	1.0E-100	BF327292.1	EST_HUMAN	Homo sapiens mRNA for KIAA1826 protein, partial cds
7834	17026	26542	3.59	1.0E-100	X94633.1	NT	MRO-BN0070-270300-008-h11 BN0070 Homo sapiens cDNA
7834	17026	26543	3.59	1.0E-100	X94633.1	NT	H. sapiens CD97 gene exon 4
7834	17026	26543	3.59	1.0E-100	X94633.1	NT	H. sapiens CD97 gene exon 4
7893	17109	26638	4.35	1.0E-100	AF111170.3	NT	Homo sapiens 14q32 Jagged2 gene, complete cds; and unknown gene
7893	17109	26639	4.35	1.0E-100	AF111170.3	NT	Homo sapiens 14q32 Jagged2 gene, complete cds; and unknown gene
7922	8269	18401	2.41	1.0E-100	AL163247.2	NT	Homo sapiens chromosome 21 segment HS21C047
8178	17311		2.07	1.0E-100	AF266285.1	NT	Homo sapiens golgin-like protein (GLP) gene, complete cds
8309	17414	26936	8.55	1.0E-100	AF240786.1	NT	Homo sapiens glutathione S-transferase theta 2 (GSTT2) and glutathione S-transferase theta 1 (GSTT1) genes, complete cds

Page 298 of 382  
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8439	18237		1.33	1.0E-100	BF446549.1	EST_HUMAN	7q88h03.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE: 3' similar to TR:Q21897 Q21897
8827	17820	23972	2.51	1.0E-100	11545732	NT	COSMID R151. [2] TR:Q8UA08
8875	17772	23941	1.51	1.0E-100	11418123	NT	Homo sapiens SH3-domain binding protein 1 (SH3BP1), mRNA
9282	18028	23854	4.18	1.0E-100	11417974	NT	Homo sapiens transcobalamin II; macrocytic anemia (TCN2), mRNA
77	9371	18500	0.89	1.0E-101	7110714	NT	Homo sapiens SEC14 (S. cerevisiae)-like 2 (SEC14L2), mRNA
77	9371	18501	0.89	1.0E-101	7110714	NT	Homo sapiens SEC14 (S. cerevisiae)-like 2 (SEC14L2), mRNA
683	8938	18068	1.7	1.0E-101	AB007815.2	NT	Homo sapiens mRNA for KIAA0448 protein, partial cds
711	9853	18082	5.91	1.0E-101	7110734	NT	Homo sapiens ventral anterior homeobox 2 (VAX2), mRNA
711	9853	18083	5.91	1.0E-101	7110734	NT	Homo sapiens ventral anterior homeobox 2 (VAX2), mRNA
780	10019	18168	2.81	1.0E-101	7657454	NT	Homo sapiens ventral anterior homeobox 2 (VAX2), mRNA
883	10099	18261	2.81	1.0E-101	4503914	NT	Homo sapiens pascadillo (zetafish) homolog 1, containing BRCT domain (PES1), mRNA
934	10167	18324	1	1.0E-101	Z20656.1	NT	Homo sapiens phosphoribosylglycinamide formyltransferase, phosphoribosylglycinamide synthetase, phosphoribosylaminimidazole synthetase (GART) mRNA
892	10223	19380	8.49	1.0E-101	BF681218.1	EST_HUMAN	Homo sapiens of cardiac alpha-myosin heavy chain gene
1059	10285	19435	1.86	1.0E-101	AJ221878.1	EST_HUMAN	602159474F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4297281 5'
1562	10776	19951	1.09	1.0E-101	5921460	NT	qg99e09.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1843336 3'
1562	10776	19952	1.09	1.0E-101	5921460	NT	Homo sapiens butyrophilin, subfamily 2, member A1 (BTN2A1), mRNA
1814	11119	20318	2.15	1.0E-101	4502898	NT	Homo sapiens butyrophilin, subfamily 2, member A1 (BTN2A1), mRNA
2023	11224	20432	5.82	1.0E-101	BE43070.1	EST_HUMAN	Homo sapiens carboxypeptidase A1 (pancreatic) (GPA1) mRNA
2318	12015	20732	1.12	1.0E-101	5729892	NT	RC3-ST0281-160600-018-H09 ST0281 Homo sapiens cDNA
2577	11763	20984	6.66	1.0E-101	X72893.1	NT	Homo sapiens A kinase (PRKA) anchor protein 8 (AKAP8), mRNA
2700	11879	21094	12.23	1.0E-101	AJ237744.1	NT	H. sapiens EWS gene, exon 5
2700	11879	21095	12.23	1.0E-101	AJ237744.1	NT	Homo sapiens RIBIR gene (partial), exon 12
2808	12148		15.41	1.0E-101	AJ252312.1	NT	Homo sapiens RIBIR gene (partial), exon 12
3167	12402	21537	2.87	1.0E-101	4885270	NT	Homo sapiens genomic downstream Rhesus box
3207	12441		2.4	1.0E-101	BF035327.1	EST_HUMAN	Homo sapiens gamma-glutamyltransferase 1 (GGT1) mRNA
3359	12587	21726	3.41	1.0E-101	AW985556.1	EST_HUMAN	601458531F1 NIH_MGC_86 Homo sapiens cDNA clone IMAGE:3862088 5'
3378	11879	21094	3.41	1.0E-101	AJ237744.1	NT	EST37029 MAGI resequences, MAGI Homo sapiens cDNA
3378	11879	21095	3.41	1.0E-101	AJ237744.1	NT	Homo sapiens RIBIR gene (partial), exon 12
3858	13074	22189	5.17	1.0E-101	AB022785.1	NT	Homo sapiens RIBIR gene (partial), exon 12
5058	14238	23327	1.2	1.0E-101	5921460	NT	Homo sapiens ASH2L gene, complete cds, similar to Drosophila ash2 gene
5058	14238	23328	1.2	1.0E-101	5921460	NT	Homo sapiens butyrophilin, subfamily 2, member A1 (BTN2A1), mRNA
5170	14349	23437	0.73	1.0E-101	BE612554.1	EST_HUMAN	Homo sapiens butyrophilin, subfamily 2, member A1 (BTN2A1), mRNA
							601452087F1 NIH_MGC_86 Homo sapiens cDNA clone IMAGE:3855781 5'

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5170	14349	23438	0.73	1.0E-101	BE612554.1	EST_HUMAN	601452087F1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3855761 5'
5654	14877	24265	4.27	1.0E-101	7427512	NT	Homo sapiens cytoplasmic linker 2 (CYLN2), mRNA
5654	14877	24266	4.27	1.0E-101	7427512	NT	Homo sapiens cytoplasmic linker 2 (CYLN2), mRNA
6218	15369	24840	4.91	1.0E-101	AF208970.1	NT	Homo sapiens Kruppel-type zinc finger protein (PEG3) mRNA, alternative splice form 4, partial cds
6218	15369	24841	4.91	1.0E-101	AF208970.1	NT	Homo sapiens Kruppel-type zinc finger protein (PEG3) mRNA, alternative splice form 4, partial cds
6283	15464	24906	4.88	1.0E-101	AW008475.1	EST_HUMAN	w55f12.x1 NCI_CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2533487 3'
6324	15505		1.73	1.0E-101	BE257384.1	EST_HUMAN	601109217F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3349901 5'
6385	15585	25022	6.59	1.0E-101	BF330759.1	EST_HUMAN	RC1-BT0313-220700-018-F12 BT0313 Homo sapiens cDNA
6483	15680	25149	4.94	1.0E-101	BF029174.1	EST_HUMAN	601764686F1 NIH_MGC_53 Homo sapiens cDNA clone IMAGE:3996837 5'
6896	15605	25070	25.34	1.0E-101	X60069.1	NT	Human mRNA for pancreatic gamma-glutamyltransferase
6896	15605	25071	25.34	1.0E-101	X60069.1	NT	Human mRNA for pancreatic gamma-glutamyltransferase
6804	16081	25528	16.67	1.0E-101	9845492	NT	Homo sapiens gamma-glutamyltransferase 1 (GGT1), transcript variant 3, mRNA
7003	16181	25653	4.96	1.0E-101	BE19687.1	EST_HUMAN	601472808T1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3875953 3'
7003	16181	25654	4.96	1.0E-101	BE19687.1	EST_HUMAN	601472808T1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3875953 3'
7188	16365	25845	2.7	1.0E-101	11429127	NT	Homo sapiens Janus kinase 2 (a protein tyrosine kinase) (JAK2), mRNA
7192	16369	25848	4.46	1.0E-101	AI570293.1	EST_HUMAN	to77d11.x1 NCI_CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2184309 3' similar to gb:M26326
7192	16369	25849	4.46	1.0E-101	AI570293.1	EST_HUMAN	KERATIN, TYPE I CYTOSKELETAL 18 (HUMAN);
8905	17798		5.23	1.0E-101	AW639051.1	EST_HUMAN	to77d11.x1 NCI_CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2184309 3' similar to gb:M26326
41	9337	18444	0.9	1.0E-102	AF012872.1	NT	QV1-DT0088-240200-085-a01 DT0088 Homo sapiens cDNA
346	9814	18740	3.75	1.0E-102	AL163303.2	NT	Homo sapiens phosphatidylinositol 4-kinase 230 (p4K230) mRNA, complete cds
626	9871	18993	1.28	1.0E-102	BE252470.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C103
784	10023	19173	1.51	1.0E-102	4557534	NT	601108292F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3344326 5'
1125	10349	19500	2.13	1.0E-102	M10976.1	NT	Homo sapiens down-regulated in adenoma (DRA) mRNA
1275	10490	19648	1.28	1.0E-102	11437148	NT	Human endogenous retroviral DNA (4-1), complete retroviral segment
1275	10490	19649	1.28	1.0E-102	11437148	NT	Homo sapiens solute carrier family 2 (facilitated glucose transporter), member 9 (SLC2A9), mRNA
1423	10636	19805	387.84	1.0E-102	BE408447.1	EST_HUMAN	Homo sapiens solute carrier family 2 (facilitated glucose transporter), member 9 (SLC2A9), mRNA
2275	11470	20691	4.52	1.0E-102	AI124669.1	EST_HUMAN	60129982F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3629901 5'
2275	11470	20692	4.52	1.0E-102	AI124669.1	EST_HUMAN	arm60c10.x1 Johnston frontal cortex Homo sapiens cDNA clone IMAGE:1539954 3' similar to
3029	12685	21393	1.55	1.0E-102	7681979	NT	SW:GG95_HUMAN Q08379 GOLGIN-95 ;
3098	12334	21480	3.08	1.0E-102	AU141005.1	EST_HUMAN	arm60c10.x1 Johnston frontal cortex Homo sapiens cDNA clone IMAGE:1539954 3' similar to



Page 300 of 382  
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3098	12334	21481	3.08	1.0E-102	AU141005.1	EST_HUMAN	AU141005 PLACE4 Homo sapiens cDNA clone PLACE4000650 5'
4217	13420	22515	1.84	1.0E-102	AL163207.2	NT	Homo sapiens chromosome 21 segment HS21C007
4406	13608	22705	1.96	1.0E-102	BE251310.1	EST_HUMAN	601107843F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3349882 5'
5145	14324	23415	0.97	1.0E-102	F68488.1	EST_HUMAN	y32c04.r1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:140634 5'
5550	14774		5.79	1.0E-102	AB034951.1	NT	Homo sapiens HSC54 mRNA for heat shock cognate protein 54, complete cds
5567	14792	24164	3.16	1.0E-102	7705398	NT	Homo sapiens histone deacetylase 7 (HDAC7), mRNA
5567	14792	24165	3.16	1.0E-102	7705398	NT	Homo sapiens histone deacetylase 7 (HDAC7), mRNA
5783	15001	24404	2.82	1.0E-102	AA59825.1	EST_HUMAN	ar82f09.x1 Barstead colon HPLRB7 Homo sapiens cDNA clone IMAGE:2151785 3' similar to TR:Q13137
6233	15414	24855	8.1	1.0E-102	AJ238964.1	NT	Q13137 NDP52 ; Homo sapiens mRNA for Centaurin-alpha2 protein
6346	15528	24974	2.87	1.0E-102	AV710738.1	EST_HUMAN	AV710738 Cu Homo sapiens cDNA clone CUAAD003 5'
6860	16050	25516	2.68	1.0E-102	T70393.1	EST_HUMAN	ydl3d07.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:67021 5'
6860	16050	25517	2.68	1.0E-102	T70393.1	EST_HUMAN	ydl3d07.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:67021 5'
6882	16073	25542	3.85	1.0E-102	AU124629.1	EST_HUMAN	AU124629 NT2RM4 Homo sapiens cDNA clone NT2RM4000309 5'
7205	16382	25862	3.09	1.0E-102	AI905037.1	EST_HUMAN	RC-BT074-260499-014 BT074 Homo sapiens cDNA
7205	16382	25863	3.09	1.0E-102	AI905037.1	EST_HUMAN	RC-BT074-260499-014 BT074 Homo sapiens cDNA
7640	16940	26337	2.15	1.0E-102	4507822	NT	Homo sapiens UDP glycosyltransferase 2 family, polypeptide B11 (UGT2B11) mRNA
7640	16940	26338	2.15	1.0E-102	4507822	NT	Homo sapiens UDP glycosyltransferase 2 family, polypeptide B11 (UGT2B11) mRNA
7842	17082	26610	3.51	1.0E-102	BF359243.1	EST_HUMAN	RC8-ET0072-150600-011-F01 ET0072 Homo sapiens cDNA
8200	17332	26875	4.71	1.0E-102	U41302.1	NT	Human chromosome 16 creatine transporter (SLC6A8) and (CDM) paralogous genes, complete cds
8315	17419		3.74	1.0E-102	AL163280.2	NT	Homo sapiens chromosome 21 segment HS21C080
8890	17785	23819	5.19	1.0E-102	AW300862.1	EST_HUMAN	x407c12.x1 NCI_CGAP_Co20 Homo sapiens cDNA clone IMAGE:2666038 3'
69	9364	18489	3.08	1.0E-103	BE908158.1	EST_HUMAN	601500405F1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3902305 5'
69	9364	18490	3.08	1.0E-103	BE908158.1	EST_HUMAN	601500405F1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3902305 5'
100	9393	18522	9.97	1.0E-103	D67078.2	NT	Homo sapiens mRNA for KIAA0235 protein, partial cds
213	9493	18625	3.06	1.0E-103	5453793	NT	Homo sapiens nucleolar protein (KKEID repeat) (NOP56) mRNA
988	10218	18373	0.89	1.0E-103	AJ278348.1	NT	Homo sapiens mRNA for pregnancy-associated plasma protein-E (PAPPE gene)
1250	10486	19630	7.51	1.0E-103	BE877541.1	EST_HUMAN	601485388F1 NIH_MGC_69 Homo sapiens cDNA clone IMAGE:3887676 5'
1576	10789	19665	2.39	1.0E-103	AF012872.1	NT	Homo sapiens phosphatidylinositol 4-kinase 230 (p4K230) mRNA, complete cds
1879	11086	20276	1.08	1.0E-103	7657592	NT	Homo sapiens smg GDS-ASSOCIATED PROTEIN (SMAP), mRNA
1944	11148	20348	1.12	1.0E-103	4502428	NT	Homo sapiens bone morphogenetic protein 8 (osteogenic protein 2) (BMP8) mRNA
1944	11148	20349	1.12	1.0E-103	4502428	NT	Homo sapiens bone morphogenetic protein 8 (osteogenic protein 2) (BMP8) mRNA
2270	11465	20866	2.26	1.0E-103	AU134991.1	EST_HUMAN	AU134991 PLACE1 Homo sapiens cDNA clone PLACE1000665 5'

Page 301 of 382  
Table 4  
Single Exon Probes Expressed in HELA Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2414	11605	20827	1.66	1.0E-103	AF060568.1	NT	Homo sapiens promyelocytic leukemia zinc finger protein (PLZF) gene, complete cds
2583	11769	20889	2.7	1.0E-103	N32770.1	EST_HUMAN	yw91d08.s1 Soares_placenta_8to9weeks_2NBP809W Homo sapiens cDNA clone IMAGE:259599 3'
3033	12269		2.84	1.0E-103	BE744722.1	EST_HUMAN	601573113F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3634315 5'
3358	12586	21725	3.16	1.0E-103	AW298245.1	EST_HUMAN	UI-H-BW0-ajf-h-11-Q-UL.s1 NCI CGAP Sub8 Homo sapiens cDNA clone IMAGE:2733165 3'
3418	12843	21772	1.28	1.0E-103	AB040892.1	NT	Homo sapiens mRNA for KIAA1459 protein, partial cds
3737	12957		24.88	1.0E-103	AF023861.1	NT	Macaca mulatta cyclophilin A mRNA, complete cds
3776	12994	22110	1.05	1.0E-103	AA485663.1	EST_HUMAN	ab10d12.s1 Strategene lung (#837210) Homo sapiens cDNA clone IMAGE:340407 3' similar to contains element LTR10 repetitive element;
3980	13194	22302	2.68	1.0E-103	T23683.1	EST_HUMAN	seq340 b4HB3MA-Cor109+10-Bio Homo sapiens cDNA clone b4HB3MA-Cor109+10-Bio-7 3'
4838	14025	23119	0.63	1.0E-103	BE600203.1	EST_HUMAN	601873135F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3955953 5'
5972	15186	24604	1.63	1.0E-103	AI590071.1	EST_HUMAN	Im58b05.x1 NCI CGAP Bm25 Homo sapiens cDNA clone IMAGE:2162289 3' similar to TR:Q13769
5972	15186	24605	1.63	1.0E-103	AI590071.1	EST_HUMAN	Im58b05.x1 NCI CGAP Bm25 Homo sapiens cDNA clone IMAGE:2162289 3' similar to TR:Q13769
6017	14507	23575	1.62	1.0E-103		NT	Homo sapiens dystrophin (muscular dystrophy, Duchenne and Becker types), includes DXS164, DXS206, DXS230, DXS238, DXS268, DXS269, DXS270, DXS272 (DMD), transcript variant Dp427m, mRNA
6017	14507	23576	1.62	1.0E-103		NT	Homo sapiens dystrophin (muscular dystrophy, Duchenne and Becker types), includes DXS164, DXS206, DXS230, DXS238, DXS268, DXS269, DXS270, DXS272 (DMD), transcript variant Dp427m, mRNA
6224	15405	24846	3.42	1.0E-103	BE748158.1	EST_HUMAN	601571537F1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:3839545 5'
6404	15585	25042	3.78	1.0E-103	AI590071.1	EST_HUMAN	Im58b05.x1 NCI CGAP Bm25 Homo sapiens cDNA clone IMAGE:2162289 3' similar to TR:Q13769
6404	15585	25043	3.78	1.0E-103	AI590071.1	EST_HUMAN	Im58b05.x1 NCI CGAP Bm25 Homo sapiens cDNA clone IMAGE:2162289 3' similar to TR:Q13769
6809	16004	25464	3.8	1.0E-103	6005921	NT	Homo sapiens triple functional domain (PTPRF interacting) (TRIO), mRNA
6809	16004	25465	3.8	1.0E-103	6005921	NT	Homo sapiens triple functional domain (PTPRF interacting) (TRIO), mRNA
7093	16270	25747	2.45	1.0E-103	Z37876.1	NT	H sapiens mRNA for latent transforming growth factor-beta binding protein (LTBP-2)
7112	16289	25770	2.96	1.0E-103	AW963876.1	EST_HUMAN	EST375749 MAGE resequences, MAGH Homo sapiens cDNA
7146	16323	25805	14.27	1.0E-103	AI878956.1	EST_HUMAN	au51g04.y1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2518326 5' similar to TR:Q15048 Q15048 KIAA0338;
7319	16536	26024	7.29	1.0E-103	AI792759.1	EST_HUMAN	PHOSPHOLIPASE C NEIGHBORING;

Page 302 of 382  
Table 4  
Single Exon Probes Expressed in HELA Cells

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7410	16622	26115	1.75	1.0E-103	11424081	NT	Homo sapiens AXL receptor tyrosine kinase (AXL), mRNA
7410	16622	26116	1.75	1.0E-103	11424081	NT	Homo sapiens AXL receptor tyrosine kinase (AXL), mRNA
7421	16632	26124	2.86	1.0E-103	AF149773.1	NT	Homo sapiens NOD1 protein (NOD1) gene, exons 1, 2, and 3
7421	16632	26125	2.86	1.0E-103	AF149773.1	NT	Homo sapiens NOD1 protein (NOD1) gene, exons 1, 2, and 3
7914	17129	26659	2.68	1.0E-103	AU136283.1	EST_HUMAN	AU136283 PLACE1 Homo sapiens cDNA clone PLACE1003923 5'
7982	16417	25904	5.33	1.0E-103	L43610.1	NT	Homo sapiens polycystic kidney disease (PKD1) gene, exons 27-30
8230	17359	26898	3.38	1.0E-103	BE944611.1	EST_HUMAN	7668a10.r1 Soares_NSF_F8_GW_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:3287610 3' similar to contains MER29.13 MER29 repetitive element
8310	17415		2.27	1.0E-103	AF224669.1	NT	Homo sapiens mannosidase, beta A, lysosomal (MANBA) gene, and ubiquitin-conjugating enzyme E2D 3 (UBE2D3) genes, complete cds
8340	17437		2.53	1.0E-103	11528291	NT	Homo sapiens hypothetical protein FLJ20454 (FLJ20454), mRNA
8546	17571	23992	2.58	1.0E-103	AB011399.1	NT	Homo sapiens gene for AF-6, complete cds
239	9518	18647	2.5	1.0E-104	AL037549.3	EST_HUMAN	DKFZp564H1072_r1 584 (synonym: hibr2) Homo sapiens cDNA clone DKFZp564H1072 5'
239	9518	18648	2.5	1.0E-104	AL037549.3	EST_HUMAN	DKFZp564H1072_r1 584 (synonym: hibr2) Homo sapiens cDNA clone DKFZp564H1072 5'
1853	11060	20251	1.92	1.0E-104	4502428	NT	Homo sapiens bone morphogenetic protein 8 (osteogenic protein 2) (BMP8) mRNA
2160	11358	20576	23.83	1.0E-104	AA132675.1	EST_HUMAN	z022008.s1 Stratagene cdn (#837204) Homo sapiens cDNA clone IMAGE:567628 3' similar to gb:Z14116.mal1 CD59 GLYCOPROTEIN PRECURSOR (HUMAN);
2170	11367	20588	10.72	1.0E-104	BE744628.1	EST_HUMAN	801577460F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3828438 5'
2337	11530	20752	10.57	1.0E-104	BF334221.1	EST_HUMAN	RC1-CT0249-110900-214-f12 CT0249 Homo sapiens cDNA
2337	11530	20753	10.57	1.0E-104	BF334221.1	EST_HUMAN	RC1-CT0249-110900-214-f12 CT0249 Homo sapiens cDNA
2400	11583	20811	7.19	1.0E-104	5031570	NT	Homo sapiens ARP2 (actin-related protein 2, yeast) homolog (ACTR2), mRNA
2487	11658	20878	4.12	1.0E-104	7662125	NT	Homo sapiens KIAA0440 protein (KIAA0440), mRNA
2487	11658	20879	4.12	1.0E-104	7662125	NT	Homo sapiens KIAA0440 protein (KIAA0440), mRNA
2823	12062	21185	13.3	1.0E-104	M34671.1	NT	Human lymphocytic antigen CD59/MEM43 mRNA, complete cds
2887	12105		2.26	1.0E-104	Y11151.1	NT	H. sapiens gene encoding phenylpyruvate tautomerase II
3230	12484	21596	1.01	1.0E-104	AU133928.1	EST_HUMAN	AU133928 OVARC1 Homo sapiens cDNA clone OVARC1000936 5'
3368	12506		2.12	1.0E-104	AA319436.1	EST_HUMAN	EST121658 Adrenal gland tumor Homo sapiens cDNA 5' end
3579	12801	21927	0.91	1.0E-104	AB033102.1	NT	Homo sapiens mRNA for KIAA1276 protein, partial cds
3579	12801	21928	0.91	1.0E-104	AB033102.1	NT	Homo sapiens mRNA for KIAA1276 protein, partial cds
3918	13134	22251	1.03	1.0E-104	AB032698.1	NT	Homo sapiens mRNA for KIAA1172 protein, partial cds
4112	13318	22419	0.85	1.0E-104	F11745.1	EST_HUMAN	HSC31A071 normalized infant brain cDNA Homo sapiens cDNA clone c-31a07
4371	13573	22689	4.33	1.0E-104	X02781.1	NT	Human mRNA for fibronectin (FN precursor)
4610	13804	22894	0.94	1.0E-104	AF231920.1	NT	Homo sapiens chromosome 21 unknown mRNA
4610	13804	22895	0.94	1.0E-104	AF231920.1	NT	Homo sapiens chromosome 21 unknown mRNA

Page 303 of 382  
Table 4  
Single Exon Probes Expressed in HELA Cells

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5855	15073	24484	8.42	1.0E-104	A1768797.1	EST_HUMAN	wj03b12.x1 NCL_CGAP_Kid12 Homo sapiens cDNA clone IMAGE:2401727 3' similar to TR:Q1414145 Q14145
5855	15073	24485	8.42	1.0E-104	A1768797.1	EST_HUMAN	KIAA0132 PROTEIN, contains element LTR7 repetitive element;
5998	15281	24713	2.3	1.0E-104	BE314182.1	EST_HUMAN	wj03b12.x1 NCL_CGAP_Kid12 Homo sapiens cDNA clone IMAGE:2401727 3' similar to TR:Q1414145 Q14145
5998	15281	24714	2.3	1.0E-104	BE314182.1	EST_HUMAN	KIAA0132 PROTEIN, contains element LTR7 repetitive element;
6178	15358	24708	1.82	1.0E-104	11425572	NT	601150451F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3503220 5'
6858	16048	25512	7.16	1.0E-104	AF091395.1	NT	Homo sapiens adaptor-related protein complex 2, beta 1 subunit (AP2B1), mRNA
6858	16048	25513	7.16	1.0E-104	AF091395.1	NT	Homo sapiens Trio isoform mRNA, complete cds
6890	15598	25059	5.48	1.0E-104	BF352841.1	EST_HUMAN	IL3-HT0618-080900-249-F07 HT0618 Homo sapiens cDNA
6890	15598	25060	6.48	1.0E-104	BF352841.1	EST_HUMAN	IL3-HT0618-080900-249-F07 HT0618 Homo sapiens cDNA
7106	16283	25763	5.13	1.0E-104	BE781713.1	EST_HUMAN	601581503F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3935977 5'
7106	16283	25764	5.13	1.0E-104	BE781713.1	EST_HUMAN	601581503F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3935977 5'
7193	16370	25850	4.72	1.0E-104	AU130765.1	EST_HUMAN	AU130765 HT2RP3 Homo sapiens cDNA clone NT2RP3001388 5'
7218	16395	25878	5.56	1.0E-104	U66535.1	NT	Human beta4-integrin (ITGB4) gene, exons 19,20,21,22,23,24 and 25
7844	17036	26551	1.89	1.0E-104	BE720191.1	EST_HUMAN	RCQ-HT0885-310700-021-b09 HT0885 Homo sapiens cDNA
7844	17036	26552	1.89	1.0E-104	BE720191.1	EST_HUMAN	RCQ-HT0885-310700-021-b09 HT0885 Homo sapiens cDNA
7872	17081	26585	5.29	1.0E-104	BF684288.1	EST_HUMAN	602141215F1 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4302507 5'
9159	17958		1.43	1.0E-104	BE383892.1	EST_HUMAN	601312181F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3558876 5'
283	11937	18691	4.48	1.0E-105	4502166	NT	Homo sapiens amyloid beta (A4) precursor protein (protease nexin-II, Alzheimer disease) (APP), mRNA
431	9298	18308	17.77	1.0E-105	4505150	NT	Homo sapiens Mals1 (mouse) homolog (MEIS1) mRNA
601	9848	18986	8.49	1.0E-105	AF032897.1	NT	Homo sapiens potassium channel subunit (HERG-3) mRNA, complete cds
601	9848	18987	8.49	1.0E-105	AF032897.1	NT	Homo sapiens potassium channel subunit (HERG-3) mRNA, complete cds
1854	10888		3.22	1.0E-105	AB020881.1	NT	Homo sapiens mRNA for cyclin B2, complete cds
1789	10959	20104	1.68	1.0E-105	AL163280.2	NT	Homo sapiens chromosome 21 segment HS21C080
1804	11101	20292	2.64	1.0E-105	D50918.1	NT	Human mRNA for KIAA0128 gene, partial cds
2156	11354	20572	5.87	1.0E-105	AA318369.1	EST_HUMAN	EST20609 Spleen 1 Homo sapiens cDNA 5' and similar to autoimmunity antigen Ku, p70/p80 subunit
2280	11485		0.92	1.0E-105	BE891788.1	EST_HUMAN	601434491F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3919511 5'
2680	11882		0.89	1.0E-105	AA584808.1	EST_HUMAN	no10005.st NCL_CGAP_Phe1 Homo sapiens cDNA clone IMAGE:1100265 3'
2866	12204		3.44	1.0E-105	AJ280411.1	NT	Homo sapiens 969 kb contig between AML1 and CBRT on chromosome 21q22, segment 1/3
3298	12530	21661	1.73	1.0E-105	BF347753.1	EST_HUMAN	602022595F1 NCL_CGAP_Bn67 Homo sapiens cDNA clone IMAGE:4158143 5'
3298	12530	21662	1.73	1.0E-105	BF347753.1	EST_HUMAN	602022595F1 NCL_CGAP_Bn67 Homo sapiens cDNA clone IMAGE:4158143 5'
3325	12554	21680	1.01	1.0E-105	7304922	NT	Homo sapiens bromodomain adjacent to zinc finger domain, 2B (BAZ2B), mRNA

Table 4

## Single Exon Probes Expressed in HELA Cells

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3325	12554	21691	1.01	1.0E-105	7304922	NT	Homo sapiens bromodomain adjacent to zinc finger domain, 2B (BAZ2B), mRNA
4075	13285	22383	2.88	1.0E-105	AW061688.1	EST_HUMAN	EST373781 IMAGE:3850156 5'
4755	13946	23046	0.64	1.0E-105	BE868881.1	EST_HUMAN	601445823F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3850156 5'
4755	13946	23047	0.64	1.0E-105	BE868881.1	EST_HUMAN	601445823F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3850156 5'
4957	14144		5.22	1.0E-105	AL163208.2	NT	Homo sapiens chromosome 21 segment HS21C008
5137	14315	23409	0.98	1.0E-105	AB018339.1	NT	Homo sapiens mRNA for KIAA0798 protein, partial cds
5195	14371	23458	0.69	1.0E-105	AW068015.1	EST_HUMAN	EST378088 IMAGE:3850156 5'
6079	14525	23546	3.33	1.0E-105	11419198	NT	Homo sapiens GTPase activating protein-like (GAPL), mRNA
6079	14525	23547	3.33	1.0E-105	11419198	NT	Homo sapiens GTPase activating protein-like (GAPL), mRNA
6473	15670	25141	8.43	1.0E-105	T05087.1	EST_HUMAN	EST02875 Fetal brain, Strategene (cat#836206) Homo sapiens cDNA clone HFBGR32
6785	15980	25440	3.95	1.0E-105	AW016879.1	EST_HUMAN	UI-H-B10p-abi-b-12.0.U1.s1 NCI_CGAP_Sub2 Homo sapiens cDNA clone IMAGE:2711782 3'
7508	16712	26200	6.62	1.0E-105	AF254822.1	NT	Homo sapiens SMARCA4 isoform (SMARCA4) gene, complete cds, alternatively spliced
7782	16977	26490	2.18	1.0E-105	D63548.1	NT	Homo sapiens COL4A6 gene for $\alpha 2(V)$ collagen, exon 31
7850	17022	26537	2.26	1.0E-105	7708636	NT	Homo sapiens Ran binding protein 11 (LOC51194), mRNA
8115	17249	26789	2.41	1.0E-105	AW027554.1	EST_HUMAN	w7407.x1 Soares_thymus_NHFT Homo sapiens cDNA clone IMAGE:2535301 3' similar to TR:P87892
154	9436		1.85	1.0E-106	AW503208.1	EST_HUMAN	UI-HF-BND-akt-g-07-0.U1.r1 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3078348 5'
210	9490	18623	1.58	1.0E-106	AI565085.1	EST_HUMAN	U79c01.x1 NCI_CGAP_U11 Homo sapiens cDNA clone IMAGE:2215008 3'
548	9799	18924	1.98	1.0E-106	AW605556.1	EST_HUMAN	EST377629 IMAGE:3850156 5'
611	9858	18977	1.87	1.0E-106	J00146.1	NT	Human dihydrofolate reductase pseudogene (psl-hd1)
612	9858	18977	2.89	1.0E-106	J00146.1	NT	Human dihydrofolate reductase pseudogene (psl-hd1)
1511	10725	18997	1.01	1.0E-106	AF145712.1	NT	Homo sapiens soluble neuropilin-1 mRNA, complete cds
1678	10898	20074	4.47	1.0E-106	U48724.1	NT	Human epidermal growth factor receptor (EGFR) precursor-mRNA, exon 4, partial cds
1694	10908	20092	1.72	1.0E-106	U04510.1	NT	Homo sapiens type IV collagen alpha 5 chain (COL4A5) gene, exon 41
1772	10982	20172	5.79	1.0E-106	AA527446.1	EST_HUMAN	ng41cd5.s1 NCI_CGAP_C03 Homo sapiens cDNA clone IMAGE:937352 3' similar to contains element LTR3 repetitive element
1772	10982	20173	5.79	1.0E-106	AA527446.1	EST_HUMAN	ng41cd5.s1 NCI_CGAP_C03 Homo sapiens cDNA clone IMAGE:937352 3' similar to contains element LTR3 repetitive element
2283	11478	20700	7.27	1.0E-106	4504184	NT	Homo sapiens glutathione S-transferase theta 1 (GSTT1), mRNA
2489	11680	20881	4.02	1.0E-106	AF003528.1	NT	Homo sapiens X-linked anhidrotic ectodermal dysplasia protein gene (EDA), exon 2 and flanking repeat regions
2561	11747	20987	1.21	1.0E-106	U84875.2	NT	Homo sapiens sperm membrane protein BS-63 mRNA, complete cds
2563	11749	20989	1.18	1.0E-106	BE260201.1	EST_HUMAN	601149783F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3502481 5'
2713	11892	21110	9.2	1.0E-106	AI276526.1	EST_HUMAN	q78h10.x1 Soares_NHMPu_S1 Homo sapiens cDNA clone IMAGE:1878307 3'

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## Single Exon Probes Expressed in HELA Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2777	10648	19821	2.45	1.0E-106	4504184	NT	Homo sapiens glutathione S-transferase theta 1 (GSTT1), mRNA
2777	10648	19822	2.45	1.0E-106	4504184	NT	Homo sapiens glutathione S-transferase theta 1 (GSTT1), mRNA
2828	12067	21188	2.2	1.0E-106	BE384296.1	EST_HUMAN	601272675F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3613818 5'
2892	12129	21263	6.26	1.0E-106	AB037747.1	NT	Homo sapiens mRNA for KIAA1326 protein, partial cds
2892	12129	21264	6.26	1.0E-106	AB037747.1	NT	Homo sapiens mRNA for KIAA1326 protein, partial cds
3145	12380	21511	2.8	1.0E-106	8922965	NT	Homo sapiens hypothetical protein FLJ11273 (FLJ11273), mRNA
3145	12380	21512	2.8	1.0E-106	8922965	NT	Homo sapiens hypothetical protein FLJ11273 (FLJ11273), mRNA
3352	12580	21720	0.65	1.0E-106	AB008681.1	NT	Homo sapiens gene for activin receptor type IIB, complete cds
3790	13008	22123	0.99	1.0E-106	AF001445.1	NT	Homo sapiens core binding factor alpha 1 subunit (CBFA1) gene, exon 2
4015	13227	22328	10.33	1.0E-106	AW974650.1	EST_HUMAN	EST386875 MAGC resequences, MAGN Homo sapiens cDNA
4015	13227	22329	10.33	1.0E-106	AW974650.1	EST_HUMAN	EST386875 MAGC resequences, MAGN Homo sapiens cDNA
4034	13244	22347	1.34	1.0E-106	5729729	NT	Homo sapiens API5-like 1 (API5L1), mRNA
4601	13795	22885	0.73	1.0E-106	BE144286.1	EST_HUMAN	MRO-HT0165:140200-008-410 HT0165 Homo sapiens cDNA
4918	14106	23200	1.48	1.0E-106	U31520.1	NT	Human alpha mannosidase II mRNA, complete cds
5381	14610	23722	2.35	1.0E-106	AA781155.1	EST_HUMAN	aj24x09.s1 Soares testis_NHT Homo sapiens cDNA clone 1391225 3' similar to gb:X12433 PROTEIN
5708	14927	24322	14.75	1.0E-106	BF679574.1	EST_HUMAN	PHPS1-2 (HUMAN);
5836	15053	24460	18.72	1.0E-106	11545913	NT	602154012F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4295067 5'
5836	15053	24461	18.72	1.0E-106	11545913	NT	Homo sapiens xylosyltransferase II (XT2), mRNA
6243	15424	24865	4.9	1.0E-106	AA663779.1	EST_HUMAN	Homo sapiens xylosyltransferase II (XT2), mRNA
6261	15442	24881	4.59	1.0E-106	11429617	NT	ae72e07.s1 Stralagene schizo brain S11 Homo sapiens cDNA clone IMAGE:969732 3' similar to gb:X65873
6341	15521	24968	8.36	1.0E-106	11425503	NT	Homo sapiens XPMC2 protein (LOC57109), mRNA
6341	15521	24969	8.36	1.0E-106	11425503	NT	Homo sapiens sorting nexin 11 (SNX11), mRNA
6458	15655	25125	6.43	1.0E-106	BE741408.1	EST_HUMAN	Homo sapiens sorting nexin 11 (SNX11), mRNA
6458	15655	25126	6.43	1.0E-106	BE741408.1	EST_HUMAN	601594331F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3948463 5'
6517	15713	25178	2.23	1.0E-106	AI523066.1	EST_HUMAN	601594331F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3948463 5'
6682	15877	25336	2.64	1.0E-106	AI654123.1	EST_HUMAN	ar68a07.x1 Barstead aorta HPLRB6 Homo sapiens cDNA clone IMAGE:2127732 3' similar to gb:X06233 CALGRANULIN B (HUMAN);
6816	16011	25474	2.41	1.0E-106	AA825307.1	EST_HUMAN	iy62a05.x1 NCI_CGAP_Kid1 Homo sapiens cDNA clone IMAGE:2283632 3' similar to SW:ICA6_HUMAN
6816	16011	25475	2.41	1.0E-106	AA825307.1	EST_HUMAN	Q05084.69 KD ISLET CELL AUTOANTIGEN ;
7148	16325	25808	6.74	1.0E-106	AA604417.1	EST_HUMAN	oc67e08.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1354790 3'
7148	16325	25809	6.74	1.0E-106	AA604417.1	EST_HUMAN	oc67e08.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1354790 3'
							np57b10.s1 NCI_CGAP_B12 Homo sapiens cDNA clone IMAGE:1130395 3'
							np57b10.s1 NCI_CGAP_B12 Homo sapiens cDNA clone IMAGE:1130395 3'

Page 306 of 382  
Table 4  
Single Exon Probes Expressed in HELA Cells

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7165	16342	25821	2.68	1.0E-106	AW363299.1	EST_HUMAN	RC0-CT0318-201199-031-a11 CT0318 Homo sapiens cDNA
7221	16398	25882	2.79	1.0E-106	AL163202.2	NT	Homo sapiens chromosome 21 segment HS21C002
7472	16680	26162	6.77	1.0E-106	BF032755.1	EST_HUMAN	601453481F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3857368 5'
7472	16680	26163	6.77	1.0E-106	BF032755.1	EST_HUMAN	601453481F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3857368 5'
7629	16830	26327	2.56	1.0E-106	J05200.1	NT	Human ryanodine receptor mRNA, complete cds
7629	16830	26328	2.56	1.0E-106	J05200.1	NT	Human ryanodine receptor mRNA, complete cds
7948	17088	26615	2.41	1.0E-106	BE257385.1	EST_HUMAN	601108219F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3349997 5'
8077	17212	26743	1.82	1.0E-106	BE010882.1	EST_HUMAN	RC5-BN0192-100500-021-B02 BN0192 Homo sapiens cDNA
8077	17212	26744	1.82	1.0E-106	BE010882.1	EST_HUMAN	RC5-BN0192-100500-021-B02 BN0192 Homo sapiens cDNA
8384	18151		4.43	1.0E-106	AW410405.1	EST_HUMAN	fn05h11.x1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:2861644 5'
8618	17615	23968	2.49	1.0E-106	BE894488.1	EST_HUMAN	601433087F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3918524 5'
8618	17615	23969	2.49	1.0E-106	BE894488.1	EST_HUMAN	601433087F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3918524 5'
8843	17752		5.27	1.0E-106	BE995905.1	EST_HUMAN	RC1-CT0249-090800-024-d05 CT0249 Homo sapiens cDNA
240	9518		3.86	1.0E-107	AJ271735.1	NT	Homo sapiens Xq pseudautosomal region; segment 1/2
269	9544		1.37	1.0E-107	X60459.1	NT	Human IFNAR gene for interferon alpha/beta receptor
636	9881	19005	1.99	1.0E-107	AF155103.1	NT	Homo sapiens NY-REN-25 antigen mRNA, partial cds
823	10081	19213	1.06	1.0E-107	X60459.1	NT	Human IFNAR gene for interferon alpha/beta receptor
896	10131	19283	1.89	1.0E-107	X60459.1	NT	Human IFNAR gene for interferon alpha/beta receptor
976	10208	19363	11.69	1.0E-107	AF154121.1	NT	Homo sapiens sodium-dependent high-affinity dicarboxylate transporter (NADC3) mRNA, complete cds
1285	10500	19661	1.31	1.0E-107	AB032253.1	NT	Homo sapiens BAZ1B mRNA for bromodomain adjacent to zinc finger domain 1B, complete cds
1550	10764	19938	4.8	1.0E-107	BF087405.1	EST_HUMAN	QV2-HT0540-120900-358-a05 HT0540 Homo sapiens cDNA
1724	10936	20119	5.69	1.0E-107	AF136275.1	NT	Homo sapiens cathepsin Z precursor (CTS2) gene, exon 3
2175	11372	20584	1.07	1.0E-107	U13729.1	NT	Human dipeptidyl peptidase IV (CD26) gene, exon 20
2330	11523	20745	10.58	1.0E-107	AW842451.1	EST_HUMAN	PM1-CN0031-190100-001-d03 CN0031 Homo sapiens cDNA
2330	11523	20746	10.58	1.0E-107	AW842451.1	EST_HUMAN	PM1-CN0031-190100-001-d03 CN0031 Homo sapiens cDNA
2500	11689	20909	2.56	1.0E-107	BE732460.1	EST_HUMAN	601567619F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3842309 5'
2500	11689	20910	2.56	1.0E-107	BE732460.1	EST_HUMAN	601567619F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3842309 5'
2967	12205	21340	3.76	1.0E-107	AW842451.1	EST_HUMAN	PM1-CN0031-190100-001-d03 CN0031 Homo sapiens cDNA
2967	12205	21341	3.76	1.0E-107	AW842451.1	EST_HUMAN	PM1-CN0031-190100-001-d03 CN0031 Homo sapiens cDNA
3065	12301	21425	3.94	1.0E-107	5902067	NT	Homo sapiens SMT3 (suppressor of mit two 3, yeast) homolog 2 (SMT3H2), mRNA
3818	13034	22145	4.53	1.0E-107	AF020671.1	NT	Homo sapiens myotubularin (MTM1) gene, exon 9
5567	14821	24168	2.68	1.0E-107	BE867469.1	EST_HUMAN	601442568F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3846494 5'
6239	15420	24860	1.82	1.0E-107	AW503913.1	EST_HUMAN	UI-HF-BND-alf-c-09-Q-UI-r1 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3076310 5'

Page 307 of 382  
Table 4  
Single Exon Probes Expressed in HELA Cells

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6239	15420	24881	1.82	1.0E-107	AW503913.1	EST_HUMAN	UI-HF-BND-af-c-08-Q-UJ1 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3079310 5'
7293	16512	26004	3.78	1.0E-107	A1392850.1	EST_HUMAN	tg10d08.x1 NCI_CGAP_GLL1 Homo sapiens cDNA clone IMAGE:2108363 3' similar to SW:AACT_DICDI
7520	16725	26216	1.91	1.0E-107	L49141.1	NT	P05095 ALPHA-ACTININ 3, NON MUSCULAR
7531	16736	26226	2.86	1.0E-107	BF666511.1	EST_HUMAN	Homo sapiens neuroendocrine-specific protein (NSP) gene, exon 4
7868	17058	26579	4.19	1.0E-107	BE540550.1	EST_HUMAN	602123933F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:4281039 5'
7831	16407	25891	4.65	1.0E-107	11419701	NT	601066881F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3452828 5'
7831	16407	25892	4.65	1.0E-107	11419701	NT	Homo sapiens HSPC049 protein (HSPC049), mRNA
8450	18293						Homo sapiens HSPC049 protein (HSPC049), mRNA
8476	18147		5.84	1.0E-107	AA001415.1	EST_HUMAN	ze45a01.s1 Soares retina N2b4HR Homo sapiens cDNA clone IMAGE:361944 3' similar to contains THR.b1 THR repetitive element
181	9481		1.52	1.0E-107	11418318	NT	Homo sapiens G-2 and S-phase expressed 1 (GTSE1), mRNA
962	10195	19350	1.35	1.0E-108	AA341834.1	EST_HUMAN	EST47363 Fetal muscle Homo sapiens cDNA 5' end
1272	10487	19645	1.48	1.0E-108	BE286042.1	EST_HUMAN	601177018F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3532348 5'
2046	11247	20457	3.83	1.0E-108	Y18000.1	NT	Homo sapiens NF2 gene
			2.49	1.0E-108	BF028728.1	EST_HUMAN	601671914F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3954939 5'
2391	11584	20802	107.38	1.0E-108	BE206894.1	EST_HUMAN	bb25b10.x1 NIH_MGC_14 Homo sapiens cDNA clone IMAGE:2963899 3' similar to gb:X63777 60S RIBOSOMAL PROTEIN L23 (HUMAN); gb:J05277 Mouse hexokinase mRNA, complete cds (MOUSE);
3323	12552	21686	0.71	1.0E-108	AF032897.1	NT	Homo sapiens potassium channel subunit (HERG-3) mRNA, complete cds
3323	12552	21687	0.71	1.0E-108	AF032897.1	NT	Homo sapiens potassium channel subunit (HERG-3) mRNA, complete cds
3802	13020	22132	1.04	1.0E-108	5453855	NT	Homo sapiens pericentriolar material 1 (PCM1) mRNA
4139	13345	22445	1.37	1.0E-108	AW684438.1	EST_HUMAN	ht12a11.x1 NCI_CGAP_GU1 Homo sapiens cDNA clone IMAGE:2972060 3' similar to SW:3BP1_MOUSE
4525	13721	22818	6.72	1.0E-108	U72861.1	NT	P55194 SH3-BINDING PROTEIN 3BP-1
4525	13721	22817	6.72	1.0E-108	U72861.1	NT	Human hepatocyte nuclear factor 4-alpha gene, exon 2
4818	14007	23107	3.11	1.0E-108	7681979	NT	Human hepatocyte nuclear factor 4-alpha gene, exon 2
4839	14126	23222	0.77	1.0E-108	AW504799.1	EST_HUMAN	Homo sapiens KIAA0187 gene product (KIAA0187), mRNA
4868	14155	23247	2.17	1.0E-108	AJ008005.1	NT	UI-HF-BND-eln-e-04-Q-UJ1 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3080168 5'
5165	14344	23433	0.99	1.0E-108	5031624	NT	Homo sapiens PSN1 gene, alternative transcript
5197	14373	23460	1.06	1.0E-108	Y12460.1	NT	Homo sapiens CCAAT-box-binding transcription factor (CBF2) mRNA
5454	14680	23840	3.03	1.0E-108	BE869016.1	EST_HUMAN	Homo sapiens mRNA for Golgi-associated microtubule-binding protein (GNAP-210)
5454	14680	23841	3.03	1.0E-108	BE869016.1	EST_HUMAN	601444922F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3848980 5'
							601444922F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3848980 5'
5729	14948	24346	5.76	1.0E-108	AF264717.1	NT	Homo sapiens FYVE domain-containing dual specificity protein phosphatase FYVE-DSP2 mRNA, complete cds



Page 308 of 382  
Table 4  
Single Exon Probes Expressed in HELA Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5729	14948	24347	5.76	1.0E-108	AF264717.1	NT	Homo sapiens FIVE domain-containing dual specificity protein phosphatase FYVE-DSP2 mRNA, complete cds
6148	15330	24768	5.4	1.0E-108	11431857	NT	Homo sapiens G protein-coupled receptor, family C, group 5, member B (GPCR5B), mRNA
6269	15449	24888	2.13	1.0E-108	4758333	NT	Homo sapiens delta-6 fatty acid desaturase (FADS6), mRNA
6485	15682		2.74	1.0E-108	AF083500.1	NT	Homo sapiens connective tissue growth factor-like protein precursor, mRNA, complete cds
7260	15591	25052	2.23	1.0E-108	BE53527.1	EST_HUMAN	601058769F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3445361 5'
7404	14373	23460	1.9	1.0E-108	Y12490.1	NT	Homo sapiens mRNA for Golgi-associated microtubule-binding protein (GMAP-210)
7632	16833	26330	1.84	1.0E-108	AF223391.1	NT	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced
7820	17013	26527	5.69	1.0E-108	AW966185.1	EST_HUMAN	EST378258 IMAGE resequences, MAGI Homo sapiens cDNA
7910	17125		2.41	1.0E-108	11441465	NT	Homo sapiens G protein-coupled receptor 48 (GPR48), mRNA
7966	17145	26679	1.7	1.0E-108	D63539.1	NT	Homo sapiens COL4A6 gene for $\alpha 6$ (IV) collagen, exon 23
8633	17623	23973	3.18	1.0E-108	AK024447.1	NT	Homo sapiens mRNA for FLJ00037 protein, partial cds
8040	17882		6.89	1.0E-108	BF346368.1	EST_HUMAN	602018571F1 NCI_CGAP_Bn67 Homo sapiens cDNA clone IMAGE:4154287 5'
44	9340	18447	1.37	1.0E-108	AW803116.1	EST_HUMAN	IL2-UM0077-260400-079-D08 UM0077 Homo sapiens cDNA
67	9362	18486	2.74	1.0E-109	D86974.1	NT	Human mRNA for KIAA0220 gene, partial cds
223	9502	18633	0.83	1.0E-109	11422486	NT	Homo sapiens hypothetical protein FLJ11318 (FLJ11316), mRNA
232	9510	18638	6.14	1.0E-109	11438391	NT	Homo sapiens reticulocalbin 1, EF-hand calcium binding domain (RCN1), mRNA
473	9726	18858	3.14	1.0E-109	4507712	NT	Homo sapiens tetratricopeptide repeat domain 2 (TTC2) mRNA
605	9852	18971	16.2	1.0E-109	AB023216.1	NT	Homo sapiens mRNA for KIAA0999 protein, partial cds
605	9852	18972	16.2	1.0E-109	AB023216.1	NT	Homo sapiens mRNA for KIAA0999 protein, partial cds
1210	10429	19585	41.99	1.0E-109	M28699.1	NT	Homo sapiens nucleolar phosphoprotein B23 (NPM1) mRNA, complete cds
1211	10429	19585	22.4	1.0E-109	M28699.1	NT	Homo sapiens nucleolar phosphoprotein B23 (NPM1) mRNA, complete cds
1528	10742	18914	1.35	1.0E-109	BE293873.1	EST_HUMAN	601186922F2 NIH_MGC_15 Homo sapiens cDNA clone IMAGE:2859636 5'
1528	10742	18915	1.35	1.0E-109	BE293873.1	EST_HUMAN	601186922F2 NIH_MGC_15 Homo sapiens cDNA clone IMAGE:2859636 5'
1840	11048	20238	5.02	1.0E-109	D13643.2	NT	Homo sapiens mRNA for KIAA0018 protein, partial cds
2206	11403	20628	4.37	1.0E-109	AL163284.2	NT	Homo sapiens chromosome 21 segment HS21C084
2215	11412	20638	2.87	1.0E-109	Y17123.1	NT	Homo sapiens SNF5/INI1 gene, exon 6
2585	11771	20991	3.53	1.0E-109	A1022328.1	EST_HUMAN	ow95a01.x1 Soares fetal_liver_spleen_INFLS_S1 Homo sapiens cDNA clone IMAGE:1654538 3' similar to TR-002197 002197 CIRCULATING CATHODIC ANTIGEN. ;
2585	11771	20992	3.53	1.0E-109	A1022328.1	EST_HUMAN	ow95a01.x1 Soares fetal_liver_spleen_INFLS_S1 Homo sapiens cDNA clone IMAGE:1654538 3' similar to TR-002197 002197 CIRCULATING CATHODIC ANTIGEN. ;
2586	11772	20993	2.16	1.0E-109	4504206	NT	Homo sapiens guanylate cyclase activator 1A (retina) (GUCA1A) mRNA

Table 4

## Single Exon Probes Expressed in HELA Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3023	12259	21387	1.32	1.0E-109	N85180.1	EST_HUMAN	J2816F Human fetal heart, Lambda ZAP Express Homo sapiens cDNA clone J2816 5' similar to ZINC FINGER PROTEIN ZNF43
3366	12594	21733	1.33	1.0E-109	AW883192.1	EST_HUMAN	GM3-NN0009-190400-150-f10 NN0009 Homo sapiens cDNA
3366	12594	21734	1.33	1.0E-109	AW883192.1	EST_HUMAN	GM3-NN0009-190400-150-f10 NN0009 Homo sapiens cDNA
3481	12715	21851	1.1	1.0E-109	AF240698.1	NT	Homo sapiens retinol dehydrogenase homolog isoform-1 (RDH) mRNA, complete cds
3828	13046		1.43	1.0E-109	BE146144.1	EST_HUMAN	MRO-HT0209-110400-108-e04 HT0209 Homo sapiens cDNA
4126	13335	22434	4.35	1.0E-109	AI855417.1	EST_HUMAN	ts98e08.x1 NCL_CGAP_GC6 Homo sapiens cDNA clone IMAGE:2239330 3' similar to WP.F53A2.8 CE16100
4144	13350	22450	1.02	1.0E-109	AA682274.1	EST_HUMAN	nu83c12.s1 NCL_CGAP_Pr22 Homo sapiens cDNA clone IMAGE:1218282 3' similar to SW.GTT2_HUMAN P30712 GLUTATHIONE S-TRANSFERASE THETA 2
4144	13350	22451	1.02	1.0E-109	AA682274.1	EST_HUMAN	nu83c12.s1 NCL_CGAP_Pr22 Homo sapiens cDNA clone IMAGE:1218282 3' similar to SW.GTT2_HUMAN P30712 GLUTATHIONE S-TRANSFERASE THETA 2
4398	13599	22700	2.55	1.0E-109	4504208	NT	Homo sapiens guanylate cyclase activator 1A (retina) (GUCA1A) mRNA
4600	13794	22884	1.26	1.0E-109	7682083	NT	Homo sapiens KIAA0377 gene product (KIAA0377) mRNA
5084	14264	23350	0.72	1.0E-109	BE283673.1	EST_HUMAN	601186922F2 NIH_MGC_15 Homo sapiens cDNA clone IMAGE:2859636 5'
5084	14264	23351	0.72	1.0E-109	BE283673.1	EST_HUMAN	601186922F2 NIH_MGC_15 Homo sapiens cDNA clone IMAGE:2859636 5'
5340	14570	23645	3.5	1.0E-109	5174822	NT	Homo sapiens placental protein 11 (serine proteinase) (P11) mRNA
6319	15501	24846	3.53	1.0E-109	11432574	NT	Homo sapiens AT-binding transcription factor 1 (ATBF1) mRNA
6320	15502	24947	5.4	1.0E-109	BF182707.1	EST_HUMAN	601809495F1 NIH_MGC_18 Homo sapiens cDNA clone IMAGE:4040279 5'
6320	15502	24948	5.4	1.0E-109	BF182707.1	EST_HUMAN	601809495F1 NIH_MGC_18 Homo sapiens cDNA clone IMAGE:4040279 5'
6692	15887	25346	12.39	1.0E-109	BE787540.1	EST_HUMAN	601479417F1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3882124 5'
6692	15887	25347	12.39	1.0E-109	BE787540.1	EST_HUMAN	601479417F1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3882124 5'
7385	18599	26087	25.47	1.0E-109	BF684831.1	EST_HUMAN	602080724F2 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4245341 5'
7539	18744	26237	2.35	1.0E-109	7662279	NT	Homo sapiens KIAA0744 gene product histone deacetylase 7 (KIAA0744) mRNA
7539	18744	26238	2.35	1.0E-109	7662279	NT	Homo sapiens KIAA0744 gene product histone deacetylase 7 (KIAA0744) mRNA
7685	18884	26392	1.97	1.0E-109	AU121370.1	EST_HUMAN	Homo sapiens KIAA0744 gene product histone deacetylase 7 (KIAA0744) mRNA
7909	17124	26655	2.23	1.0E-109	4502838	NT	Homo sapiens KIAA0744 gene product histone deacetylase 7 (KIAA0744) mRNA
7945	17085	26614	6.23	1.0E-109	W16510.1	EST_HUMAN	Homo sapiens Chediak-Higashi syndrome 1 (CHS1) mRNA
8529	11412	20636	2.3	1.0E-109	Y17123.1	NT	z008b12.r1 Soares_fetal_lung_NbHL19W Homo sapiens cDNA clone IMAGE:301439 5' similar to PIR.S43969 S43969 p54-beta stress-activated protein kinases - rat
8761	11412	20636	1.96	1.0E-109	Y17123.1	NT	Homo sapiens SNF5/INI1 gene, exon 6
8883	17778	23944	3.23	1.0E-109	AB011399.1	NT	Homo sapiens SNF5/INI1 gene, exon 6
3	6300	18402	1.41	1.0E-110	7549804	NT	Homo sapiens gene for AF-6, complete cds
39	6335	18441	4.02	1.0E-110	5803073	NT	Homo sapiens deiodinase, liothyronine, type II (DIO2), transcript variant 2, mRNA
							Homo sapiens leucine zipper-like transcriptional regulator, 1 (LZTR1) mRNA

### Single Exon Probes Expressed in HELA Cells

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Page 311 of 382  
Table 4  
Single Exon Probes Expressed in HELA Cells

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8469	17522		8.6	1.0E-110	AW062258.1	EST_HUMAN	IL0-BT0163-040899-094-g10 BT0163 Homo sapiens cDNA
8725	17677		2.64	1.0E-110	AB011399.1	NT	Homo sapiens gene for AF-6, complete cds
8868	18305		3.72	1.0E-110	BF364546.1	EST_HUMAN	PM3-NN1082-140900-006-112 NN1082 Homo sapiens cDNA
9158	11226		1.83	1.0E-110	BF508866.1	EST_HUMAN	UIH-B14-aos-b-05-0-UI.s1 NCI_CGAP_Sub8 Homo sapiens cDNA IMAGE:3085784 3'
178	9458		27.48	1.0E-111	U43701.1	NT	Human ribosomal protein L23a mRNA, complete cds
201	9481	18614	0.76	1.0E-111	4758807	NT	Homo sapiens ras GTPase activating protein-like (NGAP) mRNA
742	9983		2.19	1.0E-111	BF035327.1	EST_HUMAN	601456531F1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3882088 5'
751	9992	19138	4.09	1.0E-111	8393092	NT	Homo sapiens cat eye syndrome critical region gene 1 (CECR1), mRNA
935	10168	19325	3.28	1.0E-111	M25142.1	NT	Human cardiac alpha-myosin heavy chain (MYH6) gene, exons 32 to 34
3678	12899	22019	0.93	1.0E-111	6912641	NT	Homo sapiens sex comb on midleg homolog 1 (SCMH1), mRNA
3678	12899	22020	0.93	1.0E-111	6912641	NT	Homo sapiens sex comb on midleg homolog 1 (SCMH1), mRNA
4153	13359	22460	1.68	1.0E-111	7681569	NT	Homo sapiens DKFZP434D156 protein (DKFZP434D156), mRNA
4321	13522	22617	4.54	1.0E-111	K02268.1	NT	Human enkephalin B (enkb) gene, exon 4 and 3' flank and complete cds
4752	13943	23045	1.01	1.0E-111	4505778	NT	Homo sapiens phosphatase kinase, alpha 1 (muscle) (PHKA1), mRNA
6271	15451	24690	2.93	1.0E-111	BF366228.1	EST_HUMAN	IL2-NT0101-280700-114-E03 NT0101 Homo sapiens cDNA
6538	15734	25198	3.4	1.0E-111	U68533.1	NT	Human beta4-integrin (ITGB4) gene, exon 13
6720	15915		6.85	1.0E-111	BF214902.1	EST_HUMAN	601847132F1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:4078303 5'
6740	15935	25395	18.91	1.0E-111	X17033.1	NT	Human mRNA for Integrin alpha-2 subunit
6740	15935	25396	18.91	1.0E-111	X17033.1	NT	Human mRNA for Integrin alpha-2 subunit
6800	15995	26463	4.59	1.0E-111	AF091395.1	NT	Homo sapiens Tiro isoform mRNA, complete cds
7124	16301	25782	2.56	1.0E-111	AA504160.1	EST_HUMAN	aa58g02 s1 NCI_CGAP GC81 Homo sapiens cDNA clone IMAGE:825170 3' similar to gbL09235
7158	16335	25818	7.75	1.0E-111	AA131248.1	EST_HUMAN	VACUOLAR ATP SYNTHASE CATALYTIC SUBUNIT A, UBIQUITOUS (HUMAN);
7618	16816	26312	5.35	1.0E-111	U68159.1	NT	Z13101.1 Soares_pregnant_uterus NibHPU Homo sapiens cDNA clone IMAGE:503545 5'
8299	17407	26932	4.66	1.0E-111	11417901	NT	Human thrombopoietin receptor (MPL) gene, exons 1,2,3,4,5 and 6
8860	17763	23938	1.5	1.0E-111	AV708482.1	EST_HUMAN	Homo sapiens meningioma (disrupted in balanced translocation) 1 (MN1), mRNA
8982	18096	23804	2.08	1.0E-111	W22562.1	EST_HUMAN	AV708482 ADC Homo sapiens cDNA clone ADCAOB08 5'
9128	14505	23589	1.53	1.0E-111	AB035356.1	NT	7209 Human retina cDNA Tsp5091-cleaved sublibrary Homo sapiens cDNA not directional
614	9859	18978	0.98	1.0E-112	4501854	NT	Homo sapiens mRNA for neuraxin l-alpha protein, complete cds
616	9861	18980	6.43	1.0E-112	U29103.1	NT	Homo sapiens acetyl-Coenzyme A carboxylase beta (ACACB), mRNA
616	9861	18981	6.43	1.0E-112	U29103.1	NT	Human steroidogenic acute regulatory protein (SIAR) gene, exon 5
638	9883	18007	1.7	1.0E-112	BF509039.1	EST_HUMAN	Human steroidogenic acute regulatory protein (SIAR) gene, exon 5
638	9883	19008	1.7	1.0E-112	BF509039.1	EST_HUMAN	UIH-B14-aot-g-04-0-UI.s1 NCI_CGAP_Sub8 Homo sapiens cDNA clone IMAGE:3086023 3'
1009	10240	18392	3.97	1.0E-112	AF157623.1	NT	UIH-B14-aot-g-04-0-UI.s1 NCI_CGAP_Sub8 Homo sapiens cDNA clone IMAGE:3086023 3'

Page 312 of 382  
Table 4  
Single Exon Probes Expressed in HELA Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1069	10295	19444	1.67	1.0E-112	P52742	SWISSPROT	ZINC FINGER PROTEIN 135
1659	10872	20054	4.44	1.0E-112	7682125	NT	Homo sapiens KIAA0440 protein (KIAA0440), mRNA
1659	10872	20055	4.44	1.0E-112	7682125	NT	Homo sapiens KIAA0440 protein (KIAA0440), mRNA
2473	11664	20883	3.23	1.0E-112	BE86859.1	EST_HUMAN	601442674F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3846858 5'
3043	12280		0.82	1.0E-112	4504118	NT	Homo sapiens glutamate receptor, ionotropic, kainate 1 (GRIK1) mRNA
3211	12445	21577	1.35	1.0E-112	BE083092.1	EST_HUMAN	RC2-BT0642-030400-021-408 BT0642 Homo sapiens cDNA
3211	12445	21578	1.35	1.0E-112	BE083092.1	EST_HUMAN	RC2-BT0642-030400-021-408 BT0642 Homo sapiens cDNA
3336	12565	21703	0.61	1.0E-112	A1826511.1	EST_HUMAN	wk45b12.x1 NCI_CGAP_P722 Homo sapiens cDNA clone IMAGE:2418335 3' similar to gb:M81650_mai
3863	13079	22195	0.78	1.0E-112	BE076073.1	EST_HUMAN	SEMN0GELIN 1 PROTEIN PRECURSOR (HUMAN);
4604	13788	22888	0.82	1.0E-112	4504118	NT	MR2-BT0590-090300-113-409 BT0590 Homo sapiens cDNA
4763	13953	23053	5	1.0E-112	AB037832.1	NT	Homo sapiens glutamate receptor, ionotropic, kainate 1 (GRIK1) mRNA
4763	13953	23054	5	1.0E-112	AB037832.1	NT	Homo sapiens mRNA for KIAA1411 protein, partial cds
5521	14746	24114	37.86	1.0E-112	N46046.1	EST_HUMAN	Homo sapiens mRNA for KIAA1411 protein, partial cds
6526	15722	25187	3.4	1.0E-112	AU118031.1	EST_HUMAN	y95d07.1 Soares melanocyte 2bBHM Homo sapiens cDNA clone IMAGE:273229 5'
6756	15951	25408	3.08	1.0E-112	BE867635.1	EST_HUMAN	AU118031 HEMBA1 Homo sapiens cDNA clone HEMBA1002773 5'
6756	15951	25409	3.08	1.0E-112	BE867635.1	EST_HUMAN	601443151F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3847285 5'
7359	16575	26067	2.88	1.0E-112	AW863327.1	EST_HUMAN	601443151F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3847285 5'
7322	16727	26218	5.43	1.0E-112	AJ248900.1	NT	MR3-SN0009-100400-108-b12 SN0009 Homo sapiens cDNA
7662	16862	26364	1.98	1.0E-112	BE280479.1	EST_HUMAN	Homo sapiens mRNA for secreted modular calcium-binding protein (smoc1 gene)
7739	16835	26443	4.55	1.0E-112	AW377670.1	EST_HUMAN	601155323F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3138989 5'
8550	17757		1.37	1.0E-112	AF106656.1	NT	PMO-C70237-141099-001-h02 CT0237 Homo sapiens cDNA
750	9991	19134	5.03	1.0E-113	AJ365586.1	EST_HUMAN	Homo sapiens adenylosuccinate lyase gene, complete cds
750	9991	19135	5.03	1.0E-113	AJ365586.1	EST_HUMAN	ac95f01.x1 Schiller meningioma Homo sapiens cDNA clone IMAGE:1953625 3'
950	10183	19339	17.13	1.0E-113	M11965.1	NT	ac95f01.x1 Schiller meningioma Homo sapiens cDNA clone IMAGE:1953625 3'
1527	10741	19913	3.46	1.0E-113	AJ365586.1	EST_HUMAN	Human X-linked phosphoglycerate kinase gene, exon 8
1908	11948	20309	1.11	1.0E-113	AF240775.1	NT	ac95f01.x1 Schiller meningioma Homo sapiens cDNA clone IMAGE:1953625 3'
2064	11265	20478	0.98	1.0E-113	BF15218.1	EST_HUMAN	Homo sapiens eIF4E-transporter mRNA, complete cds
3094	12330	21456	1.75	1.0E-113	AJ23948.1	NT	UIH-BW1-enl-f-03-0-UJ.s1 NCI_CGAP_Sub7 Homo sapiens cDNA clone IMAGE:3082876 3'
5301	18134		3.33	1.0E-113	BE780858.1	EST_HUMAN	Homo sapiens mRNA for putative RNA helicase, 3' and
5439	14666	23819	6.09	1.0E-113	AU127214.1	EST_HUMAN	601469465F1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3872536 5'
5625	14849	24231	4.06	1.0E-113	AU140291.1	EST_HUMAN	AU127214 NT2RP2 Homo sapiens cDNA clone NT2RP2000807 5'
5698	14918	24312	2.36	1.0E-113	11525737	NT	AU140291 PLACE2 Homo sapiens cDNA clone PLACE2000274 5'
							Homo sapiens UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylglucosaminyltransferase 8 (GalNAc-T8) (GALNT8), mRNA

Page 313 of 382  
Table 4  
Single Exon Probes Expressed in HELA Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6803	15998	25456	3.64	1.0E-113	BE382842.1	EST_HUMAN	601297709F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3627554 5'
6803	15998	25457	3.64	1.0E-113	BE382842.1	EST_HUMAN	601297709F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3627554 5'
7683	16882	26390	1.75	1.0E-113	AW500518.1	EST_HUMAN	U1-HF-BND-ak4-b-12-0-U1.1 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3077326 5'
7691	16890	26397	3.01	1.0E-113	AW630291.1	EST_HUMAN	hh81a09.y1 NCL_CGAP_GU1 Homo sapiens cDNA clone IMAGE:2669176 5' similar to TR:O60327 O60327 KIAA0584 PROTEIN;
7691	16890	26398	3.01	1.0E-113	AW630291.1	EST_HUMAN	hh81a09.y1 NCL_CGAP_GU1 Homo sapiens cDNA clone IMAGE:2669176 5' similar to TR:O60327 O60327 KIAA0584 PROTEIN;
7812	17005	26518	3.6	1.0E-113	BE262968.1	EST_HUMAN	601105529F1 NIH_MGC_15 Homo sapiens cDNA clone IMAGE:2888368 5'
8031	17168	26708	3.34	1.0E-113	AA580720.1	EST_HUMAN	nc80603.r1 NCL_CGAP_GC1 Homo sapiens cDNA clone IMAGE:797089 5' similar to SW:FEN1_HUMAN P39748 FLAP ENDONUCLEASE-1;
8031	17168	26707	3.34	1.0E-113	AA580720.1	EST_HUMAN	nc80603.r1 NCL_CGAP_GC1 Homo sapiens cDNA clone IMAGE:797089 5' similar to SW:FEN1_HUMAN P39748 FLAP ENDONUCLEASE-1;
60	9356	18474	1.21	1.0E-114	Y17151.2	NT	Homo sapiens mRNA for multidrug resistance protein 3 (ABCC3)
60	9356	18475	1.21	1.0E-114	Y17151.2	NT	Homo sapiens mRNA for multidrug resistance protein 3 (ABCC3)
60	9356	18476	1.21	1.0E-114	Y17151.2	NT	Homo sapiens mRNA for multidrug resistance protein 3 (ABCC3)
651	9887	19023	8.43	1.0E-114	T70551.1	EST_HUMAN	Yd15c01.s1 Soares fetal liver spleen 1NLS Homo sapiens cDNA clone IMAGE:108288 3' similar to gb:A21187 ALPHA-2-MACROGLOBULIN PRECURSOR (HUMAN); contains Alu repetitive element;
1078	10303	19454	1.39	1.0E-114	8823087	NT	Homo sapiens hypothetical protein FLJ20080 (FLJ20080), mRNA
1320	10535	19699	4.23	1.0E-114	7657529	NT	Homo sapiens rhabdoid tumor deletion region protein 1 (RTDR1), mRNA
1619	10832	20007	4.87	1.0E-114	6631094	NT	Homo sapiens minichromosome maintenance deficient (S. cerevisiae) 3 (MCM3), mRNA
1647	10861	20042	8.45	1.0E-114	6679073	NT	Homo sapiens nucleoporin-like protein 1 (NLP_1), mRNA
2220	11417	20842	1.26	1.0E-114	AB002374.1	NT	Human mRNA for KIAA0376 gene, partial cds
2756	9342	18450	1.22	1.0E-114	AB033102.1	NT	Homo sapiens mRNA for KIAA1276 protein, partial cds
2756	9342	18451	1.22	1.0E-114	AB033102.1	NT	Homo sapiens mRNA for KIAA1276 protein, partial cds
3095	12331	21457	2.27	1.0E-114	X04086.1	NT	Human gene for catalase (EC 1.11.1.6) exon 2 mapping to chromosome 11, band p13
3136	12371	21502	1.26	1.0E-114	BF206374.1	EST_HUMAN	60186963F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4100214 5'
3992	13206	22312	1.54	1.0E-114	AF149773.1	NT	Homo sapiens NOD1 protein (NOD1) gene, exons 1, 2, and 3
4385	13586	22688	0.77	1.0E-114	J03171.1	NT	Human interferon-alpha receptor (HuIFN-alpha-Rec) mRNA, complete cds
5168	14347	23435	1.03	1.0E-114	BE275324.1	EST_HUMAN	601122173F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3348069 5'
5208	14381	23467	0.94	1.0E-114	AF004949.1	NT	Homo sapiens PKY protein kinase mRNA, complete cds
6201	15382	24823	9.02	1.0E-114	Y18000.1	NT	Homo sapiens NF2 gene
6201	15382	24824	9.02	1.0E-114	Y18000.1	NT	Homo sapiens NF2 gene
6425	15622	25086	2.57	1.0E-114	4557600	NT	Homo sapiens gamma-aminobutyric acid (GABA) A receptor, alpha 2 (GABRA2) mRNA

Page 314 of 382  
Table 4  
Single Exon Probes Expressed in HELA Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6680	15875	25334	4.26	1.0E-114	U63041.1	NT	Human neural cell adhesion molecule CD56 mRNA, complete cds
6706	15901	25362	7.86	1.0E-114	AB011133.1	NT	Homo sapiens mRNA for KIAA0561 protein, partial cds
6706	15901	25363	7.86	1.0E-114	AB011133.1	NT	Homo sapiens mRNA for KIAA0561 protein, partial cds
6884	16075		10.62	1.0E-114	AW327455.1	EST_HUMAN	dq0305 x1 NIH_MGC_2 Homo sapiens cDNA clone IMAGE:2846744 5'
6900	15606	25072	4.01	1.0E-114	AF077754.1	NT	Homo sapiens tyrosine kinase pp60c-src (SRC) gene, exon 12 and partial cds
							ba73g12.y1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:2906086 5' similar to gb:X17206 40S RIBOSOMAL PROTEIN S4 (HUMAN); gb:M20632 Mouse LLRep3 protein mRNA from a repetitive element, complete (MOUSE);
7368	16584		15.17	1.0E-114	BE302666.1	EST_HUMAN	
7745	16941	26452	3.76	1.0E-114	AV733454.1	EST_HUMAN	AV733454 cdA Homo sapiens cDNA clone cdABA08 5'
7745	16941	26453	3.76	1.0E-114	AV733454.1	EST_HUMAN	AV733454 cdA Homo sapiens cDNA clone cdABA08 5'
8767	18368		2.74	1.0E-114	11418041	NT	Homo sapiens TNF-Inducible protein CG12-1 (CG12-1), mRNA
9033	17878	23891	3.22	1.0E-114	11034850	NT	Homo sapiens hypothetical protein (DJ1042K10.2), mRNA
9033	17878	23892	3.22	1.0E-114	11034850	NT	Homo sapiens hypothetical protein (DJ1042K10.2), mRNA
23	9319	18423	5.81	1.0E-115	4758111	NT	Homo sapiens HLA-B associated transcript-1 (D6S81E) mRNA
127	9410	18544	2.5	1.0E-115	4505938	NT	Homo sapiens polymerase (RNA) II (DNA directed) polypeptide A (220kD) (POLR2A) mRNA
131	9414		16.52	1.0E-115	4557887	NT	
297	9570	18702	2.23	1.0E-115	AW604759.1	EST_HUMAN	Homo sapiens keratin 18 (KRT18) mRNA
							QV4-UMD094-300300-156-b08 UM0094 Homo sapiens cDNA
542	9793	18916	0.6	1.0E-115	AI339206.1	EST_HUMAN	q06f01.x1 NCJ_CGAP_GC4 Homo sapiens cDNA clone IMAGE:1946809 3' similar to TR:O00536 O00536 TTF-I INTERACTING PEPTIDE 5;
542	9793	18917	0.6	1.0E-115	AI339206.1	EST_HUMAN	q06f01.x1 NCJ_CGAP_GC4 Homo sapiens cDNA clone IMAGE:1946809 3' similar to TR:O00536 O00536 TTF-I INTERACTING PEPTIDE 5;
796	10035	19185	1.09	1.0E-115	5174702	NT	Homo sapiens transforming growth factor beta-activated kinase-binding protein 1 (TAB1), mRNA
796	10035	19186	1.09	1.0E-115	5174702	NT	Homo sapiens transforming growth factor beta-activated kinase-binding protein 1 (TAB1), mRNA
798	10037	19188	349.13	1.0E-115	4503794	NT	Homo sapiens ferritin, heavy polypeptide 1 (FTH1) mRNA
1808	11017	20210	1.36	1.0E-115	U78027.1	NT	Homo sapiens Bruton's tyrosine kinase (BTK), alpha-D-galactosidase A (GLA), L44-like ribosomal protein (L44L) and FTP3 (FTP3) genes, complete cds
2048	11249	20459	1.05	1.0E-115	BE745469.1	EST_HUMAN	601579838F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3928832 5'
2048	11249	20460	1.05	1.0E-115	BE745469.1	EST_HUMAN	601579838F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3928832 5'
2054	11255	20468	0.94	1.0E-115	AB007902.1	NT	Homo sapiens KIAA0442 mRNA, partial cds
2264	11459	20678	1.92	1.0E-115	AF231124.1	NT	Homo sapiens testican-1 mRNA, complete cds
3079	12315	21437	5.51	1.0E-115	AJ245922.1	NT	Homo sapiens mRNA for alpha-tubulin 8 (TUBA8 gene)
3079	12315	21438	5.51	1.0E-115	AJ245922.1	NT	Homo sapiens mRNA for alpha-tubulin 8 (TUBA8 gene)
3449	12674	21809	2.12	1.0E-115	AJ277892.1	NT	Homo sapiens partial TTN gene for titin
4019	13231	22334	3.93	1.0E-115	AB002348.2	NT	Homo sapiens mRNA for KIAA0350 protein, partial cds

Page 315 of 382  
Table 4  
Single Exon Probes Expressed in HELA Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4253	13456	22548	1.31	1.0E-115	AL137163.1	NT	Novel human gene mapping to chromosome X
4385	13598	22697	3.42	1.0E-115	6912659	NT	Homo sapiens sir2-like 3 (SIRT3), mRNA
4428	13628	22722	4.3	1.0E-115	4758279	NT	Homo sapiens EphA4 (EPHA4), mRNA
4591	13785	22876	1.84	1.0E-115	8922435	NT	Homo sapiens hypothetical protein FLJ10466 (FLJ10466), mRNA
4591	13785	22877	1.84	1.0E-115	8922435	NT	Homo sapiens hypothetical protein FLJ10466 (FLJ10466), mRNA
4678	13872	22971	2.9	1.0E-115	AL096857.1	NT	Novel human mRNA from chromosome 1, which has similarities to BAT2 genes
4679	13872	22972	2.9	1.0E-115	AL096857.1	NT	Novel human mRNA from chromosome 1, which has similarities to BAT2 genes
4827	14115	23210	3.92	1.0E-115	AL163268.2	NT	Homo sapiens chromosome 21 segment HS21C068
4827	14115	23211	3.92	1.0E-115	AL163268.2	NT	Homo sapiens chromosome 21 segment HS21C068
5363	14593	23670	1.74	1.0E-115	AW970335.1	EST_HUMAN	EST382416 IMAGE resequences, MAGK Homo sapiens cDNA
5463	14689	24040	1.79	1.0E-115	11425128	NT	Homo sapiens similar to ER to nucleus signalling 1 (H. sapiens) (LOC63433), mRNA
5463	14689	24041	1.79	1.0E-115	11425128	NT	Homo sapiens similar to ER to nucleus signalling 1 (H. sapiens) (LOC63433), mRNA
5828	15045	24449	14.79	1.0E-115	11426038	NT	Homo sapiens similar to ribosomal protein S28 (H. sapiens) (LOC63438), mRNA
5890	15107	24517	1.86	1.0E-115	7661883	NT	Homo sapiens KIAA0054 gene product; Helicase (KIAA0054), mRNA
5890	15107	24518	1.86	1.0E-115	7661883	NT	Homo sapiens KIAA0054 gene product; Helicase (KIAA0054), mRNA
6255	15436	24875	7.4	1.0E-115	AB023212.1	NT	Homo sapiens mRNA for KIAA0995 protein, partial cds
6511	15707	25172	6.99	1.0E-115	BE830187.1	EST_HUMAN	RC8-ET0081-130700-011-G01 ET0081 Homo sapiens cDNA
6511	15707	25173	6.99	1.0E-115	BE830187.1	EST_HUMAN	RC8-ET0081-130700-011-G01 ET0081 Homo sapiens cDNA
6722	15917	25376	9.46	1.0E-115	11434772	NT	Homo sapiens eukaryotic translation initiation factor 4B (EIF4B), mRNA
7305	16523	26014	3.52	1.0E-115	AW571544.1	EST_HUMAN	xc32f08.x1 NCI CGAP U91 Homo sapiens cDNA clone IMAGE:2839239 3' similar to SW:CAVP_CANFA
7838	17076	26804	2.64	1.0E-115	4502528	NT	P10463 CALYPHOSINE
8252	17380	26914	4.28	1.0E-115	BF361864.1	EST_HUMAN	Homo sapiens calcium channel, voltage-dependent, alpha 1E subunit (CACNA1E), mRNA
8324	17425		1.76	1.0E-115	AF240786.1	NT	QV2-NN0044-210800-308-610 NN0044 Homo sapiens cDNA
579	9828	18947	0.93	1.0E-116	BE275502.1	EST_HUMAN	Homo sapiens glutathione S-transferase theta 2 (GSTT2) and glutathione S-transferase theta 1 (GSTT1) genes, complete cds
810	10049	19200	1.33	1.0E-116	4507334	NT	601121347F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:2888875 5'
869	10105		0.8	1.0E-116	4507334	NT	Homo sapiens synaptotagmin 1 (SYNJ1), mRNA
1866	11170	20375	2.57	1.0E-116	5174478	NT	Homo sapiens synaptotagmin 1 (SYNJ1), mRNA
1866	11170	20376	2.57	1.0E-116	5174478	NT	Homo sapiens pericentrin (PCNT), mRNA
1985	11198	20408	1.19	1.0E-116	AU133080.1	EST_HUMAN	AU133080 NT2RP4 Homo sapiens cDNA clone NT2RP4001228 5'
2067	12009	20480	1	1.0E-116	M19824.1	NT	Human apolipoprotein B-100 (apoB) gene, exons 17 and 18
2067	12009	20481	1	1.0E-116	M19824.1	NT	Human apolipoprotein B-100 (apoB) gene, exons 17 and 18
2273	11468	20689	1.85	1.0E-116	5453941	NT	Homo sapiens protein phosphatase, EF hand calcium-binding domain 1 (PPEF1) mRNA



Page 316 of 382  
Table 4  
Single Exon Probes Expressed in HELA Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2309	11503		4.25	1.0E-116	U78308.1	NT	Human olfactory receptor olfr17-201-1 (OR17-201-1) gene, olfactory receptor olfr17-32 (OR17-32) gene and olfactory receptor pseudo olfr17-01 (OR17-01) pseudogene, complete cds
2419	11610	20832	2.52	1.0E-116	AB018333.1	NT	Homo sapiens mRNA for KIAA0780 protein, partial cds
2691	11958	21086	8.61	1.0E-116	BE889258.1	EST_HUMAN	601513337F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3914600 5'
3130	12365		8.84	1.0E-116	T07515.1	EST_HUMAN	EST05405 Fetal brain, Stragene (cat#636206) Homo sapiens cDNA clone HFBK28 similar to EST containing L1 repeat
3139	12374	21504	6.18	1.0E-116	L77570.1	NT	Homo sapiens DiGeorge syndrome critical region, centromeric end
3139	12374	21505	6.18	1.0E-116	L77570.1	NT	Homo sapiens DiGeorge syndrome critical region, centromeric end
4372	13574	22670	2.17	1.0E-116	5031954	NT	Homo sapiens sodium phosphate transporter 3 (NPT3) mRNA
4470	13688	22759	1.39	1.0E-116	AB026898.1	NT	Homo sapiens DNA, DLEC1 to ORCTL4 gene region, section 1/2 (DLEC1, ORCTL3, ORCTL4 genes, complete cds)
4872	14060	23154	1.55	1.0E-116	AI907068.1	EST_HUMAN	PM-BT135-070499-016 BT135 Homo sapiens cDNA
5644	14867	24262	2.81	1.0E-116	W42822.1	EST_HUMAN	zc24d07.r1 Soares_senescent_fibroblasts_NHISF Homo sapiens cDNA clone IMAGE:323245 5' similar to SW:MDHM_MOUSE P08249 MALATE DEHYDROGENASE, MITOCHONDRIAL PRECURSOR;
5757	14976	24374	1.87	1.0E-116	AB046858.1	NT	Homo sapiens mRNA for KIAA1638 protein, partial cds
5757	14976	24375	1.87	1.0E-116	AB046858.1	NT	Homo sapiens mRNA for KIAA1638 protein, partial cds
5981	15098		2.13	1.0E-116	BE158133.1	EST_HUMAN	MR2-HT0379-210200-102-804 HT0379 Homo sapiens cDNA
6060	15250	24672	1.77	1.0E-116	C02844.1	EST_HUMAN	C02844 Human heart cDNA (YNakamura) Homo sapiens cDNA clone 3NHCO567
6167	15349	24787	8.61	1.0E-116	AV716314	EST_HUMAN	AV716314 DCB Homo sapiens cDNA clone DCBCCG06 5'
6586	15782	25242	2.68	1.0E-116	AA354256.1	EST_HUMAN	EST62685 Jurkat T-cells V Homo sapiens cDNA 5' end similar to similar to keratin 2
6586	15782	25243	2.68	1.0E-116	AA354256.1	EST_HUMAN	EST62685 Jurkat T-cells V Homo sapiens cDNA 5' end similar to similar to keratin 2
6805	16000	25458	6.84	1.0E-116	AI216352.1	EST_HUMAN	qh09c05.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1844168 3' similar to gbX53741_ma1 FIBULIN-1, ISOFORM A PRECURSOR (HUMAN);
7279	16498	25980	4.18	1.0E-116	BF335849.1	EST_HUMAN	GM2-CT0482-300800-349-e08 CT0482 Homo sapiens cDNA
7695	16894	26403	3.79	1.0E-116	AI367140.1	EST_HUMAN	qq41e04.x1 Soares_NHMPu_S1 Homo sapiens cDNA clone IMAGE:1835102 3' similar to WP:B0495.7 CE01765;
8253	17381	26915	3.94	1.0E-116	D44816.1	EST_HUMAN	HUMSUPY287 Human brain cDNA Homo sapiens cDNA clone NF187-S
8880	18361		1.69	1.0E-116	BE258569.1	EST_HUMAN	601108350F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3344580 5'
9081	18225		2.02	1.0E-116	AL134889.1	EST_HUMAN	DKFZp762L1110.r1 762 (synonym: hmel2) Homo sapiens cDNA clone DKFZp762L1110 5'
565	9815	18937	1.67	1.0E-117	4928636	NT	Homo sapiens acetyl-Coenzyme A carboxylase alpha (ACACA), mRNA
1085	11985	19462	2.51	1.0E-117	AF124393.1	NT	Mus musculus fragile-X-related protein 1 (Fxr1h) gene, exons 13a through 15
1725	10637	20120	1.74	1.0E-117	AF123320.1	NT	Homo sapiens lymphocyte activation-associated protein mRNA, complete cds
1799	11008	20201	2.17	1.0E-117	AI69816.1	NT	Human apolipoprotein B-100 (apoB) gene, exon 10

Page 317 of 382  
Table 4  
Single Exon Probes Expressed in HELA Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2178	11375	20597	3.14	1.0E-117	AW957699.1	EST_HUMAN	EST1369769 MAGE resequences, MAGE Homo sapiens cDNA
2672	11757	20977	4.99	1.0E-117	M63488.1	NT	Human alpha-5 collagen type IV gene, exon 5
3235	12469	21601	2.35	1.0E-117	AA978114.1	EST_HUMAN	op32c11.s1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1578548 3'
3688	13183	22283	10.3	1.0E-117	AA316723.1	EST_HUMAN	EST188414 HCC cell line (metastasis to liver in mouse) II Homo sapiens cDNA 5' end similar to ribosomal protein L29
4000	13213	22317	0.69	1.0E-117	AL163209.2	NT	Homo sapiens chromosome 21 segment HS21C009
4337	13538	22629	3.11	1.0E-117	8659584	NT	Homo sapiens collagen, type IV, alpha 5 (Alport syndrome) (COL4A5), mRNA
4575	13769	22864	2.19	1.0E-117	AL042120.1	EST_HUMAN	DKFZp434C1120_r1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434C1120 5'
4736	13927	23030	0.99	1.0E-117	X89670.1	NT	H. sapiens mRNA for TPOR16 protein
4736	13927	23031	0.99	1.0E-117	X89670.1	NT	H. sapiens mRNA for TPOR16 protein
4824	14013	23112	10.37	1.0E-117	AF134304.2	NT	Homo sapiens Scar2 (SCAR2) gene, partial cds
4824	14013	23113	10.37	1.0E-117	AF134304.2	NT	Homo sapiens Scar2 (SCAR2) gene, partial cds
4885	14073	23170	1.62	1.0E-117	U58109.1	NT	Mus musculus nebulin mRNA, partial cds
4885	14073	23171	1.62	1.0E-117	U58109.1	NT	Mus musculus nebulin mRNA, partial cds
4858	14145	23237	3.13	1.0E-117	AB020673.1	NT	Homo sapiens mRNA for KIAA0866 protein, complete cds
5274	14448	23518	0.61	1.0E-117	6912461	NT	Homo sapiens atrophin-1 interacting protein 1: activin receptor interacting protein 1 (KIAA0705), mRNA
5285	14456	23525	15.42	1.0E-117	6997248	NT	Homo sapiens sal (Drosophila)-like 1 (SALL1), mRNA
5364	14594	23671	3.1	1.0E-117	BE730508.1	EST_HUMAN	601582657F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3832214 5'
6273	15453	24893	5.21	1.0E-117	L76571.1	NT	Homo sapiens nuclear hormone receptor (shp) gene, 3' end of cds
6273	15453	24894	5.21	1.0E-117	L76571.1	NT	Homo sapiens nuclear hormone receptor (shp) gene, 3' end of cds
6311	15492	24937	4.74	1.0E-117	AV717788.1	EST_HUMAN	AV717788 DCB Homo sapiens cDNA clone DCBBAE01 5'
6311	15492	24938	4.74	1.0E-117	AV717788.1	EST_HUMAN	AV717788 DCB Homo sapiens cDNA clone DCBBAE01 5'
6454	15651	25119	6.33	1.0E-117	AI850145.1	EST_HUMAN	wp88b07.x1 NCL_CGAP_Bm25 Homo sapiens cDNA clone IMAGE:2468629 3' similar to TR:O75065
7434	16643	26135	1.68	1.0E-117	D83776.1	NT	O75065 KIAA0477 PROTEIN.
7822	17014	26528	2.73	1.0E-117	AB011541.1	NT	Human mRNA for KIAA0191 gene, partial cds
7822	17014	26529	2.73	1.0E-117	AB011541.1	NT	Homo sapiens mRNA for MEGF8, partial cds
7832	17072	26786	32.7	1.0E-117	BE269858.1	EST_HUMAN	Homo sapiens mRNA for MEGF8, partial cds
8121	17255	26786	2.27	1.0E-117	4501848	NT	601186203F1 NIH_MGC_8 Homo sapiens cDNA clone IMAGE:3544286 5'
8121	17255	26787	2.27	1.0E-117	4501848	NT	Homo sapiens ATP-binding cassette, sub-family A (ABC1), member 3 (ABCA3), mRNA
8567	18304		1.98	1.0E-117	AF224669.1	NT	Homo sapiens ATP-binding cassette, sub-family A (ABC1), member 3 (ABCA3), mRNA
9277	11985	19462	1.98	1.0E-117	AF124393.1	NT	Homo sapiens mannosidase, beta A, lysosomal (MANBA) gene, and ubiquitin-conjugating enzyme E2D 3 (UBE2D3) genes, complete cds
						NT	Mus musculus fragile-X-related protein 1 (Furth) gene, exons 13a through 15

Table 4

## Single Exon Probes Expressed in HELA Cells

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
70	9385	18491	3.8	1.0E-118	AF161500.1	NT	Homo sapiens HSPC151 mRNA, complete cds
95	9388	18517	0.66	1.0E-118	AL045854.1	EST_HUMAN	DKFZp434i056_r1 434 (synonym: hhes3) Homo sapiens cDNA clone DKFZp434i056 5'
523	9774	18899	7.45	1.0E-118	7657016	NT	Homo sapiens hypothetical protein (DJ328E19.C1.1), mRNA
924	11081	19316	0.92	1.0E-118	5174880	NT	Homo sapiens sine oculis homeobox (Drosophila) homolog 1 (SIX1), mRNA
2199	11396	20818	4.13	1.0E-118	BE389705.1	EST_HUMAN	601281947F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3804019 5'
2199	11396	20819	4.13	1.0E-118	BE389705.1	EST_HUMAN	601281947F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3804019 5'
2199	11396	20820	4.13	1.0E-118	BE389705.1	EST_HUMAN	601281947F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3804019 5'
2298	11493		12.88	1.0E-118	AW951728.1	EST_HUMAN	EST363798 IMAGE resequences, MAGB Homo sapiens cDNA
2697	11877	21091	4.25	1.0E-118	U07000.1	NT	Human breakpoint cluster region (BCR) gene, complete cds
2697	11877	21092	4.25	1.0E-118	U07000.1	NT	Human breakpoint cluster region (BCR) gene, complete cds
3088	12304		4.88	1.0E-118	Y13932.1	NT	Homo sapiens PRKY exon 7
3159	12394	21529	5.35	1.0E-118	A1347694.1	EST_HUMAN	qp01f05.x1 NCI_CGAP_Kid5 Homo sapiens cDNA clone IMAGE:1916769 3'
3159	12394	21530	5.35	1.0E-118	A1347694.1	EST_HUMAN	qp01f05.x1 NCI_CGAP_Kid5 Homo sapiens cDNA clone IMAGE:1916769 3'
3925	13141	22258	1.12	1.0E-118	AB024469.1	NT	Pongo pygmaeus DNA, similar to pol gene of HERSV-W and MSRV, isolate ORW3-3
4064	13274	22374	7.45	1.0E-118	D23690.1	NT	Human mRNA for ribosomal protein, complete cds
4718	13909	23011	1.8	1.0E-118	11425783	NT	Homo sapiens KIAA0478 gene product (KIAA0478), mRNA
5405	14633	23744	1.89	1.0E-118	AF142624.1	NT	Homo sapiens calcium channel gamma 4 subunit (CACNG4) gene, exon 3
5405	14633	23745	1.89	1.0E-118	AF142624.1	NT	Homo sapiens calcium channel gamma 4 subunit (CACNG4) gene, exon 3
5634	14858	24241	1.65	1.0E-118	11420764	NT	Homo sapiens transient receptor potential channel 5 (TRPC5), mRNA
6333	15514	24981	4.89	1.0E-118	11431050	NT	Homo sapiens chromosome 2 open reading frame 3 (C2ORF3), mRNA
6592	15788	25247	7.57	1.0E-118	BE062855.1	EST_HUMAN	QVO-BT0263-090200-097-h03 BT0263 Homo sapiens cDNA
6592	15788	25248	7.57	1.0E-118	BE062855.1	EST_HUMAN	QVO-BT0263-090200-097-h03 BT0263 Homo sapiens cDNA
6595	15791	25249	3.03	1.0E-118	AA443024.1	EST_HUMAN	z68d07.r1 Soares_NHMPu_S1 Homo sapiens cDNA clone IMAGE:811789 5'
6595	15791	25250	3.03	1.0E-118	AA443024.1	EST_HUMAN	z68d07.r1 Soares_NHMPu_S1 Homo sapiens cDNA clone IMAGE:811789 5'
6775	15970	25426	3.19	1.0E-118	BE263134.1	EST_HUMAN	601144863F2 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3160502 5'
7826	17018	26534	5.5	1.0E-118	AA315007.1	EST_HUMAN	EST198814 HCC cell line (metastasis to liver in mouse) II Homo sapiens cDNA 5' end similar to dynein, light chain 1, cytoplasmic
8096	17230	26768	1.71	1.0E-118	BF093687.1	EST_HUMAN	QVO-UM0091-120900-385-b12 UM0091 Homo sapiens cDNA
8096	17230	26769	1.71	1.0E-118	BF093687.1	EST_HUMAN	QVO-UM0091-120900-385-b12 UM0091 Homo sapiens cDNA
8218	17349		1.97	1.0E-118	6325465	NT	Homo sapiens flap structure-specific endonuclease 1 (FEN1), mRNA
765	10005	19154	0.77	1.0E-119	AF170492.1	NT	Homo sapiens chloride channel CLC4 (CLC4) mRNA, complete cds
1044	11984	19420	1.88	1.0E-119	7705607	NT	Homo sapiens CGI-105 protein (LOC51011), mRNA
1902	11108	20301	2.49	1.0E-119	AB023147.1	NT	Homo sapiens mRNA for KIAA0930 protein, partial cds

PCT/US 01/00670

Page 319 of 382  
Table 4  
Single Exon Probes Expressed in HELA Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3206	12440		0.74	1.0E-119	AA916760.1	EST_HUMAN	on10b05.s1 NCI_CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1556241 3' similar to WP:E04F6.2
3928	13145	22282	0.87	1.0E-119	4504116	NT	CE01214 ;
5357	14587	23684	2.81	1.0E-119	AU133399.1	EST_HUMAN	Homo sapiens glutamate receptor, ionotropic, kainate 1 (GRIK1) mRNA
5365	14595	23672	10.86	1.0E-119	M89914.1	NT	AU133399 NT2RP4 Homo sapiens cDNA clone NT2RP4001981 5'
5368	14598	23676	3.46	1.0E-119	BE636121.1	EST_HUMAN	Human neurofibromin (NF1) gene, complete cds
5409	14637	23765	1.8	1.0E-119	AV693731.1	EST_HUMAN	RC1-NN0073-250800-018-g08 NN0073 Homo sapiens cDNA
5723	14941	24337	8.85	1.0E-119	AI150703.1	EST_HUMAN	AV693731 GKC Homo sapiens cDNA clone GKCDHB03 5'
5852	15070	24480	2.4	1.0E-119	X06262.1	NT	qb77c09.x1 Soares fetal heart NBHH19W Homo sapiens cDNA clone IMAGE:1706128 3' similar to
5858	15078	24489	4.25	1.0E-119	AW974183.1	EST_HUMAN	SW-K1CJ_MOUSE P02535 KERA1IN, TYPE I CYTOSKELETAL 10 ;
7150	16327	25810	3.05	1.0E-119	AA465124.1	EST_HUMAN	Human c-fes/fps proto-oncogene
7225	16402	25887	5.18	1.0E-119	AB032281.1	NT	EST386288 MAGe resequences, MAGM Homo sapiens cDNA
7755	16951		11.08	1.0E-119	BF569571.1	EST_HUMAN	es3205.r1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:814977 5'
8624	18291		7.48	1.0E-119	AW847519.1	EST_HUMAN	Homo sapiens Scl mRNA for stearoyl-CoA desaturase, complete cds
306	9578	18711	0.7	1.0E-120	4507334	NT	Homo sapiens synapjanin 1 (SYNJ1), mRNA
1048	10274	19426	5.48	1.0E-120	AF248540.1	NT	Homo sapiens synapjanin 1 (SYNJ1), mRNA
1048	10274	19427	5.48	1.0E-120	AF248540.1	NT	Homo sapiens intersectin 2 (SH3D1B) mRNA, complete cds
1429	10842	19813	3.03	1.0E-120	NA4873.1	EST_HUMAN	Homo sapiens intersectin 2 (SH3D1B) mRNA, complete cds
1581	10784	19971	4.29	1.0E-120	AF167706.1	NT	y40g12.r1 Soares melanocyte 2NBHM Homo sapiens cDNA clone IMAGE:273766 5'
1775	10985	20177	1.78	1.0E-120	4537250	NT	Homo sapiens cysteine-rich repeat-containing protein S52 precursor, mRNA, complete cds
2077	11277	20483	1.44	1.0E-120	AB011399.1	NT	Homo sapiens disintegrin and metalloprotease domain 10 (ADAM10) mRNA
2077	11277	20494	1.44	1.0E-120	AB011399.1	NT	Homo sapiens gene for AF-6, complete cds
3278	9578	18711	0.95	1.0E-120	4507334	NT	Homo sapiens gene for AF-6, complete cds
4351	13553	22648	1.8	1.0E-120	AF056480.1	NT	Homo sapiens synapjanin 1 (SYNJ1), mRNA
4351	13553	22649	1.8	1.0E-120	AF056480.1	NT	Homo sapiens cAMP-specific phosphodiesterase 8A (PDE8A) mRNA, partial cds
4666	13860	22860	1.74	1.0E-120	AF098463.1	NT	Homo sapiens cAMP-specific phosphodiesterase 8A (PDE8A) mRNA, partial cds
4666	13860	22861	1.74	1.0E-120	AF098463.1	NT	Homo sapiens stanniocalcin (STC) gene, partial cds
5179	14356		0.69	1.0E-120	BE296720.1	EST_HUMAN	Homo sapiens stanniocalcin (STC) gene, partial cds
5200	14376	23463	1.38	1.0E-120	AB04151.1	EST_HUMAN	600B4362F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:2860414 5'
5545	14768	24135	13.47	1.0E-120	BF568222.1	EST_HUMAN	CM-BT043-090289-075 BT043 Homo sapiens cDNA
5545	14769	24136	13.47	1.0E-120	BF568222.1	EST_HUMAN	602183994F1 NIH_MGC_42 Homo sapiens cDNA clone IMAGE:4300174 5'
6426	15623	25087	2.58	1.0E-120	Y00067.1	NT	602183994F1 NIH_MGC_42 Homo sapiens cDNA clone IMAGE:4300174 5'
6426	15623	25088	2.58	1.0E-120	Y00067.1	NT	Human gene for neurofilament subunit M (NF-M)

Page 320 of 382  
Table 4  
Single Exon Probes Expressed in HELA Cells

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6573	15789	25232	2.78	1.0E-120	BF37599.1	EST_HUMAN	602035352F1 NCI CGAP_Brn64 Homo sapiens cDNA clone IMAGE:4183333 5'
6803	15788	25256	2.72	1.0E-120	AB007984.1	NT	Homo sapiens mRNA, chromosome 1 specific transcript KIAA0495
6803	15789	25257	2.72	1.0E-120	AB007984.1	NT	Homo sapiens mRNA, chromosome 1 specific transcript KIAA0495
6911	16098	25565	6.03	1.0E-120	BE382102.1	EST_HUMAN	601307739F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3825544 5'
6911	16098	25586	6.03	1.0E-120	BE382102.1	EST_HUMAN	601307739F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3825544 5'
7000	16178	25649	3.59	1.0E-120	BF306541.1	EST_HUMAN	601888958F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4122876 5'
7004	16182	25655	12.1	1.0E-120	AU133205.1	EST_HUMAN	AU133205 NT2RP4 Homo sapiens cDNA clone NT2RP4001541 5'
7099	16276	25756	2.58	1.0E-120	AB029000.1	NT	Homo sapiens mRNA for KIAA1077 protein, partial cds
7686	16885	26360	10.02	1.0E-120	BE286387.1	EST_HUMAN	601178727F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3532015 5'
7884	17100	26630	1.7	1.0E-120	BE867619.1	EST_HUMAN	601443135F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3847281 5'
7884	17100	26631	1.7	1.0E-120	BE867619.1	EST_HUMAN	601443135F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3847281 5'
8782	17711	23957	1.24	1.0E-120	11417862	NT	Homo sapiens calcineurin binding protein 1 (KIAA0330), mRNA
73	9367	18495	1.82	1.0E-121	Y18000.1	NT	Homo sapiens NF2 gene
383	9847	18782	1.32	1.0E-121	AU134983.1	EST_HUMAN	AU134983 PLACE1 Homo sapiens cDNA clone PLACE1000898 5'
731	11875	18111	1.23	1.0E-121	5032182	NT	Homo sapiens TNF receptor-associated factor 1 (TRAF1) mRNA
1835	11139	20335	0.96	1.0E-121	4755139	NT	Homo sapiens inositol polyphosphate-4-phosphatase, type I, 107KD (INPP4A), splice variant a, mRNA
1935	11139	20336	0.96	1.0E-121	4755139	NT	Homo sapiens inositol polyphosphate-4-phosphatase, type I, 107KD (INPP4A), splice variant a, mRNA
2072	11272	20487	1.12	1.0E-121	L76631.1	NT	Homo sapiens metabotropic glutamate receptor 1 beta (mGluR1beta) mRNA, complete cds
2540	11728	20845	1.42	1.0E-121	BF344378.1	EST_HUMAN	602014759F1 NCI CGAP_Brn64 Homo sapiens cDNA clone IMAGE:4150286 5'
2540	11728	20846	1.42	1.0E-121	BF344378.1	EST_HUMAN	602014759F1 NCI CGAP_Brn64 Homo sapiens cDNA clone IMAGE:4150286 5'
3046	12282	21408	4.5	1.0E-121	Y19208.1	NT	Homo sapiens hHb3 gene for hair keratin, exons 1 to 9
3048	12282	21410	4.5	1.0E-121	Y19208.1	NT	Homo sapiens hHb3 gene for hair keratin, exons 1 to 9
3510	12734	21872	1	1.0E-121	AB037758.1	NT	Homo sapiens mRNA for KIAA1337 protein, partial cds
3510	12734	21873	1	1.0E-121	AB037758.1	NT	Homo sapiens mRNA for KIAA1337 protein, partial cds
3657	12878	21998	8.82	1.0E-121	AF155156.2	NT	Homo sapiens adaptor-related protein complex AP-4 epsilon subunit mRNA, complete cds
3704	12924	22043	0.74	1.0E-121	A1904151.1	EST_HUMAN	GM-BT043-090289-075 BT043 Homo sapiens cDNA
4322	13523	22618	15.63	1.0E-121	A1263284.1	EST_HUMAN	q57601.x1 NCI CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2005417 3'
4886	14183	23271	3.41	1.0E-121	X91897.1	NT	H.sapiens ECE-1 gene (exon 17)
5139	14318	23408	1.18	1.0E-121	A1904151.1	EST_HUMAN	GM-BT043-090289-075 BT043 Homo sapiens cDNA
6437	15634	25099	2.45	1.0E-121	11438217	NT	Homo sapiens gamma-aminobutyric acid (GABA) A receptor, alpha 2 (GABRA2), mRNA
6438	15635	25100	2.34	1.0E-121	D84122.1	NT	Homo sapiens DNA for prostacyclin synthase, exon 8
6438	15635	25101	2.34	1.0E-121	D84122.1	NT	Homo sapiens DNA for prostacyclin synthase, exon 8

Page 321 of 382  
Table 4  
Single Exon Probes Expressed in HELA Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7357	16573	26065	3.21	1.0E-121	11427788	NT	Homo sapiens COX11 (yeast) homodolog, cytochrome c oxidase assembly protein (COX11), mRNA
7364	16580	26071	2.22	1.0E-121	AF064200.1	NT	Homo sapiens UDP-glucuronosyltransferase 2B4 precursor (UGT2B4) mRNA, UGT2B4*E458 allele, complete cds
7540	16745	26239	4.58	1.0E-121	7390334	NT	Homo sapiens chloride intracellular channel 4 like (CLIC4L), mRNA
7567	16772	26264	1.92	1.0E-121	N59624.1	EST_HUMAN	w74c01.s1 Soares fetal liver spleen 1NLS Homo sapiens cDNA clone IMAGE:248448 3'
272	9547	18676	1.18	1.0E-122	11526176	NT	Homo sapiens T-cell lymphoma invasion and metastasis 1 (TIAM1), mRNA
341	9609	18736	3.68	1.0E-122	AF114488.1	NT	Homo sapiens intersectin short isoform (ITSN) mRNA, complete cds
363	9629	18761	1.23	1.0E-122	11526176	NT	Homo sapiens T-cell lymphoma invasion and metastasis 1 (TIAM1), mRNA
892	10127	19260	3.5	1.0E-122	AF114488.1	NT	Homo sapiens intersectin short isoform (ITSN) mRNA, complete cds
1227	10445	19801	4.46	1.0E-122	M20707.1	NT	Human kappa-immunoglobulin germline pseudogene (Chr22.4) variable region (subgroup V kappa II)
1688	10881	20085	3.77	1.0E-122	AF167706.1	NT	Homo sapiens cysteine-rich repeat-containing protein S52 precursor, mRNA, complete cds
1687	10869	20087	2.46	1.0E-122	11418424	NT	Homo sapiens collagen, type XII, alpha 1 (COL12A1), mRNA
1687	10869	20088	2.46	1.0E-122	11418424	NT	Homo sapiens collagen, type XII, alpha 1 (COL12A1), mRNA
1783	10963	20189	6.26	1.0E-122	BE906024.1	EST_HUMAN	601497032F1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3899358 5'
2454	11645	20865	22.45	1.0E-122	BF316170.1	EST_HUMAN	601896173F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4125234 5'
2454	11645	20866	22.45	1.0E-122	BF316170.1	EST_HUMAN	601896173F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4125234 5'
2792	12032	21157	1.28	1.0E-122	AF264717.1	NT	Homo sapiens FYVE domain-containing dual specificity protein phosphatase FYVE-DSP2 mRNA, complete cds
4863	14051	23145	3.37	1.0E-122	4502166	NT	Homo sapiens amyloid beta (A4) precursor protein (protease nexin-II, Alzheimer disease) (APP), mRNA
5011	14188	23145	1.3	1.0E-122	AW504645.1	EST_HUMAN	UI-HF-BND-ali-a-03-0-U1.r1 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3078948 5'
5982	14700	24054	6.1	1.0E-122	BE256039.1	EST_HUMAN	601113567F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3354232 5'
8362	17453		3.75	1.0E-122	11418187	NT	Homo sapiens phosphomannomutase 1 (PMM1), mRNA
777	10016	19164	1.53	1.0E-123	BF345274.1	EST_HUMAN	602018058F1 NCI_CGAP_Bn67 Homo sapiens cDNA clone IMAGE:4153670 5'
777	10016	19165	1.53	1.0E-123	BF345274.1	EST_HUMAN	602018058F1 NCI_CGAP_Bn67 Homo sapiens cDNA clone IMAGE:4153670 5'
1020	10248	19399	6.17	1.0E-123	AL163249.2	NT	Homo sapiens chromosome 21 segment HS21C049
1029	10255	19408	3.73	1.0E-123	5803114	NT	Homo sapiens inner membrane protein, mitochondrial (mitofilin) (NMT), mRNA
1245	10461	19621	4.94	1.0E-123	4505818	NT	Homo sapiens phosphatidylinositol-4-phosphate 5-kinase, type II, beta (PIP5K2B) mRNA, and translated products
1245	10461	19622	4.94	1.0E-123	4505818	NT	Homo sapiens phosphatidylinositol-4-phosphate 5-kinase, type II, beta (PIP5K2B) mRNA, and translated products
2089	11269	20483	2.16	1.0E-123	M55419.1	NT	Human amelogenin (AMELY) gene, 3' end of cds
2089	11269	20484	2.16	1.0E-123	M55419.1	NT	Human amelogenin (AMELY) gene, 3' end of cds

Page 322 of 382  
Table 4  
Single Exon Probes Expressed in HELA Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2069	11269	20485	2.18	1.0E-123	M55419.1	NT	Human amelogenin (AMELY) gene, 3' end of cds
2281	11476		3.68	1.0E-123	7705962	NT	Homo sapiens RAB9-like protein (LOC51209), mRNA
5417	14845	23777	1.83	1.0E-123	L34219.1	NT	Homo sapiens retinaldehyde-binding protein (CRALBP) gene, complete cds
5417	14845	23778	1.83	1.0E-123	L34219.1	NT	Homo sapiens retinaldehyde-binding protein (CRALBP) gene, complete cds
5857	15075	24488	1.97	1.0E-123	AU118435.1	EST_HUMAN	AU118435 HEMBA1 Homo sapiens cDNA clone HEMBA1003591 5'
6357	15537	24991	1.92	1.0E-123	BE263001.1	EST_HUMAN	601152815F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3509162 5'
6870	16092	25560	3.52	1.0E-123	AB007923.1	NT	Homo sapiens mRNA for KIAA0454 protein, partial cds
6912	16100	25587	31.08	1.0E-123	U09823.1	NT	Oryctolagus cuniculus New Zealand white elongation factor 1 alpha (Rabefla2) mRNA, complete cds
8211	17342	26881	5.75	1.0E-123	BF677282.1	EST_HUMAN	602086791F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4250879 5'
8211	17342	26882	5.75	1.0E-123	BF677282.1	EST_HUMAN	602086791F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4250879 5'
273	9548	19877	1.3	1.0E-124	4507500	NT	Homo sapiens T-cell lymphoma invasion and metastasis 1 (TIAM1) mRNA
273	9548	19878	1.3	1.0E-124	4507500	NT	Homo sapiens T-cell lymphoma invasion and metastasis 1 (TIAM1) mRNA
279	9554		1.47	1.0E-124	D87675.1	NT	Homo sapiens DNA for amyloid precursor protein, complete cds
492	9745	18876	2.96	1.0E-124	AL163246.2	NT	Homo sapiens chromosome 21 segment HS21C048
698	9940	19073	4.88	1.0E-124	AA397551.1	EST_HUMAN	z81b04.r1 Stralagene schizo brain S11 Homo sapiens cDNA clone IMAGE:728719 5' similar to TR:G300482
698	9940	19074	4.88	1.0E-124	AA397551.1	EST_HUMAN	G300482 POL=REVERSE TRANSCRIPTASE HOMOLOG (RETROVIRAL ELEMENT) ;
766	10006	19155	6.95	1.0E-124	AF155654.1	NT	z81b04.r1 Stralagene schizo brain S11 Homo sapiens cDNA clone IMAGE:728719 5' similar to TR:G300482
818	10056	19209	1.35	1.0E-124	4507500	NT	Human putative ribosomal protein S1 mRNA
914	10149	18309	1.76	1.0E-124	7705446	NT	Homo sapiens T-cell lymphoma invasion and metastasis 1 (TIAM1) mRNA
1354	10569	19733	7.35	1.0E-124	AF274892.1	NT	Homo sapiens hypothetical protein (HSPC088), mRNA
1354	10569	19734	7.35	1.0E-124	AF274892.1	NT	Homo sapiens glucose transporter 3 gene, exons 9, 10, and complete cds
1784	10894	20190	4.41	1.0E-124	AJ131712.1	NT	Homo sapiens glucose transporter 3 gene, exons 9, 10, and complete cds
2029	11250	20438	1.29	1.0E-124	BE79524.1	EST_HUMAN	Homo sapiens mRNA for nuclear RNA-helicase (nrlh1 gene)
2420	11611	20833	2.16	1.0E-124	AB024069.1	NT	601491715F1 NIH_MGC_89 Homo sapiens cDNA clone IMAGE:3883954 5'
3341	12570	21709	0.6	1.0E-124	4504116	NT	Homo sapiens gene for B120, exon 11
3465	12690	21826	0.73	1.0E-124	S76694.1	NT	Homo sapiens glutamate receptor, ionotropic, kainate 1 (GRIK1) mRNA
3465	12690	21827	0.73	1.0E-124	S76694.1	NT	Homo sapiens ATP-sensitive inwardly rectifying K-channel subunit (KCNJ6/BIR1) gene, exon
3628	12849	21968	3.42	1.0E-124	X13794.1	NT	Homo sapiens ATP-sensitive inwardly rectifying K-channel subunit (KCNJ6/BIR1) gene, exon
3876	13092	22208	0.7	1.0E-124	4507500	NT	H. sapiens lactate dehydrogenase B gene exon 1 and 2 (EC 1.1.2.7) (and joined CDS)
4044	13254	22356	0.6	1.0E-124	4504116	NT	Homo sapiens T-cell lymphoma invasion and metastasis 1 (TIAM1) mRNA
4053	13263	22366	0.99	1.0E-124	4504116	NT	Homo sapiens glutamate receptor, ionotropic, kainate 1 (GRIK1) mRNA

Page 323 of 382  
Table 4  
Single Exon Probes Expressed in HELA Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4757	13948	23049	1.91	1.0E-124	AB024089.1	NT	Homo sapiens gene for B120, exon 11
5327	14559	23631	9.25	1.0E-124	8922337	NT	Homo sapiens hypothetical protein FLJ10300 (FLJ10300), mRNA
5609	14833	24208	6.87	1.0E-124	BF696135.1	EST_HUMAN	602124644F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:4281635 5'
6094	15294	24727	3.05	1.0E-124	Y11717.1	NT	M. musculus mRNA for hoxa3 gene
6545	15741	25202	12.36	1.0E-124	4506654	NT	Homo sapiens ribosomal protein L5 (RPL5) mRNA
6909	16097	25563	2.65	1.0E-124	AV645633.1	EST_HUMAN	AV645633 GLC Homo sapiens cDNA clone GLCACE04 3'
6909	16097	25564	2.65	1.0E-124	AV645633.1	EST_HUMAN	AV645633 GLC Homo sapiens cDNA clone GLCACE04 3'
6967	16145	25615	9.53	1.0E-124	AI767133.1	EST_HUMAN	w93f02.x1 NCI_CGAP_Kid12 Homo sapiens cDNA clone IMAGE:2400891 3'
6967	16145	25616	9.53	1.0E-124	AI767133.1	EST_HUMAN	w93f02.x1 NCI_CGAP_Kid12 Homo sapiens cDNA clone IMAGE:2400891 3'
7877	17065	26589	3.49	1.0E-124	AW656563.1	EST_HUMAN	hJ05c06.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2980906 3'
8008	16443	25932	3.27	1.0E-124	AI446455.1	EST_HUMAN	ij19e03.x1 NCI_CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2141980 3' similar to TR:O31662 O31662 YKRS PROTEIN.;
8008	16443	25933	3.27	1.0E-124	AI446455.1	EST_HUMAN	ij19e03.x1 NCI_CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2141980 3' similar to TR:O31662 O31662 YKRS PROTEIN.;
8437	9940	19073	5.82	1.0E-124	AA397551.1	EST_HUMAN	z181b04.r1 Stratagene schizo brain S11 Homo sapiens cDNA clone IMAGE:728719 5' similar to TR:G300482 G300482 POL=REVERSE TRANSCRIPTASE HOMOLOG (RETROVIRAL ELEMENT);
8437	9940	19074	5.82	1.0E-124	AA397551.1	EST_HUMAN	z181b04.r1 Stratagene schizo brain S11 Homo sapiens cDNA clone IMAGE:728719 5' similar to TR:G300482 G300482 POL=REVERSE TRANSCRIPTASE HOMOLOG (RETROVIRAL ELEMENT);
8895	17789	23922	1.72	1.0E-124	AB029016.1	NT	Homo sapiens mRNA for KIAA1093 protein, partial cds
9164	18238	23704	1.62	1.0E-124	11417862	NT	Homo sapiens calcineurin binding protein 1 (KIAA0330), mRNA
9164	18238	23705	1.62	1.0E-124	11417862	NT	Homo sapiens calcineurin binding protein 1 (KIAA0330), mRNA
153	9435	18569	3.63	1.0E-125	BE219510.1	EST_HUMAN	hV59a08.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3177686 3' similar to TR:Q25058 Q25058 FIBROPELLEIN IA.;
153	9435	18570	3.63	1.0E-125	BE219510.1	EST_HUMAN	hV59a08.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3177686 3' similar to TR:Q25058 Q25058 FIBROPELLEIN IA.;
324	9595		9.19	1.0E-125	AB032998.1	NT	Homo sapiens mRNA for KIAA1172 protein, partial cds
432	9297	18399	5.96	1.0E-125	BE743922.1	EST_HUMAN	601577981F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3926685 5'
650	9896	19021	4.06	1.0E-125	AI110656.1	EST_HUMAN	HA0086 Human fetal liver cDNA library Homo sapiens cDNA
650	9896	19022	4.06	1.0E-125	AI110656.1	EST_HUMAN	HA0086 Human fetal liver cDNA library Homo sapiens cDNA
735	9976	19115	1.92	1.0E-125	AF264750.1	NT	Homo sapiens ALR-like protein mRNA, partial cds
870	10106	19268	1.99	1.0E-125	AA042813.1	EST_HUMAN	z163d07.s1 Soares_pregnant_uterus_NBHPU Homo sapiens cDNA clone IMAGE:486540 3' similar to gb:X65657_cds1 OLFACTORY RECEPTOR-LIKE PROTEIN HGMP07E (HUMAN);
1006	10237	19389	1.04	1.0E-125	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C010
1162	10384	19534	1.97	1.0E-125	7662279	NT	Homo sapiens KIAA0744 gene product; histone deacetylase 7 (KIAA0744), mRNA



Page 324 of 382  
Table 4  
Single Exon Probes Expressed in HELA Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1780	10990	20185	2.74	1.0E-125	AF015450.1	NT	Homo sapiens Usurpin-alpha mRNA, complete cds
1780	10990	20186	2.74	1.0E-125	AF015450.1	NT	Homo sapiens Usurpin-alpha mRNA, complete cds
2326	11519	20739	4.04	1.0E-125	AA011278.1	EST_HUMAN	z01g09.r1 Soares_fetal_liver_spleen_TNFSF_S1 Homo sapiens cDNA clone IMAGE:429568 5'
2468	11659	20880	3.16	1.0E-125	AA042813.1	EST_HUMAN	zK53c07.s1 Soares_pregnant_uterus_NbHPU Homo sapiens cDNA clone IMAGE:486540 3' similar to gb:X65857.cds1 OLFACTORY RECEPTOR-LIKE PROTEIN HGMP07E (HUMAN);
2556	11743	20961	2.42	1.0E-125	4504696	NT	Homo sapiens inhibin, alpha (INH A) mRNA
2556	11743	20962	2.42	1.0E-125	4504696	NT	Homo sapiens inhibin, alpha (INH A) mRNA
2971	14464	21345	1.26	1.0E-125	BE018009.1	EST_HUMAN	ZINC FINGER PROTEIN.; zK53c07.s1 Soares_pregnant_uterus_NbHPU Homo sapiens cDNA clone IMAGE:486540 3' similar to gb:X65857.cds1 OLFACTORY RECEPTOR-LIKE PROTEIN HGMP07E (HUMAN);
3841	13058	22173	1.21	1.0E-125	AA042813.1	EST_HUMAN	Homo sapiens zinc finger protein ZNF287 (ZNF287), mRNA
4547	13742	22842	2.2	1.0E-125	11425114	NT	Homo sapiens zinc finger protein ZNF287 (ZNF287), mRNA
4547	13742	22843	2.2	1.0E-125	11425114	NT	Homo sapiens zinc finger protein ZNF287 (ZNF287), mRNA
4619	13813	22903	1.18	1.0E-125	BE315412.1	EST_HUMAN	601141152F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3140796 5'
5056	9435	18569	1.71	1.0E-125	BE219510.1	EST_HUMAN	hV59a08.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3177686 3' similar to TR:Q25058 Q25058 FIBROPELLEIN A ;
5056	9435	18570	1.71	1.0E-125	BE219510.1	EST_HUMAN	hV59a08.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3177686 3' similar to TR:Q25058 Q25058 FIBROPELLEIN A ;
5629	14853	24236	3.41	1.0E-125	BE892560.1	EST_HUMAN	601433472F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3918952 5'
5919	15136	24546	4.5	1.0E-125	BE562526.1	EST_HUMAN	601335826F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3689790 5'
5919	15136	24547	4.5	1.0E-125	BE562526.1	EST_HUMAN	601335826F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3689790 5'
6109	15203	24621	4.08	1.0E-125	X03427.1	NT	Homo sapiens IGF-II gene, exon 5
6109	15203	24622	4.08	1.0E-125	X03427.1	NT	Homo sapiens IGF-II gene, exon 5
6812	16007	25468	12.48	1.0E-125	BE181640.1	EST_HUMAN	QV1-HT0638-070500-191-d12 HT0638 Homo sapiens cDNA
6812	16007	25469	12.48	1.0E-125	BE181640.1	EST_HUMAN	QV1-HT0638-070500-191-d12 HT0638 Homo sapiens cDNA
7274	16483	25985	3.47	1.0E-125	AF043458.1	NT	Homo sapiens I-REL gene, exon 5
7696	16895	26404	4.49	1.0E-125	AB014567.1	NT	Homo sapiens mRNA for KIAA0667 protein, partial cds
7837	17029	28545	1.76	1.0E-125	7669505	NT	Homo sapiens myosin, heavy polypeptide 1, skeletal muscle, adult (MYH1), mRNA
7842	17034	26550	5.99	1.0E-125	AF026029.1	NT	Homo sapiens poly(A) binding protein II (PABP2) gene, complete cds
7939	17079	26607	3.23	1.0E-125	AW812899.1	EST_HUMAN	RC3-ST0186-250200-018-c11 ST0186 Homo sapiens cDNA
8035	17171	26709	5.52	1.0E-125	BE074267.1	EST_HUMAN	QV3-BT0569-020200-075-g09 BT0569 Homo sapiens cDNA
8035	17171	26710	5.52	1.0E-125	BE074267.1	EST_HUMAN	QV3-BT0569-020200-075-g09 BT0569 Homo sapiens cDNA
783	10022	19172	1.06	1.0E-126	4758007	NT	Homo sapiens CDC-like kinase (CLK) mRNA
786	10025	19175	1.61	1.0E-126	M61936.1	NT	Human laminin B1 chain gene, exon 20

Page 325 of 382  
Table 4  
Single Exon Probes Expressed in HELA Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2313	11507	20728	1.65	1.0E-126	8923056	NT	Homo sapiens hypothetical protein FLJ20048 (FLJ20048), mRNA
2313	11507	20728	1.65	1.0E-126	8923056	NT	Homo sapiens hypothetical protein FLJ20048 (FLJ20048), mRNA
2557	11744	20963	6.17	1.0E-126	6382078	NT	Homo sapiens RAN binding protein 2 (RANBP2), mRNA
3037	12274	21403	11.07	1.0E-126	AA160709.1	EST_HUMAN	z072c03.r1 Stragelene pancreas (#937208) Homo sapiens cDNA clone IMAGE:592420 5'
3037	12274	21404	11.07	1.0E-126	AA160709.1	EST_HUMAN	z072c03.r1 Stragelene pancreas (#937208) Homo sapiens cDNA clone IMAGE:592420 5'
3607	12828	21948	0.94	1.0E-126	X53941.1	NT	H. sapiens DNA for liver cytochrome b5 pseudogene
3635	12858	21975	1.42	1.0E-126	7657038	NT	Homo sapiens death receptor 6 (DR6), mRNA
4787	13986	23091	1.09	1.0E-126	AF101108.1	NT	Homo sapiens collagen type XI alpha-1 (COL11A1) gene, exon 63
4787	13986	23092	1.09	1.0E-126	AF101108.1	NT	Homo sapiens collagen type XI alpha-1 (COL11A1) gene, exon 63
4851	14040	23133	1.81	1.0E-126	N34078.1	EST_HUMAN	y78c06.r1 Soares melanocyte 2N6HM Homo sapiens cDNA clone IMAGE:267850 5'
5184	14360	23448	0.81	1.0E-126	BE743922.1	EST_HUMAN	601577981F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3926685 5'
5767	14986	24386	4.09	1.0E-126	AA460075.1	EST_HUMAN	z066c03.r1 Soares_total_fetus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:786444 5' similar to TR:G1145880 G1145880 TITIN
5781	14989	24401	3.92	1.0E-126	AB040958.1	NT	Homo sapiens mRNA for KIAA1525 protein, partial cds
5781	14989	24402	3.92	1.0E-126	AB040958.1	NT	Homo sapiens mRNA for KIAA1525 protein, partial cds
6459	16056	25127	3.09	1.0E-126	X16809.1	NT	Human mRNA for ankryrin (variant 2.1)
7435	16644	26136	3.63	1.0E-126	BF683175.1	EST_HUMAN	602139136F1 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4298240 5'
8049	17185	26724	2.23	1.0E-126	BE261690.1	EST_HUMAN	601149404F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3502129 5'
8933	14360	23448	5.06	1.0E-126	BE743922.1	EST_HUMAN	601577981F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3926685 5'
175	9456	18588	7.09	1.0E-127	AB024597.1	NT	Homo sapiens mRNA for casein kinase I epsilon, complete cds
175	9456	18589	7.09	1.0E-127	AB024597.1	NT	Homo sapiens mRNA for casein kinase I epsilon, complete cds
176	9456	18588	6.74	1.0E-127	AB024597.1	NT	Homo sapiens mRNA for casein kinase I epsilon, complete cds
176	9456	18589	6.74	1.0E-127	AB024597.1	NT	Homo sapiens mRNA for casein kinase I epsilon, complete cds
278	9553	18685	1.51	1.0E-127	D87675.1	NT	Homo sapiens DNA for amyloid precursor protein, complete cds
278	9553	18686	1.51	1.0E-127	D87675.1	NT	Homo sapiens DNA for amyloid precursor protein, complete cds
891	10126	19289	0.9	1.0E-127	AF114488.1	NT	Homo sapiens interseitin short isoform (ITSN) mRNA, complete cds
928	10160	19318	1.07	1.0E-127	U72621.2	NT	Homo sapiens lost on transformation LOT1 mRNA, complete cds
1668	10879	20063	2.02	1.0E-127	4827053	NT	Homo sapiens ubiquitin specific protease 8 (USP8) mRNA
2033	11234	20441	2.82	1.0E-127	5803065	NT	Homo sapiens leukocyte immunoglobulin-like receptor, subfamily A (with TM domain), member 1 (LILRA1), mRNA
2033	11234	20442	2.82	1.0E-127	5803065	NT	Homo sapiens leukocyte immunoglobulin-like receptor, subfamily A (with TM domain), member 1 (LILRA1), mRNA
2166	11364	20583	85.3	1.0E-127	4506620	NT	Homo sapiens ribosomal protein L26 (RPL26) mRNA
2310	11504	20725	2.49	1.0E-127	AF245505.1	NT	Homo sapiens adican mRNA, complete cds

Page 326 of 382  
Table 4  
Single Exon Probes Expressed in HELA Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2568	11754	20974	40.25	1.0E-127	X12881.1	NT	Human mRNA for cytokeratin 18
3670	12891	22012	0.63	1.0E-127	AF114488.1	NT	Homo sapiens intersectin short isoform (ITSN) mRNA, complete cds
3799	13017	22130	1.23	1.0E-127	AW191297.1	EST_HUMAN	au80a06.y1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2782594 5' similar to TR:Q15170 Q15170 TRANSCRIPTION FACTOR S-IL-RELATED PROTEIN, contains element MER22 repetitive element;
4094	13302	22402	0.68	1.0E-127	AF135188.1	NT	Homo sapiens delayed rectifier potassium channel subunit isK mRNA, complete cds
4241	13444	22534	22.24	1.0E-127	7706239	NT	Homo sapiens neuroblastoma-amplified protein (LOC51594), mRNA
4241	13444	22535	22.24	1.0E-127	7706239	NT	Homo sapiens neuroblastoma-amplified protein (LOC51594), mRNA
4499	13697	22791	0.82	1.0E-127	AF252297.1	NT	Homo sapiens cytochrome P450 retinoid metabolizing protein P450RAL-2 mRNA, complete cds
4603	13797	22887	4.81	1.0E-127	4506384	NT	Homo sapiens RAD1 (S. pombe) homolog (RAD1) mRNA, and translated products
4835	13829		2.81	1.0E-127	AL163268.2	NT	Homo sapiens chromosome 21 segment HS21C088
4878	13870	22969	0.86	1.0E-127	8912639	NT	Homo sapiens Ring1 and YY1 binding protein (RYBP), mRNA
5186	14362	23447	0.88	1.0E-127	AF105699.1	NT	Homo sapiens acetylcholine receptor epsilon subunit (CHRNA) gene, complete cds
5186	14362	23448	0.88	1.0E-127	AF105699.1	NT	Homo sapiens acetylcholine receptor epsilon subunit (CHRNA) gene, complete cds
5186	14362	23449	0.88	1.0E-127	AF105699.1	NT	Homo sapiens acetylcholine receptor epsilon subunit (CHRNA) gene, complete cds
5538	14783	24130	2.03	1.0E-127	W03547.1	EST_HUMAN	z01a10.r1 Soares melanocyte 2NbrHM Homo sapiens cDNA clone IMAGE:281258 5' similar to SW:PIP6_RAT P10688 1-PHOSPHATIDYLINOSITOL-4,5-BISPHOSPHATE PHOSPHODIESTERASE DELTA 1;
5573	14797	24171	4.34	1.0E-127	X65784.1	NT	H.sapiens NOS2 gene, exon 6
5737	14956	24355	2.24	1.0E-127	X84080.1	NT	H.sapiens TCF11 gene, exon 3-6
5788	15015	24418	6.1	1.0E-127	4504778	NT	Homo sapiens integrin, beta 8 (ITGB8) mRNA
6978	16156	25627	4.37	1.0E-127	AF274863.1	NT	Homo sapiens secretory pathway component Sec31B-1 mRNA, alternatively spliced, complete cds
6978	16156	25628	4.37	1.0E-127	AF274863.1	NT	Homo sapiens secretory pathway component Sec31B-1 mRNA, alternatively spliced, complete cds
7179	16356	25834	3.58	1.0E-127	11427235	NT	Homo sapiens Chediak-Higashi syndrome 1 (CHS1), mRNA
7718	16917	26424	6.61	1.0E-127	11417339	NT	Homo sapiens similar to heat shock 70kD protein 9B (mortalin-2) (H. sapiens) (LOC63184), mRNA
7718	16917	26425	6.51	1.0E-127	11417339	NT	Homo sapiens similar to heat shock 70kD protein 9B (mortalin-2) (H. sapiens) (LOC63184), mRNA
8146	17278	26822	1.83	1.0E-127	BE895415.1	EST_HUMAN	601434794F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3919917 5'
8146	17278	26823	1.83	1.0E-127	BE895415.1	EST_HUMAN	601434794F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3919917 5'
8674	9456	18589	3.11	1.0E-127	AB024597.1	NT	Homo sapiens mRNA for casein kinase I epsilon, complete cds
8674	9456	18589	3.11	1.0E-127	AB024597.1	NT	Homo sapiens mRNA for casein kinase I epsilon, complete cds
8894	17779	23945	1.58	1.0E-127	AB011399.1	NT	Homo sapiens gene for AF-6, complete cds
466	9719	18851	3.7	1.0E-128	BE365617.1	EST_HUMAN	601278127F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3618822 5'

Page 327 of 382  
Table 4  
Single Exon Probes Expressed in HELA Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2038	11239	20448	30.04	1.0E-128	U02523.1	NT	Human FAU1P pseudogene, trinucleotide repeat regions
2038	11239	20447	30.04	1.0E-128	U02523.1	NT	Human FAU1P pseudogene, trinucleotide repeat regions
2178	11373	20596	153.58	1.0E-128	4508718	NT	Homo sapiens ribosomal protein S2 (RPS2) mRNA
2408	11600		6.88	1.0E-128	11437455	NT	Homo sapiens chromatin-specific transcription elongation factor, 140 kDa subunit (FACTP140), mRNA
3371	12599	21735	1.23	1.0E-128	AB033073.1	NT	Homo sapiens mRNA for KIAA1247 protein, partial cds
4687	13881	22862	4.92	1.0E-128	11428673	NT	Homo sapiens prospero-related homeobox 1 (PROX1), mRNA
5835	15052	24459	1.84	1.0E-128	11420986	NT	Homo sapiens phosphodiesterase 1C, calmodulin-dependent (70kD) (PDE1C), mRNA
6056	15225	24644	6.7	1.0E-128	BF224345.1	EST_HUMAN	7q86b10.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE: 3'
7120	16297	25779	3.35	1.0E-128	AA639198.1	EST_HUMAN	CHROMOSOME SEGREGATION GENE HOMOLOG CAS. ;
7298	16517	26008	5.1	1.0E-128	11425254	NT	Homo sapiens glutamate receptor, ionotropic, N-methyl D-aspartate 2D (GRIN2D), mRNA
7306	16524	26015	8.5	1.0E-128	AA926959.1	EST_HUMAN	om88h08.s1 NCI_CGAP_GC4 Homo sapiens cDNA clone IMAGE:1552383 3' similar to gb:X54941 CYCLIN-
8533	17559		5.07	1.0E-128	AW955290.1	EST_HUMAN	DEPENDENT KINASES REGULATORY SUBUNIT 1 (HUMAN);
419	8872	18814	0.67	1.0E-129	S37722.1	NT	EST387360 MAGE resequences, MAGC Homo sapiens cDNA
1693	10605	20091	3.35	1.0E-128	AL066880.1	NT	insulin-like growth factor binding protein-2 [human, placenta, Genomic, 1019 nt, segment 2 of 4]
1698	10910	20096	1.46	1.0E-129	AF240786.1	NT	Novel human mRNA containing Zinc finger C2H2 type domains
1698	10910	20097	1.46	1.0E-129	AF240786.1	NT	Homo sapiens glutathione S-transferase theta 2 (GSTT2) and glutathione S-transferase theta 1 (GSTT1)
1813	11021	20214	2.67	1.0E-128	11418522	NT	genes, complete cds
3092	12328	21451	1.51	1.0E-129	Q14585	SWISSPROT	Homo sapiens zinc finger protein 76 (expressed in testis) (ZNF76), mRNA
3092	12328	21452	1.51	1.0E-129	Q14585	SWISSPROT	ZINC FINGER PROTEIN HZF10
3092	12328	21453	1.51	1.0E-129	Q14585	SWISSPROT	ZINC FINGER PROTEIN HZF10
4146	13352	22454	2.08	1.0E-129	AB040882.1	NT	Homo sapiens mRNA for KIAA1459 protein, partial cds
4285	13468	22559	2.19	1.0E-128	AW755254.1	EST_HUMAN	CMYA5 Human cardiac muscle expression library Homo sapiens cDNA clone 4151835 similar to CMYA5
4285	13468	22560	2.19	1.0E-128	AW755254.1	EST_HUMAN	Cardiomyopathy associated gene 5
5704	14923	24318	4.43	1.0E-129	AJ006345.1	NT	CMYA5 Human cardiac muscle expression library Homo sapiens cDNA clone 4151835 similar to CMYA5
6130	15314	24748	4.22	1.0E-128	AJ006345.1	NT	Homo sapiens KVLQ11 gene
6161	15344	24781	9.49	1.0E-128	11420850	NT	Homo sapiens KVLQ11 gene
6587	15763		8.3	1.0E-129	AB014534.1	NT	Homo sapiens similar to ribosomal protein S26 (H. sapiens) (LOC63694), mRNA
							Homo sapiens mRNA for KIAA0634 protein, partial cds

Page 328 of 382  
Table 4

## Single Exon Probes Expressed in HELA Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7778	16971	26484	3.53	1.0E-129	AA625528.1	EST_HUMAN	af7207.r1 Soares_NHMPu_S1 Homo sapiens cDNA clone IMAGE:1047589 5'
7845	15344	24781	10.01	1.0E-129	11420850	NT	Homo sapiens similar to ribosomal protein S28 (H. sapiens) (LOC636894), mRNA
8520	17551		4.44	1.0E-128	H83155.1	EST_HUMAN	y49c05.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:199112 5' similar to
8925	17808		1.73	1.0E-128	AL120739.1	EST_HUMAN	SP:B48150 B48150 HP-23=HIBERNATION-RELATED PROTEIN - TAMIAS ASIATICUS=ASIAN ;
78	9370	18499	3.47	1.0E-130	7705530	NT	DKFZp762K171_r1 762 (synonym: hmed2) Homo sapiens cDNA clone DKFZp762K171 5'
1178	10399	19552	0.7	1.0E-130	AB037835.1	NT	Homo sapiens hypothetical protein (HSPC242), mRNA
1842	10858	20037	36.76	1.0E-130	BE275192.1	EST_HUMAN	Homo sapiens mRNA for KIAA1414 protein, partial cds
1842	10858	20038	36.76	1.0E-130	BE275192.1	EST_HUMAN	601121995F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3346386 5'
1952	11158		1.9	1.0E-130	X04092.1	NT	601121995F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3346386 5'
2728	11905		8.45	1.0E-130	AJ010230.1	NT	Human gene for catalase (EC 1.11.1.6) exon 9 mapping to chromosome 11, band p13
2832	12071	21192	1.26	1.0E-130	BE564219.1	EST_HUMAN	Homo sapiens RET finger protein-like 1 antisense transcript, partial
2832	12071	21193	1.28	1.0E-130	BE564219.1	EST_HUMAN	Homo sapiens RET finger protein-like 1 antisense transcript, partial
3553	12776	21905	1.13	1.0E-130	AF240698.1	NT	601343016F1 NIH_MGC_53 Homo sapiens cDNA clone IMAGE:3885468 5'
3750	12071	21192	5.96	1.0E-130	BE564219.1	EST_HUMAN	601343016F1 NIH_MGC_53 Homo sapiens cDNA clone IMAGE:3885468 5'
3750	12071	21193	5.96	1.0E-130	BE564219.1	EST_HUMAN	601343016F1 NIH_MGC_53 Homo sapiens cDNA clone IMAGE:3885468 5'
3910	13128	22243	1.57	1.0E-130	AW503580.1	EST_HUMAN	Homo sapiens retinol dehydrogenase homolog isoform-1 (RDH) mRNA, complete cds
4049	13259	22361	0.97	1.0E-130	M97710.1	NT	601343016F1 NIH_MGC_53 Homo sapiens cDNA clone IMAGE:3885468 5'
4535	13731	22828	8.08	1.0E-130	AW843983.1	EST_HUMAN	601343016F1 NIH_MGC_53 Homo sapiens cDNA clone IMAGE:3885468 5'
5127	14306	23396	1.16	1.0E-130	AW363269.1	EST_HUMAN	U1-HF-BN0-aky-g-06-o-U1.r1 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3078731 5'
5127	14306	23397	1.16	1.0E-130	AW363299.1	EST_HUMAN	Human T-cell receptor (V alpha 22.1, J alpha RPM14265-variant, C alpha 1) mRNA
6187	15389	24809	2.09	1.0E-130	11416777	NT	Human T-cell receptor (V alpha 22.1, J alpha RPM14265-variant, C alpha 1) mRNA
6832	16026	25492	2.38	1.0E-130	AB037756.1	NT	GM4-CN0045-180200-511-f02 CN0045 Homo sapiens cDNA
4	9301	18403	2.48	0.0E+00	AA228126.1	EST_HUMAN	RC0-CT0318-201199-031-a11 CT0318 Homo sapiens cDNA
4	9301	18404	2.48	0.0E+00	AA228126.1	EST_HUMAN	RC0-CT0318-201199-031-a11 CT0318 Homo sapiens cDNA
7	9303	18407	1.29	0.0E+00	4885136	NT	Homo sapiens solute carrier family 8 (neurotransmitter transporter, L-proline), member 7 (SLC8A7), mRNA
15	9311	18413	0.72	0.0E+00	8923349	NT	Homo sapiens mRNA for KIAA1335 protein, partial cds
15	9311	18414	0.72	0.0E+00	8923349	NT	z58c04.r1 Soares_NHMPu_S1 Homo sapiens cDNA clone IMAGE:667590 5' similar to TR:G222811
22	9318	18421	3.45	0.0E+00	D83327.1	NT	G222811 ALPHA 1 CHAIN OF TYPE XII COLLAGEN ;
22	9318	18422	3.45	0.0E+00	D83327.1	NT	z58c04.r1 Soares_NHMPu_S1 Homo sapiens cDNA clone IMAGE:667590 5' similar to TR:G222811
28	9324	18427	23.31	0.0E+00	AF141349.1	NT	G222811 ALPHA 1 CHAIN OF TYPE XII COLLAGEN ;
							Homo sapiens checkpoint suppressor 1 (CHEST), mRNA
							Homo sapiens hypothetical protein FLJ20371 (FLJ20371), mRNA
							Homo sapiens hypothetical protein FLJ20371 (FLJ20371), mRNA
							Homo sapiens DORR1 mRNA, partial cds
							Homo sapiens DORR1 mRNA, partial cds
							Homo sapiens beta-tubulin mRNA, complete cds

Table 4

## Single Exon Probes Expressed in HELA Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
36	9332	18437	2.44	0.0E+00	5802687	NT	Homo sapiens Cdc42 effector protein 2 (CEP2), mRNA
38	9334	18440	0.64	0.0E+00	M58600.1	NT	Human heparin cofactor II (HCF2) gene, exons 1 through 5
42	9338	18445	5.94	0.0E+00	6857825	NT	Homo sapiens RNA-binding protein S1, serine-rich domain (RNPS1), mRNA
59	9355	18472	2.5	0.0E+00	Y17151.2	NT	Homo sapiens mRNA for multidrug resistance protein 3 (ABCC3)
59	9355	18473	2.5	0.0E+00	Y17151.2	NT	Homo sapiens mRNA for multidrug resistance protein 3 (ABCC3)
61	9357	18477	1.28	0.0E+00	D78804.1	EST_HUMAN	HUM516H08B Human placenta polyA+ (TFujwara) Homo sapiens cDNA clone GEN-516H08 5'
61	9357	18478	1.28	0.0E+00	D78804.1	EST_HUMAN	HUM516H08B Human placenta polyA+ (TFujwara) Homo sapiens cDNA clone GEN-516H08 5'
62	9359	18479	27.64	0.0E+00	L16558.1	NT	Human ribosomal protein L7 (RPL7) mRNA, complete cds
64	9360	18482	8.6	0.0E+00	AW069534.1	EST_HUMAN	cr48a07.x1 Jia bone marrow stroma Homo sapiens cDNA clone HBMSC_cr48a07 3'
64	9360	18483	8.6	0.0E+00	AW069534.1	EST_HUMAN	cr48a07.x1 Jia bone marrow stroma Homo sapiens cDNA clone HBMSC_cr48a07 3'
75	9369	18497	0.73	0.0E+00	4758977	NT	Homo sapiens protein tyrosine phosphatase, non-receptor type substrate 1 (PTPNS1) mRNA
75	9369	18498	0.73	0.0E+00	4758977	NT	Homo sapiens protein tyrosine phosphatase, non-receptor type substrate 1 (PTPNS1) mRNA
78	9369	18497	0.62	0.0E+00	4758977	NT	Homo sapiens protein tyrosine phosphatase, non-receptor type substrate 1 (PTPNS1) mRNA
78	9369	18498	0.62	0.0E+00	4758977	NT	Homo sapiens protein tyrosine phosphatase, non-receptor type substrate 1 (PTPNS1) mRNA
81	9374	18504	0.87	0.0E+00	4501850	NT	Homo sapiens amiloride binding protein 1 (amine oxidase (copper-containing)) (ABP1), nuclear gene encoding mitochondrial protein, mRNA
82	9375		33.19	0.0E+00	4504444	NT	Homo sapiens heterogeneous nuclear ribonucleoprotein A1 (HNRPA1) mRNA
91	9384	18513	38.94	0.0E+00	5016088	NT	Homo sapiens actin, beta (ACTB) mRNA
94	9387	18516	25.33	0.0E+00	U82277.1	NT	Human polyhomeotic 1 homolog (HPH1) mRNA, partial cds
101	9394	18523	1.41	0.0E+00	A1114743.1	EST_HUMAN	HA1347 Human fetal liver cDNA library Homo sapiens cDNA
102	9395	18524	1.65	0.0E+00	AB037784.1	NT	Homo sapiens mRNA for KIAA1363 protein, partial cds
107	9397	18527	0.68	0.0E+00	XG1213.1	NT	H. sapiens ncx1 gene (exon 2)
118	9404	18533	2.12	0.0E+00	A1823701.1	EST_HUMAN	ts38b05.x1 NCL_CGAP_U14 Homo sapiens cDNA clone IMAGE:2230833 3' similar to TR:Q99551 Q99551 MITOCHONDRIAL TRANSCRIPTION TERMINATION FACTOR PRECURSOR.
117	9404	18533	1.15	0.0E+00	A1823701.1	EST_HUMAN	ts38b05.x1 NCL_CGAP_U14 Homo sapiens cDNA clone IMAGE:2230833 3' similar to TR:Q99551 Q99551 MITOCHONDRIAL TRANSCRIPTION TERMINATION FACTOR PRECURSOR.
118	11836	18534	2.65	0.0E+00	N36040.1	EST_HUMAN	yo1h08.r1 Soares melanocyte 2NbHM Homo sapiens cDNA clone IMAGE:270017 5'
118	11836	18535	2.65	0.0E+00	N36040.1	EST_HUMAN	yo1h08.r1 Soares melanocyte 2NbHM Homo sapiens cDNA clone IMAGE:270017 5'
128	9411	18545	4.14	0.0E+00	4505838	NT	Homo sapiens polymerase (RNA) II (DNA directed) polypeptide A (220kD) (POLR2A) mRNA
128	9411	18546	4.14	0.0E+00	4505838	NT	Homo sapiens polymerase (RNA) II (DNA directed) polypeptide A (220kD) (POLR2A) mRNA
137	9419	18553	1.13	0.0E+00	T56945.1	EST_HUMAN	ye83g04.r2 Stratagene fetal spleen (8937205) Homo sapiens cDNA clone IMAGE:68310 5'
137	9419	18554	1.13	0.0E+00	T56945.1	EST_HUMAN	ye83g04.r2 Stratagene fetal spleen (8937205) Homo sapiens cDNA clone IMAGE:68310 5'
156	9438		34.89	0.0E+00	4504444	NT	Homo sapiens heterogeneous nuclear ribonucleoprotein A1 (HNRPA1) mRNA
160	9442	18575	2.05	0.0E+00	BF036881.1	EST_HUMAN	601480375F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3863803 5'

Table 4

## Single Exon Probes Expressed in HELA Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
736	9977	19116	4.24	0.0E+00	AF264750.1	NT	Homo sapiens ALR-like protein mRNA, partial cds
736	9977	19117	4.24	0.0E+00	AF264750.1	NT	Homo sapiens ALR-like protein mRNA, partial cds
738	9979	19120	13.52	0.0E+00	11545800	NT	Homo sapiens hypothetical protein FLJ21634 (FLJ21634), mRNA
744	9985	19128	2.08	0.0E+00	BE241577.1	EST_HUMAN	TCAAP1D0778 Pediatric acute myelogenous leukemia cell (FAB M1) Baylor-HGSC project=TCAA Homo sapiens cDNA clone TCAAP0779
764	10004	19152	1.52	0.0E+00	AF226890.2	NT	Homo sapiens MHC class I antigen (HLA-G) mRNA, HLA-G1 allele, complete cds
764	10004	19153	1.52	0.0E+00	AF226890.2	NT	Homo sapiens MHC class I antigen (HLA-G) mRNA, HLA-G1 allele, complete cds
767	10007	19156	1.76	0.0E+00	J03784.1	NT	Human, plasminogen activator inhibitor-1 gene, exons 2 to 9
767	10007	19157	1.76	0.0E+00	J03784.1	NT	Human, plasminogen activator inhibitor-1 gene, exons 2 to 9
770	10010	19158	1.02	0.0E+00	AB037760.1	NT	Homo sapiens mRNA for KIAA1339 protein, partial cds
771	10011	19159	2.04	0.0E+00	5912749	NT	Homo sapiens zinc finger protein 212 (ZNF212), mRNA
773	11977	19161	2.38	0.0E+00	D30612.1	NT	Homo sapiens mRNA for repressor protein, partial cds
774	10013	19162	2.78	0.0E+00	BE869735.1	EST_HUMAN	601445647F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3848903 5'
776	10017	19166	3.28	0.0E+00	R48915.1	EST_HUMAN	Y65908.1 Soares breast 2NB-Hst Homo sapiens cDNA clone IMAGE:154046 5'
778	10018	19167	3	0.0E+00	5032086	NT	Homo sapiens splicing factor 3a, subunit 1, 120kD (SF3A1), mRNA
788	10027	19178	1.78	0.0E+00	AB011389.1	NT	Homo sapiens gene for AF-6, complete cds
791	10031	19180	3.24	0.0E+00	7681965	NT	Homo sapiens KIAA0170 gene product (KIAA0170), mRNA
802	10041	19192	0.95	0.0E+00	D80006.1	NT	Human mRNA for KIAA0184 gene, partial cds
802	10041	19193	0.95	0.0E+00	D80006.1	NT	Human mRNA for KIAA0184 gene, partial cds
807	10046	19197	2.72	0.0E+00	X89772.1	NT	H. sapiens mRNA for interferon alpha/beta receptor (long form)
811	10050	19201	3.81	0.0E+00	AB020717.1	NT	Homo sapiens mRNA for KIAA0910 protein, partial cds
811	10050	19202	3.81	0.0E+00	AB020717.1	NT	Homo sapiens mRNA for KIAA0910 protein, partial cds
816	10054	19208	12.64	0.0E+00	5174478	NT	Homo sapiens pericentrin (PCNT) mRNA
817	10055		10.04	0.0E+00	4507500	NT	Homo sapiens T-cell lymphoma invasion and metastasis 1 (TIAM1) mRNA
834	10072	19229	1.56	0.0E+00	7657213	NT	Homo sapiens hormonally upregulated neu tumor-associated kinase (HUNK), mRNA
835	10073	19230	2.71	0.0E+00	7657213	NT	Homo sapiens hormonally upregulated neu tumor-associated kinase (HUNK), mRNA
837	10075	19232	2.56	0.0E+00	4557680	NT	Homo sapiens potassium voltage-gated channel, Isk-related family, member 1 (KCNE1) mRNA
843	10080	19236	1.38	0.0E+00	AF108830.1	NT	Homo sapiens serine-threonine protein kinase (MNBH) mRNA, complete cds
843	10080	19239	1.38	0.0E+00	AF108830.1	NT	Homo sapiens serine-threonine protein kinase (MNBH) mRNA, complete cds
844	10081	19240	0.85	0.0E+00	AF108830.1	NT	Homo sapiens serine-threonine protein kinase (MNBH) mRNA, complete cds
849	10086	19245	1.3	0.0E+00	4503854	NT	Homo sapiens GA-binding protein transcription factor, alpha subunit (GABPA), mRNA
853	10089	19250	2.26	0.0E+00	4507500	NT	Homo sapiens T-cell lymphoma invasion and metastasis 1 (TIAM1) mRNA
853	10089	19251	2.26	0.0E+00	4507500	NT	Homo sapiens T-cell lymphoma invasion and metastasis 1 (TIAM1) mRNA
860	10096		1.51	0.0E+00	AF027153.1	NT	Homo sapiens sodium/myo-inositol cotransporter (SLC5A3) gene, complete cds

Page 336 of 382  
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Single Exon Probes Expressed in HELA Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
864	10100	19262	6.12	0.0E+00	AB028942.1	NT	Homo sapiens mRNA for KIAA1019 protein, partial cds
864	10100	19263	6.12	0.0E+00	AB028942.1	NT	Homo sapiens mRNA for KIAA1019 protein, partial cds
865	10101	19264	8.12	0.0E+00	4507152	NT	Homo sapiens SON DNA binding protein (SON) mRNA
866	10102	19265	3.01	0.0E+00	AB028942.1	NT	Homo sapiens mRNA for KIAA1019 protein, partial cds
867	10103	19266	9.08	0.0E+00	4506728	NT	Homo sapiens ribosomal protein S5 (RPS5) mRNA
871	10107	19269	1.87	0.0E+00	AB020717.1	NT	Homo sapiens mRNA for KIAA0910 protein, partial cds
871	10107	19270	1.87	0.0E+00	AB020717.1	NT	Homo sapiens mRNA for KIAA0910 protein, partial cds
872	10108	19271	2.32	0.0E+00	AA533272.1	EST_HUMAN	U66407.s1 NCI CGAP_P10 Homo sapiens cDNA clone IMAGE:597453
872	10108	19272	2.32	0.0E+00	AA533272.1	EST_HUMAN	U66407.s1 NCI CGAP_P10 Homo sapiens cDNA clone IMAGE:597453
873	10109		8.85	0.0E+00	BF677694.1	EST_HUMAN	602085579F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4249815 5'
877	10113	19273	1.37	0.0E+00	7657213	NT	Homo sapiens hormonally upregulated neu tumor-associated kinase (HUNK), mRNA
877	10113	19274	1.37	0.0E+00	7657213	NT	Homo sapiens hormonally upregulated neu tumor-associated kinase (HUNK), mRNA
878	10114	19275	2.16	0.0E+00	7657213	NT	Homo sapiens hormonally upregulated neu tumor-associated kinase (HUNK), mRNA
878	10114	19276	2.16	0.0E+00	7657213	NT	Homo sapiens hormonally upregulated neu tumor-associated kinase (HUNK), mRNA
901	10136	19288	1.84	0.0E+00	AL163203.2	NT	Homo sapiens chromosome 21 segment HS21C003
908	10143	19304	1.71	0.0E+00	BE089592.1	EST_HUMAN	QV0-BT0703-280400-211-g11 BT0703 Homo sapiens cDNA
908	10143	19305	1.71	0.0E+00	BE089592.1	EST_HUMAN	QV0-BT0703-280400-211-g11 BT0703 Homo sapiens cDNA
918	10153	19314	2.88	0.0E+00	AL163203.2	NT	Homo sapiens chromosome 21 segment HS21C003
928	10162		38.57	0.0E+00	4504958	NT	Homo sapiens lamellipodin receptor 1 (67kD, ribosomal protein SA) (LAMR1), mRNA
930	10162		32.73	0.0E+00	4504958	NT	Homo sapiens lamellipodin receptor 1 (67kD, ribosomal protein SA) (LAMR1), mRNA
931	10164	19321	0.76	0.0E+00	AF089747.1	NT	Homo sapiens alpha-1-antichymotrypsin precursor, mRNA, partial cds
932	10165	19322	1.87	0.0E+00	L28101.1	NT	Homo sapiens kallistatin (P14) gene, exons 1-4, complete cds
958	10191	19345	1.41	0.0E+00	M37180.1	NT	Human ras inhibitor mRNA, 3' end
959	10192	19346	8.37	0.0E+00	M37180.1	NT	Human ras inhibitor mRNA, 3' end
960	10193	19347	0.83	0.0E+00	M37180.1	NT	Human ras inhibitor mRNA, 3' end
961	10194	19348	1.68	0.0E+00	4507430	NT	Homo sapiens thymotrophic embryonic factor (TEF), mRNA
961	10194	19349	1.68	0.0E+00	4507430	NT	Homo sapiens thymotrophic embryonic factor (TEF), mRNA
969	11982	19356	2.74	0.0E+00	A001948.1	EST_HUMAN	cs98e03.s1 NCI CGAP_GC3 Homo sapiens cDNA clone IMAGE:1613404 3'
969	11982	19357	2.74	0.0E+00	A001948.1	EST_HUMAN	cs98e03.s1 NCI CGAP_GC3 Homo sapiens cDNA clone IMAGE:1613404 3'
971	10203	19359	7.12	0.0E+00	7657268	NT	Homo sapiens KIAA0928 protein Mx2 interacting nuclear target (MINT) homolog (KIAA0928), mRNA
982	10213	19369	2.97	0.0E+00	AB030566.1	NT	Homo sapiens mRNA for PSP24, complete cds
990	10221	19375	1.29	0.0E+00	BF366974.1	EST_HUMAN	PM2-GN0014-050900-001-f02 GN0014 Homo sapiens cDNA
990	10221	19376	1.29	0.0E+00	BF366974.1	EST_HUMAN	PM2-GN0014-050900-001-f02 GN0014 Homo sapiens cDNA



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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
980	10221	19377	1.29	0.0E+00	BF366974.1	EST_HUMAN	PM2-GN0014-050800-001-02 GN0014 Homo sapiens cDNA
991	10222	19378	2.96	0.0E+00	X52207.1	NT	Homo sapiens partial c-fgr gene, exons 2 and 3
991	10222	19379	2.96	0.0E+00	X52207.1	NT	Homo sapiens partial c-fgr gene, exons 2 and 3
1000	10231	19386	2.42	0.0E+00	4757869	NT	Homo sapiens chromodomain protein, Y chromosome-like (CDYL) mRNA
1012	10242	19394	2.4	0.0E+00	U83668.1	NT	Human beta-tubulin (TUB4q) gene, complete cds
1013	10243	19395	37.53	0.0E+00	U83668.1	NT	Human beta-tubulin (TUB4q) gene, complete cds
1014	10243	19395	9.7	0.0E+00	U83668.1	NT	Human beta-tubulin (TUB4q) gene, complete cds
1017	10246		13.45	0.0E+00	AF198490.1	NT	Homo sapiens 8q22.1 region and MTG8 (CBFA2T1) gene, partial cds
1018	10246		12.78	0.0E+00	AF198490.1	NT	Homo sapiens 8q22.1 region and MTG8 (CBFA2T1) gene, partial cds
1021	10249	19400	2.19	0.0E+00	AF111170.3	NT	Homo sapiens 14q32 Jagged2 gene, complete cds; and unknown gene
1022	10249	19400	2.09	0.0E+00	AF111170.3	NT	Homo sapiens 14q32 Jagged2 gene, complete cds; and unknown gene
1023	10249	19400	1.72	0.0E+00	AF111170.3	NT	Homo sapiens 14q32 Jagged2 gene, complete cds; and unknown gene
1024	10250	19401	2.61	0.0E+00	AF111170.3	NT	Homo sapiens 14q32 Jagged2 gene, complete cds; and unknown gene
1027	10253	19404	3.31	0.0E+00	7661685	NT	Homo sapiens DKFZP586M0122 protein (DKFZP586M0122), mRNA
1031	10257	19408	4.14	0.0E+00	5803114	NT	Homo sapiens inner membrane protein, mitochondrial (IMMT), mRNA
1033	10259		4.94	0.0E+00	AA458880.1	EST_HUMAN	aa88g07.61 Stratagene fetal retina 937202 Homo sapiens cDNA clone IMAGE:838236 3' similar to SW:PRS8_HUMAN P47210 26S PROTEASE REGULATORY SUBUNIT 8;
1036	10262	19413	0.95	0.0E+00	N43182.1	EST_HUMAN	EST5124 WATM1 Homo sapiens cDNA clone 51124 similar to DNA-DIRECTED RNA POLYMERASE II (alignment Ser and Pro with BLASTx or p)
1036	10262	19414	0.95	0.0E+00	N43182.1	EST_HUMAN	EST5124 WATM1 Homo sapiens cDNA clone 51124 similar to DNA-DIRECTED RNA POLYMERASE II (alignment Ser and Pro with BLASTx or p)
1037	10263	19415	2.06	0.0E+00	4759249	NT	Homo sapiens TRAF family member-associated NFKB activator (TANK) mRNA
1037	10263	19416	2.08	0.0E+00	4759249	NT	Homo sapiens TRAF family member-associated NFKB activator (TANK) mRNA
1040	10266		5.28	0.0E+00	8922833	NT	Homo sapiens hypothetical protein FLJ111198 (FLJ111198), mRNA
1054	10280	19431	9.66	0.0E+00	4759569	NT	Homo sapiens heat shock 70kD protein 98 (mortalin-2) (HSPA98) mRNA
1072	10297	19446	2.84	0.0E+00	4829672	NT	Homo sapiens cadherin 6, K-cadherin (fetal kidney) (CDH6) mRNA
1072	10297	19447	2.84	0.0E+00	4829672	NT	Homo sapiens cadherin 6, K-cadherin (fetal kidney) (CDH6) mRNA
1076	10301	19451	7.53	0.0E+00	8923624	NT	Homo sapiens hypothetical protein FLJ20695 (FLJ20695), mRNA
1076	10301	19452	7.53	0.0E+00	8923624	NT	Homo sapiens hypothetical protein FLJ20695 (FLJ20695), mRNA
1077	10302	19453	88.63	0.0E+00	AJ245922.1	NT	Homo sapiens mRNA for alpha-tubulin 8 (TUBA8 gene)
1079	10304		0.78	0.0E+00	8923087	NT	Homo sapiens hypothetical protein FLJ20080 (FLJ20080), mRNA
1081	10306	19457	3.29	0.0E+00	5174384	NT	Homo sapiens alkylation repair, alkB homolog (ABH), mRNA
1080	10314	19468	10.32	0.0E+00	4758117	NT	Homo sapiens Death associated protein 3 (DAP3) mRNA
1104	10328	19478	2.49	0.0E+00	BE005208.1	EST_HUMAN	MRO-BN0115-200300-003-108 BN0115 Homo sapiens cDNA

Page 338 of 382  
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Single Exon Probes Expressed in HELA Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1127	10351	19502	4.27	0.0E+00	7706134	NT	Homo sapiens potassium channel, subfamily K, member 9 (KCNK9), mRNA
1127	10351	19503	4.27	0.0E+00	7706134	NT	Homo sapiens potassium channel, subfamily K, member 9 (KCNK9), mRNA
1140	10363	19513	1.08	0.0E+00	4826947	NT	Homo sapiens protein kinase, X-linked (PRKX), mRNA
1140	10363	19514	1.06	0.0E+00	4826947	NT	Homo sapiens protein kinase, X-linked (PRKX), mRNA
1141	10364	19515	18.48	0.0E+00	4506712	NT	Homo sapiens ribosomal protein S27a (RPS27A), mRNA
1143	10366	19517	0.74	0.0E+00	8923280	NT	Homo sapiens hypothetical protein FLJ20309 (FLJ20309), mRNA
1148	10369	19520	8.75	0.0E+00	AB002059.1	NT	Homo sapiens DNA for Human P2XM, complete cds
1148	10371	19521	27.94	0.0E+00	AB002059.1	NT	Homo sapiens DNA for Human P2XM, complete cds
1149	10372	19522	3.79	0.0E+00	7657488	NT	Homo sapiens similar to rat integral membrane glycoprotein POM121 (POM121L1), mRNA
1149	10372	19523	3.79	0.0E+00	7657488	NT	Homo sapiens similar to rat integral membrane glycoprotein POM121 (POM121L1), mRNA
1153	10375	19526	1.82	0.0E+00	7706500	NT	Homo sapiens Npw38-binding protein NpwBP (LOC51729), mRNA
1154	10376	19527	0.63	0.0E+00	X95826.1	NT	H. sapiens ART4 gene
1154	10376	19528	0.63	0.0E+00	X95826.1	NT	H. sapiens ART4 gene
1155	10377	19528	0.79	0.0E+00	A1147950.1	EST_HUMAN	gb22d10.x1 Soares, pregnant uterus NBHPU Homo sapiens cDNA clone IMAGE:1697011 3'
1167	10378	19531	1.09	0.0E+00	AB020710.1	NT	Homo sapiens mRNA for KIAA0903 protein, partial cds
1164	10386	19537	2.81	0.0E+00	9986844	NT	Homo sapiens chromosome 12 open reading frame 3 (C12ORF3), mRNA
1176	10397	19549	2.31	0.0E+00	7305076	NT	Homo sapiens glutamate decarboxylase 1 (brain, 67kD) (GAD1), transcript variant GAD25, mRNA
1176	10397	19550	2.31	0.0E+00	7305076	NT	Homo sapiens glutamate decarboxylase 1 (brain, 67kD) (GAD1), transcript variant GAD25, mRNA
1179	10400	19553	0.8	0.0E+00	AB037835.1	NT	Homo sapiens mRNA for KIAA1414 protein, partial cds
1186	10407	19562	34.92	0.0E+00	4557897	NT	Homo sapiens keratin 18 (KRT18), mRNA
1217	10435		1.33	0.0E+00	7657336	NT	Homo sapiens mult. (E. coli) homolog 3 (MLH3), mRNA
1230	10448	19604	1.02	0.0E+00	8922593	NT	Homo sapiens hypothetical protein FLJ10697 (FLJ10697), mRNA
1233	10451	19607	1.44	0.0E+00	AF264750.1	NT	Homo sapiens ALR-like protein mRNA, partial cds
1233	10451	19608	1.44	0.0E+00	AF264750.1	NT	Homo sapiens ALR-like protein mRNA, partial cds
1234	10452	19609	1.02	0.0E+00	AF264750.1	NT	Homo sapiens ALR-like protein mRNA, partial cds
1235	11988	19610	1.63	0.0E+00	AF264750.1	NT	Homo sapiens ALR-like protein mRNA, partial cds
1253	10469	19633	5.36	0.0E+00	AF109718.1	NT	Homo sapiens chromosome 3 subtelomeric region
1254	10470	19634	1.58	0.0E+00	4503098	NT	Homo sapiens chondroitin sulfate proteoglycan 4 (melanoma-associated) (CSPG4), mRNA
1264	10479	19640	1.06	0.0E+00	4505740	NT	Homo sapiens prefoldin 4 (PFDN4), mRNA
1273	10488		2.95	0.0E+00	Y18000.1	NT	Homo sapiens NF2 gene
1281	10496	19655	97.05	0.0E+00	4506718	NT	Homo sapiens ribosomal protein S2 (RPS2), mRNA
1288	10503	19664	3.99	0.0E+00	AF084479.1	NT	Homo sapiens Williams-Beuren syndrome deletion transcript 9 (WBSOR9), mRNA, complete cds
1294	10509	19668	3.05	0.0E+00	AB040940.1	NT	Homo sapiens mRNA for KIAA1507 protein, partial cds
1294	10509	19669	3.05	0.0E+00	AB040940.1	NT	Homo sapiens mRNA for KIAA1507 protein, partial cds

Table 4

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162	9444		61.78	0.0E+00	4504444	NT	Homo sapiens heterogeneous nuclear ribonucleoprotein A1 (HNRPA1) mRNA
165	9447	18578	0.97	0.0E+00	AF111168.2	NT	Homo sapiens serine palmitoyl transferase, subunit II gene, complete cds; and unknown genes
167	9449	18579	0.94	0.0E+00	BE285973.1	EST_HUMAN	601174270F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3528864 5'
168	9449	18579	0.75	0.0E+00	BE285973.1	EST_HUMAN	601174270F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3528864 5'
169	9450	18580	3.95	0.0E+00	W73973.1	EST_HUMAN	zsf2005.f1 Soares_fetal heart_NbHH19W Homo sapiens cDNA clone IMAGE:345201 5' similar to gb:X16282_cds1 ZINC FINGER PROTEIN CLONE 647 (HUMAN);
170	9451	18581	0.69	0.0E+00	BE162832.1	EST_HUMAN	QV3-HT0457-140200-088-404 HT0457 Homo sapiens cDNA
170	9451	18582	0.69	0.0E+00	BE162832.1	EST_HUMAN	QV3-HT0457-140200-088-404 HT0457 Homo sapiens cDNA
171	9452	18583	2.33	0.0E+00	AF24-088.1	NT	Homo sapiens zinc finger protein mRNA, complete cds
174	9455	18586	7.31	0.0E+00	AL163202.2	NT	Homo sapiens chromosome 21 segment HS21C002
174	9455	18587	7.31	0.0E+00	AL163202.2	NT	Homo sapiens chromosome 21 segment HS21C002
185	9464	18594	4.28	0.0E+00	BE018970.1	EST_HUMAN	bb24e12.y1 NIH_MGC_14 Homo sapiens cDNA clone IMAGE:2863854 5' similar to WP:Y57A10A.Z CE22831;
185	9464	18595	4.28	0.0E+00	BE018970.1	EST_HUMAN	bb24e12.y1 NIH_MGC_14 Homo sapiens cDNA clone IMAGE:2863854 5' similar to WP:Y57A10A.Z CE22831;
190	9469	18598	2.81	0.0E+00	AB018327.1	NT	Homo sapiens mRNA for KIAA0784 protein, partial cds
190	9469	18599	2.81	0.0E+00	AB018327.1	NT	Homo sapiens mRNA for KIAA0784 protein, partial cds
191	9470	18600	1.3	0.0E+00	AB018327.1	NT	Homo sapiens mRNA for KIAA0784 protein, partial cds
191	9470	18601	1.3	0.0E+00	AB018327.1	NT	Homo sapiens mRNA for KIAA0784 protein, partial cds
199	9479	18612	122.25	0.0E+00	D50659.1	NT	Human gamma-cytoplasmic actin (ACTGP9) pseudogene
204	9484	18617	4.3	0.0E+00	AF273045.1	NT	Homo sapiens CTCL tumor antigen se14-3 mRNA, complete cds
204	9484	18618	4.3	0.0E+00	AF273045.1	NT	Homo sapiens CTCL tumor antigen se14-3 mRNA, complete cds
208	9486	18620	12.98	0.0E+00	AF167174.1	NT	Homo sapiens chromosome X MSL3-2 protein mRNA, complete cds
208	9486	18621	12.98	0.0E+00	AF167174.1	NT	Homo sapiens chromosome X MSL3-2 protein mRNA, complete cds
215	11862	18627	28.1	0.0E+00	AI587308.1	EST_HUMAN	tp04f08.x1 NCI_CGAP_U13 Homo sapiens cDNA clone IMAGE:2207847 3' similar to gb:J03191 PROFILIN1 (HUMAN);
215	11862	18628	28.1	0.0E+00	AI587308.1	EST_HUMAN	tp04f08.x1 NCI_CGAP_U13 Homo sapiens cDNA clone IMAGE:2207847 3' similar to gb:J03191 PROFILIN1 (HUMAN);
217	9486	18630	2	0.0E+00	AF195659.1	NT	Homo sapiens DNA mismatch repair protein (MLH3) gene, complete cds
219	9488		39.28	0.0E+00	4506832	NT	Homo sapiens ribosomal protein L31 (RPL31) mRNA
220	9489		11.09	0.0E+00	AF132000.1	NT	Homo sapiens TADA1 protein mRNA, complete cds
226	9505	18635	1.91	0.0E+00	AB018284.1	NT	Homo sapiens mRNA for KIAA0721 protein, partial cds
227	9505	18635	1.98	0.0E+00	AB018284.1	NT	Homo sapiens mRNA for KIAA0721 protein, partial cds
228	9508	18636	2.02	0.0E+00	6878444	NT	Mus musculus testis-specific protein, Y-encoded-like (Tspyl), mRNA

Table 4

## Single Exon Probes Expressed in HELA Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
242	9520	18651	8.91	0.0E+00	5453805	NT	Homo sapiens NS1-associated protein 1 (NSAP1) mRNA
244	9522		10.25	0.0E+00	AL163201.2	NT	Homo sapiens chromosome 21 segment HS21C001
251	9527	18657	4.08	0.0E+00	AF231919.1	NT	Homo sapiens chromosome 21 unknown mRNA
253	9529	18660	1.78	0.0E+00	X89772.1	NT	H. sapiens mRNA for Interferon alpha/beta receptor (long form)
261	9537		8.15	0.0E+00	AF231919.1	NT	Homo sapiens chromosome 21 unknown mRNA
274	9549	18678	1.3	0.0E+00	4507500	NT	Homo sapiens T-cell lymphoma invasion and metastasis 1 (TIAM1) mRNA
274	9549	18680	1.3	0.0E+00	4507500	NT	Homo sapiens T-cell lymphoma invasion and metastasis 1 (TIAM1) mRNA
278	9551	18682	2.35	0.0E+00	7706028	NT	Homo sapiens hypothetical protein (LOC51250), mRNA
287	9561		1.27	0.0E+00	D83327.1	NT	Homo sapiens DORR1 mRNA, partial cds
288	9562	18695	3.32	0.0E+00	D83327.1	NT	Homo sapiens DORR1 mRNA, partial cds
288	9562	18698	3.32	0.0E+00	D83327.1	NT	Homo sapiens DORR1 mRNA, partial cds
289	9563		0.81	0.0E+00	AW845293.1	EST_HUMAN	IL2-CT0031-181199-020-B03 CT0031 Homo sapiens cDNA
288	9571	18703	8.24	0.0E+00	4557029	NT	Homo sapiens potassium inwardly-rectifying channel, subfamily J, member 15 (KCNJ15) mRNA
309	9592	18714	3.6	0.0E+00	4557029	NT	Homo sapiens potassium inwardly-rectifying channel, subfamily J, member 15 (KCNJ15) mRNA
310	9593	18715	3.82	0.0E+00	AB028942.1	NT	Homo sapiens mRNA for KIAA1019 protein, partial cds
311	11865		14.42	0.0E+00	4506728	NT	Homo sapiens ribosomal protein S5 (RPS5) mRNA
312	9594	18716	0.88	0.0E+00	4503914	NT	Homo sapiens phosphoribosylglycylamide formyltransferase, phosphoribosylglycylamide synthetase, phosphoribosylaminimidazole synthetase (GART) mRNA
313	9595		4.5	0.0E+00	AA480002.1	EST_HUMAN	z18c06.r1 Soares_NHMPu_S1 Homo sapiens cDNA clone IMAGE:753994.5
314	9598	18717	21.53	0.0E+00	4507152	NT	Homo sapiens SON DNA binding protein (SON) mRNA
315	9598	18717	17.61	0.0E+00	4507152	NT	Homo sapiens SON DNA binding protein (SON) mRNA
319	9599	18721	1.63	0.0E+00	AF114488.1	NT	Homo sapiens Intersectin short isoform (ITSN) mRNA, complete cds
332	9602	18730	1.09	0.0E+00	O14867	SWISSPROT	TRANSCRIPTION REGULATOR PROTEIN BACH1 (BTB AND CNC HOMOLOG 1) (HA2303)
332	9602	18731	1.09	0.0E+00	O14867	SWISSPROT	TRANSCRIPTION REGULATOR PROTEIN BACH1 (BTB AND CNC HOMOLOG 1) (HA2303)
333	9603	18732	3.8	0.0E+00	7657213	NT	Homo sapiens hormonally upregulated neu tumor-associated kinase (HUNK), mRNA
334	9603	18732	2.51	0.0E+00	7657213	NT	Homo sapiens hormonally upregulated neu tumor-associated kinase (HUNK), mRNA
349	9617	18744	1.86	0.0E+00	5174574	NT	Homo sapiens myeloid/lymphoid or mixed-lineage leukemia (trithorax (Drosophila) homolog), translocated to, 4 (MLLT4) mRNA
350	9618	18746	1.11	0.0E+00	4505256	NT	Homo sapiens moesin (MSN), mRNA
353	9621	18749	22.13	0.0E+00	4827057	NT	Homo sapiens X-box binding protein 1 (XBP1) mRNA
356	9624	18754	1.89	0.0E+00	U71600.1	NT	Human zinc finger protein zfp31 (zfp31) mRNA, partial cds
361	9628	18758	2.54	0.0E+00	AF231919.1	NT	Homo sapiens chromosome 21 unknown mRNA
361	9628	18759	2.54	0.0E+00	AF231919.1	NT	Homo sapiens chromosome 21 unknown mRNA

Table 4

## Single Exon Probes Expressed in HELA Cells

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
362	11966	18760	4.02	0.0E+00	AF231918.1	NT	Homo sapiens chromosome 21 unknown mRNA
364	9630	18762	0.8	0.0E+00	4507500	NT	Homo sapiens T-cell lymphoma invasion and metastasis 1 (TIAM1) mRNA
366	9633	18768	1.94	0.0E+00	4503854	NT	Homo sapiens GA-binding protein transcription factor, alpha subunit (GABPA), mRNA
367	9634	18767	1.2	0.0E+00	D80006.1	NT	Human mRNA for KIAA0184 gene, partial cds
368	9634	18767	1	0.0E+00	D80006.1	NT	Human mRNA for KIAA0184 gene, partial cds
370	9636	18769	0.69	0.0E+00	4507500	NT	Homo sapiens T-cell lymphoma invasion and metastasis 1 (TIAM1) mRNA
381	9645	18780	2.68	0.0E+00	AU134963.1	EST_HUMAN	AU134963 PLACE1 Homo sapiens cDNA clone PLACE1000898 5'
392	9686	18824	7.13	0.0E+00	AB028942.1	NT	Homo sapiens mRNA for KIAA1019 protein, partial cds
393	9687	18825	2.49	0.0E+00	AI363014.1	EST_HUMAN	q61h05.x1 NCI_CGAP_Bm25 Homo sapiens cDNA clone IMAGE:2018457 3' similar to gb:X54199
397	9652	18787	2.84	0.0E+00	AW754180.1	EST_HUMAN	PHOSPHORIBOSYLAMINE-GLYCINE LIGASE (HUMAN);
400	9654	18790	12.1	0.0E+00	4503680	NT	RC2-CT0320-300100-016-a09 CT0320 Homo sapiens cDNA
401	9655	18791	2.32	0.0E+00	4503680	NT	Homo sapiens IgG Fc binding protein (FC(GAMMA)BP) mRNA
401	9655	18792	2.32	0.0E+00	4503680	NT	Homo sapiens IgG Fc binding protein (FC(GAMMA)BP) mRNA
402	9656	18793	1.17	0.0E+00	4503680	NT	Homo sapiens IgG Fc binding protein (FC(GAMMA)BP) mRNA
403	9657	18794	1.8	0.0E+00	4503680	NT	Homo sapiens IgG Fc binding protein (FC(GAMMA)BP) mRNA
403	9657	18795	1.6	0.0E+00	4503680	NT	Homo sapiens IgG Fc binding protein (FC(GAMMA)BP) mRNA
404	9658	18796	0.59	0.0E+00	4503680	NT	Homo sapiens IgG Fc binding protein (FC(GAMMA)BP) mRNA
405	9659	18797	3.48	0.0E+00	4503680	NT	Homo sapiens IgG Fc binding protein (FC(GAMMA)BP) mRNA
406	9660	18798	0.61	0.0E+00	4503680	NT	Homo sapiens IgG Fc binding protein (FC(GAMMA)BP) mRNA
407	9661	18799	1.85	0.0E+00	X74870.1	NT	H. sapiens gene for RNA pol II largest subunit, exons 23-28
407	9661	18800	1.85	0.0E+00	X74870.1	NT	H. sapiens gene for RNA pol II largest subunit, exons 23-28
408	9661	18799	1.89	0.0E+00	X74870.1	NT	H. sapiens gene for RNA pol II largest subunit, exons 23-28
408	9661	18800	1.89	0.0E+00	X74870.1	NT	H. sapiens gene for RNA pol II largest subunit, exons 23-28
412	9665		51.35	0.0E+00	4506608	NT	Homo sapiens ribosomal protein L19 (RPL19) mRNA
426	8291	18393	1.21	0.0E+00	R17795.1	EST_HUMAN	Y098402.1 Soares Infant brain 1N1B Homo sapiens cDNA clone IMAGE:31652 5'
434	9668	18826	1.24	0.0E+00	4503914	NT	Homo sapiens phosphoribosylglycinamide formyltransferase, phosphoribosylglycinamide synthetase,
435	9669		19.94	0.0E+00	4506728	NT	phosphoribosylaminimidazole synthetase (GART) mRNA
436	9669	18827	7.31	0.0E+00	AB028942.1	NT	Homo sapiens ribosomal protein S5 (RPS5) mRNA
437	9691	18828	4.64	0.0E+00	4507152	NT	Homo sapiens mRNA for KIAA1019 protein, partial cds
437	9691	18829	4.64	0.0E+00	4507152	NT	Homo sapiens SON DNA binding protein (SON) mRNA
438	9692	18830	3.52	0.0E+00	AF193607.1	NT	Homo sapiens SON DNA binding protein (SON) mRNA
450	9703		0.92	0.0E+00	AL163201.2	NT	Mus musculus truncated SON protein (Son) mRNA, complete cds
							Homo sapiens chromosome 21 segment HS21C001

Table 4

## Single Exon Probes Expressed in HELA Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
452	9705	18943	1.28	0.0E+00	4557879	NT	Homo sapiens interferon gamma receptor 1 (IFNGR1) mRNA
457	9710		1.48	0.0E+00	AA324262.1	EST_HUMAN	EST27054 Cerebellum II Homo sapiens cDNA 5' end
458	9711		2.54	0.0E+00	BE254447.1	EST_HUMAN	601111520F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3352348 5'
474	9727	18957	6.06	0.0E+00	4504532	NT	Homo sapiens 6-hydroxytryptamine (serotonin) receptor 1B (HTR1B) mRNA
474	9727	18958	6.06	0.0E+00	4504532	NT	Homo sapiens 5-hydroxytryptamine (serotonin) receptor 1B (HTR1B) mRNA
480	9732	18966	15.14	0.0E+00	4557887	NT	Homo sapiens keratin 18 (KRT18) mRNA
480	9732	18967	15.14	0.0E+00	4557887	NT	Homo sapiens keratin 18 (KRT18) mRNA
490	9743	18873	3.04	0.0E+00	AL163246.2	NT	Homo sapiens chromosome 21 segment HS21C046
490	9743	18874	7.23	0.0E+00	AL163246.2	NT	Homo sapiens chromosome 21 segment HS21C046
491	9744	18875	7.23	0.0E+00	AL163246.2	NT	Homo sapiens chromosome 21 segment HS21C046
500	9752	18880	2.83	0.0E+00	AB033035.1	NT	Homo sapiens mRNA for KIAA1209 protein, partial cds
502	9754	18882	1.89	0.0E+00	AU132898.1	EST_HUMAN	AU132898 NT2RP4 Homo sapiens cDNA clone NT2RP4000837 5'
510	9762	18888	3.47	0.0E+00	BE385144.1	EST_HUMAN	601274951F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3615756 5'
511	11969	18889	1.89	0.0E+00	AW938825.1	EST_HUMAN	PMO-DT0065-130400-002-c06 DT0065 Homo sapiens cDNA
514	9765	18891	1.14	0.0E+00	AL117233.1	NT	Novel human gene mapping to chromosome 1
515	9766	18892	1.09	0.0E+00	8923955	NT	Homo sapiens PC326 protein (PC326), mRNA
518	9769		0.75	0.0E+00	BF379403.1	EST_HUMAN	IL2-FT0159-070800-120-F07 FT0159 Homo sapiens cDNA
525	9776	18901	6.28	0.0E+00	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C010
532	11970	18905	1.5	0.0E+00	BE081527.1	EST_HUMAN	QV2-BT0635-160400-142-h05 BT0635 Homo sapiens cDNA
537	9788	18911	1.08	0.0E+00	BF028005.1	EST_HUMAN	601764858F1 NIH_MGC_53 Homo sapiens cDNA clone IMAGE:3986998 5'
543	9794	18918	1.13	0.0E+00	AB040909.1	NT	Homo sapiens mRNA for KIAA1476 protein, partial cds
546	9797	18921	9.28	0.0E+00	6006030	NT	Homo sapiens mRNA for KIAA1476 protein, partial cds
547	9798	18922	4.75	0.0E+00	4504036	NT	Homo sapiens polypeptide 1-like (TCCEB1L) mRNA
547	9798	18923	4.75	0.0E+00	4504036	NT	Homo sapiens guanine nucleotide binding protein (G protein), alpha 11 (Gq class) (GNA11) mRNA
548	9800	18925	1.77	0.0E+00	8923831	NT	Homo sapiens guanine nucleotide binding protein (G protein), alpha 11 (Gq class) (GNA11) mRNA
550	9801	18926	1.44	0.0E+00	8923831	NT	Homo sapiens anillin (LOC544443), mRNA
550	9801	18927	1.44	0.0E+00	8923831	NT	Homo sapiens anillin (LOC544443), mRNA
							Homo sapiens X-linked anhidrotic ectodermal dysplasia protein gene (EDA), exon 2 and flanking repeat regions
555	9805		5.12	0.0E+00	AF003528.1	NT	UJ-H-B11-acb-H-04-0-U1.s1 NCI_CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2713951 3'
563	9813	18936	1.42	0.0E+00	AW135324.1	EST_HUMAN	Homo sapiens RGH1 gene, retrovirus-like element
573	9823		7.59	0.0E+00	D10063.1	NT	Homo sapiens ubiquinol-cytochrome c reductase, Rieske iron-sulfur polypeptide 1 (UQCRCF1), nuclear gene
593	9841	18961	3.94	0.0E+00	5174742	NT	encoding mitochondrial protein, mRNA
606	9853		5.9	0.0E+00	J04066.1	NT	Human apolipoprotein A-I (ApoA-I) gene, exon 1

Table 4

## Single Exon Probes Expressed in HELA Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
609	9856	18975	3.34	0.0E+00	BF104988.1	EST_HUMAN	601822627F1 NIH_MGC_75 Homo sapiens cDNA clone IMAGE:4045447 5'
615	9860	18979	1.28	0.0E+00	4501854	NT	Homo sapiens acetyl-Coenzyme A carboxylase beta (ACACB), mRNA
620	9865	18985	0.9	0.0E+00	AF221712.1	NT	Homo sapiens Smed- and Olf-interacting zinc finger protein mRNA, partial cds
620	9865	18986	0.9	0.0E+00	AF221712.1	NT	Homo sapiens Smed- and Olf-interacting zinc finger protein mRNA, partial cds
628	9873	18984	2.56	0.0E+00	AF149773.1	NT	Homo sapiens NOD1 protein (NOD1) gene, exons 1, 2, and 3
630	9875	18987	0.93	0.0E+00	AB037807.1	NT	Homo sapiens mRNA for KIAA1388 protein, partial cds
632	9877	18988	1.89	0.0E+00	6806918	NT	Homo sapiens low density lipoprotein-related protein 2 (LRP2), mRNA
633	9878	18989	2.11	0.0E+00	6806918	NT	Homo sapiens low density lipoprotein-related protein 2 (LRP2), mRNA
633	9878	19000	2.11	0.0E+00	6806918	NT	Homo sapiens low density lipoprotein-related protein 2 (LRP2), mRNA
634	9879	19001	0.94	0.0E+00	6806918	NT	Homo sapiens low density lipoprotein-related protein 2 (LRP2), mRNA
634	9879	19002	0.94	0.0E+00	6806918	NT	Homo sapiens low density lipoprotein-related protein 2 (LRP2), mRNA
641	9887	19012	1.32	0.0E+00	AA399488.1	EST_HUMAN	z60c07.1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:726732 5'
645	9891	19016	12.08	0.0E+00	D11078.1	NT	Homo sapiens RGH2 gene, retrovirus-like element
649	9895	19019	3.5	0.0E+00	W78811.1	EST_HUMAN	zh51b04.r1 Soares_fetal_liver_spleen_TNFSL_S1 Homo sapiens cDNA clone IMAGE:415587 5' similar to gb:A21187 ALPHA-2-MACROGLOBULIN PRECURSOR (HUMAN);
649	9895	19020	3.5	0.0E+00	W78811.1	EST_HUMAN	zh51b04.r1 Soares_fetal_liver_spleen_TNFSL_S1 Homo sapiens cDNA clone IMAGE:415587 5' similar to gb:A21187 ALPHA-2-MACROGLOBULIN PRECURSOR (HUMAN);
652	9898		3.55	0.0E+00	4885528	NT	Homo sapiens novel SH2-containing protein 3 (NSP3) mRNA
659	9905	19032	2.48	0.0E+00	6006003	NT	Homo sapiens glutamate receptor, ionotropic, N-methyl D-aspartate 2B (GRIN2B) mRNA
661	9907	19035	1.88	0.0E+00	5031624	NT	Homo sapiens CCAAT-box-binding transcription factor (CBF2) mRNA
664	9910	19039	1.49	0.0E+00	U05235.1	NT	Human neutral amino acid transporter (ASCT1) gene, exon 8
668	9914	19042	0.87	0.0E+00	AF108389.1	NT	Homo sapiens sodium/calcium exchanger isoform NaCa3 (NCX1) mRNA, complete cds
668	9914	19043	0.87	0.0E+00	AF108389.1	NT	Homo sapiens sodium/calcium exchanger isoform NaCa3 (NCX1) mRNA, complete cds
674	9919	19048	4.8	0.0E+00	4826847	NT	Homo sapiens protein kinase, X-linked (PRKX) mRNA
674	9919	19049	4.8	0.0E+00	4826847	NT	Homo sapiens protein kinase, X-linked (PRKX) mRNA
680	11973		1.26	0.0E+00	X57147.1	NT	Human endogenous retrovirus pHE.1 (ERV8)
689	9902	19063	17.16	0.0E+00	4504424	NT	Homo sapiens high-mobility group (nonhistone chromosomal) protein 1 (HMG1) mRNA
694	9937	19067	4.7	0.0E+00	AB028012.1	NT	Homo sapiens mRNA for KIAA1089 protein, partial cds
704	9946	19082	3.3	0.0E+00	7657468	NT	Homo sapiens similar to rat integral membrane glycoprotein POM121 (POM121L1), mRNA
716	9958	19096	106.67	0.0E+00	AA614537.1	EST_HUMAN	mp49d01.s1 NCI_CGAP_Br.1.1 Homo sapiens cDNA clone IMAGE:1128633 3' similar to gb:X57352 INTERFERON-INDUCIBLE PROTEIN 1-3U (HUMAN);
720	9962	19100	4.1	0.0E+00	M60675.1	NT	Human von Willebrand factor gene, exons 23 through 34
720	9962	19101	4.1	0.0E+00	M60675.1	NT	Human von Willebrand factor gene, exons 23 through 34
730	9972	19110	1.35	0.0E+00	5032192	NT	Homo sapiens TNF receptor-associated factor 1 (TRAF1) mRNA

Table 4

## Single Exon Probes Expressed in HELA Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1307	10523	19882	2.46	0.0E+00	5174748	NT	Homo sapiens Wolfram syndrome (WFS) mRNA
1307	10523	19883	2.46	0.0E+00	5174748	NT	Homo sapiens Wolfram syndrome (WFS) mRNA
1307	10523	19884	2.46	0.0E+00	5174748	NT	Homo sapiens Wolfram syndrome (WFS) mRNA
1308	10524		3.13	0.0E+00	AF068156.1	NT	Homo sapiens protein phosphatase 2A BR gamma subunit gene, exon 5
1318	11990	19898	1.32	0.0E+00	7657529	NT	Homo sapiens rhabdoid tumor deletion region protein 1 (RTDR1), mRNA
1318	11990	19897	1.32	0.0E+00	7657529	NT	Homo sapiens rhabdoid tumor deletion region protein 1 (RTDR1), mRNA
1323	10538	19702	1.51	0.0E+00	5803146	NT	Homo sapiens ring finger protein 9 (RNF9), mRNA
1324	10539	19703	2.45	0.0E+00	4508004	NT	Homo sapiens zinc finger protein 173 (ZNF173) mRNA
1326	10541	19704	0.63	0.0E+00	Y07826.2	NT	Homo sapiens RFB30 gene for RING finger protein
1327	10542	19705	0.68	0.0E+00	5803146	NT	Homo sapiens ring finger protein 9 (RNF9), mRNA
1328	10543	19706	2.48	0.0E+00	4508004	NT	Homo sapiens zinc finger protein 173 (ZNF173) mRNA
1330	10545	19708	4.21	0.0E+00	AB011149.1	NT	Homo sapiens mRNA for KIAA0577 protein, complete cds
1331	10546	19709	5.75	0.0E+00	7661965	NT	Homo sapiens KIAA0170 gene product (KIAA0170), mRNA
1332	10547	19710	5.16	0.0E+00	7661965	NT	Homo sapiens KIAA0170 gene product (KIAA0170), mRNA
1333	10548	19711	4.94	0.0E+00	8567387	NT	Homo sapiens KIAA0170 gene product (KIAA0170), mRNA
1333	10548	19712	4.94	0.0E+00	8567387	NT	Homo sapiens KIAA0170 gene product (KIAA0170), mRNA
1345	10559	19725	2.1	0.0E+00	M14123.1	NT	Homo sapiens period (Drosophila) homolog 3 (PER3), mRNA
1402	10616	19780	1.83	0.0E+00	BE257955.1	EST_HUMAN	Human endogenous retrovirus HERV-K10
1402	10616	19781	1.83	0.0E+00	BE257955.1	EST_HUMAN	601109792F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3350471 5'
1412	10625	19791	1.3	0.0E+00	AJ250014.1	NT	601109792F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3350471 5'
1421	10634	19803	0.91	0.0E+00	AJ208756.1	EST_HUMAN	Homo sapiens mRNA for Familial Cylindromatosis cyl gene
							eg38b06.x1 Scarses_tests_NHT Homo sapiens cDNA clone IMAGE:1837427 3' similar to WP.T27A1.5
							CE14213
1422	10635	19804	44.87	0.0E+00	6042206	NT	RAN, member RAS oncogene family/Homo sapiens RAN, member RAS oncogene family (RAN), mRNA
1431	10644	19816	2.73	0.0E+00	7705565	NT	Homo sapiens KIAA1114 protein (KIAA1114), mRNA
1431	10644	19817	2.73	0.0E+00	7705565	NT	Homo sapiens KIAA1114 protein (KIAA1114), mRNA
1433	10646	19818	7.39	0.0E+00	AJ238093.1	NT	Homo sapiens partial AF-4 gene, exons 2 to 7 and Alu repeat elements
1441	10655	19829	3.3	0.0E+00	AF038280.1	NT	Homo sapiens alpha1-8fucosyltransferase (alpha1-8FucT) gene, exon 7
1459	10672	19844	3.25	0.0E+00	AL132998.1	NT	Novel human gene on chromosome 20
1463	10676	19849	2.09	0.0E+00	D87077.1	NT	Human mRNA for KIAA0240 gene, partial cds
1466	10679	19852	9.32	0.0E+00	6912457	NT	Homo sapiens calnexin binding protein 1 (KIAA0330), mRNA
1488	10681	19854	2.31	0.0E+00	7661965	NT	Homo sapiens KIAA0170 gene product (KIAA0170), mRNA
1488	10681	19855	2.31	0.0E+00	7661965	NT	Homo sapiens KIAA0170 gene product (KIAA0170), mRNA
1500	10713	19895	1.19	0.0E+00	7708434	NT	Homo sapiens hHDC for homolog of Drosophila headcase (LOC51898), mRNA



Table 4  
Single Exon Probes Expressed in HELA Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1512	10728	19898	3.05	0.0E+00	AA481172.1	EST_HUMAN	aa34403.1 NCI CGAP_GCB1 Homo sapiens cDNA clone IMAGE:815116 5'
1518	10732	19901	111.36	0.0E+00	AF023880.1	NT	Cercopithecus aethiops cyclophilin A mRNA, complete cds
1518	10732	19902	111.36	0.0E+00	AF023880.1	NT	Cercopithecus aethiops cyclophilin A mRNA, complete cds
1520	10734	19905	1.22	0.0E+00	AW976097.1	EST_HUMAN	EST388206 IMAGE resequences, MAGN Homo sapiens cDNA
1520	10734	19906	1.22	0.0E+00	AW976097.1	EST_HUMAN	EST388206 IMAGE resequences, MAGN Homo sapiens cDNA
1521	10735	19907	1.09	0.0E+00	D10884.1	NT	Bovine mRNA for neurocalcin
1523	10737		4.77	0.0E+00	U78027.1	NT	Homo sapiens Bruton's tyrosine kinase (BTK), alpha-D-galactosidase A (GLA), L44-like ribosomal protein (L44L) and FTP3 (FTP3) genes, complete cds
1524	10738	19910	5.07	0.0E+00	4505404	NT	Homo sapiens transmembrane glycoprotein (GPNMB) mRNA
1524	10738	19911	5.07	0.0E+00	4505404	NT	Homo sapiens transmembrane glycoprotein (GPNMB) mRNA
1525	10739	19912	2.82	0.0E+00	7662405	NT	Homo sapiens KIAA0957 protein (KIAA0957), mRNA
1526	10740		6.07	0.0E+00	7656972	NT	Homo sapiens TNF-inducible protein CG12-1 (CG12-1), mRNA
1531	10745	19918	3.66	0.0E+00	M88478.1	NT	Human transglutaminase mRNA, complete cds
1533	10747	19919	0.95	0.0E+00	4507720	NT	Homo sapiens titin (TTN) mRNA
1533	10747	19920	0.95	0.0E+00	4507720	NT	Homo sapiens titin (TTN) mRNA
1534	11997		72.34	0.0E+00	4506854	NT	Homo sapiens ribosomal protein L5 (RPL5) mRNA
1535	10748	19921	74.68	0.0E+00	M14199.1	NT	Human laminin receptor (2H5 epitope) mRNA, 5' end
1545	10759	19932	13.15	0.0E+00	4503098	NT	Homo sapiens chondroitin sulfate proteoglycan 4 (melanoma-associated) (CSPG4), mRNA
1551	10765		2.44	0.0E+00	D00333.1	NT	human c-yes-2 gene
1559	10773	19946	8.95	0.0E+00	Z83738.1	NT	H. sapiens HH2B/e gene
1560	10774	19947	2.11	0.0E+00	5921460	NT	Homo sapiens butyrophilin, subfamily 2, member A1 (BTN2A1), mRNA
1560	10774	19948	2.11	0.0E+00	5921460	NT	Homo sapiens butyrophilin, subfamily 2, member A1 (BTN2A1), mRNA
1561	10775	19949	9.8	0.0E+00	AV690831.1	EST_HUMAN	AV690831 GKC Homo sapiens cDNA clone GKCBOF02 5'
1561	10775	19950	9.8	0.0E+00	AV690831.1	EST_HUMAN	AV690831 GKC Homo sapiens cDNA clone GKCBOF02 5'
1564	11988	19953	3.17	0.0E+00	AB040905.1	NT	Homo sapiens mRNA for KIAA1472 protein, partial cds
1568	10781	19954	1.39	0.0E+00	AF157476.1	NT	Homo sapiens DNA polymerase zeta catalytic subunit (REV3) mRNA, complete cds
1570	10783	19957	3.7	0.0E+00	7662183	NT	Homo sapiens KIAA0569 gene product (KIAA0569), mRNA
1570	10783	19958	3.7	0.0E+00	7662183	NT	Homo sapiens KIAA0569 gene product (KIAA0569), mRNA
1572	10785	19959	43.92	0.0E+00	5729876	NT	Homo sapiens heat shock 70KD protein 10 (HSC71) (HSPA10), mRNA
1572	10785	19960	43.92	0.0E+00	5729876	NT	Homo sapiens heat shock 70KD protein 10 (HSC71) (HSPA10), mRNA
1574	10787	19962	1.25	0.0E+00	M91803.1	NT	Human sodium channel mRNA
1588	10801	19977	8.91	0.0E+00	H26873.1	EST_HUMAN	yo76c05.s1 Soares adult brain N2b4HB55Y Homo sapiens cDNA clone IMAGE:183848 3'
1598	10810	19987	9.46	0.0E+00	AB046829.1	NT	Homo sapiens mRNA for KIAA1609 protein, partial cds
1598	10810	19988	9.46	0.0E+00	AB046829.1	NT	Homo sapiens mRNA for KIAA1609 protein, partial cds

Page 341 of 382  
Table 4  
Single Exon Probes Expressed in HELA Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1615	10828	20033	1.28	0.0E+00	AW444637.1	EST_HUMAN	UI-H-B13-gw-c-04-01-01 NCI CGAP_Sub5 Homo sapiens cDNA clone IMAGE:2733284 3'
1640	10854	20034	1.25	0.0E+00	BE144364.1	EST_HUMAN	MRO-HT0168-191189-004-b11 HTO168 Homo sapiens cDNA
1640	10854	20035	1.25	0.0E+00	BE144364.1	EST_HUMAN	MRO-HT0168-191189-004-b11 HTO168 Homo sapiens cDNA
1644	10858	20039	13.17	0.0E+00	AI768104.1	EST_HUMAN	wg81b07.x1 Soares NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:2371477 3' similar to TR:Q62788 Q62788 CYS2/HIS2 ZINC FINGER PROTEIN ;
1645	10859	20040	3.17	0.0E+00	AF057177.1	NT	Homo sapiens T-cell receptor gamma V1 gene region
1648	10862	20043	2.18	0.0E+00	M29580.1	NT	Human zinc-finger protein 7 (ZFP7) mRNA, complete cds
1648	10862	20044	2.18	0.0E+00	M29580.1	NT	Human zinc-finger protein 7 (ZFP7) mRNA, complete cds
1650	10864	20048	39.38	0.0E+00	4557887	NT	Homo sapiens keratin 18 (KRT18) mRNA
1651	10865	20047	1.68	0.0E+00	7657065	NT	Homo sapiens v-ets avian erythroblastosis virus E26 oncogene related (ERG), mRNA
1655	10869	20050	1	0.0E+00	BE222374.1	EST_HUMAN	hu11d05.x1 NCI CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3166281 3' similar to TR:O95147 O95147 MKP-1 LIKE PROTEIN TYROSINE PHOSPHATASE ;
1655	10869	20051	1	0.0E+00	BE222374.1	EST_HUMAN	hu11d05.x1 NCI CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3166281 3' similar to TR:O95147 O95147 MKP-1 LIKE PROTEIN TYROSINE PHOSPHATASE ;
1657	10870	20053	1.59	0.0E+00	4557610	NT	Homo sapiens gamma-aminobutyric acid (GABA) A receptor, gamma 2 (GABRG2) mRNA
1660	10873	20058	4.61	0.0E+00	H30132.1	EST_HUMAN	yo59e08.r1 Soares breast 3NBHst Homo sapiens cDNA clone IMAGE:182246 5' similar to gb:M64099 GAMMA-GLUTAMYL TRANSPEPTIDASE 5 PRECURSOR (HUMAN);
1660	10873	20057	4.61	0.0E+00	H30132.1	EST_HUMAN	GAMMA-GLUTAMYL TRANSPEPTIDASE 5 PRECURSOR (HUMAN);
1662	10875	20059	5.52	0.0E+00	Z80780.1	NT	yo59e08.r1 Soares breast 3NBHst Homo sapiens cDNA clone IMAGE:182246 5' similar to gb:M64099 GAMMA-GLUTAMYL TRANSPEPTIDASE 5 PRECURSOR (HUMAN);
1662	10875	20060	5.52	0.0E+00	Z80780.1	NT	yo59e08.r1 Soares breast 3NBHst Homo sapiens cDNA clone IMAGE:182246 5' similar to gb:M64099 GAMMA-GLUTAMYL TRANSPEPTIDASE 5 PRECURSOR (HUMAN);
1665	10878		17.97	0.0E+00	5031748	NT	H. sapiens H2B/h gene
1674	10886	20072	5.65	0.0E+00	8823841	NT	H. sapiens H2B/h gene
1677	10888	20075	1	0.0E+00	8453855	NT	Homo sapiens high-mobility group (nonhistone chromosomal) protein 17 (HMG17), mRNA
1682	10894	20082	2.52	0.0E+00	4826973	NT	Homo sapiens pericentriolar material 1 (PCM1) mRNA
1688	10900	20089	5.88	0.0E+00	AB026542.1	NT	Homo sapiens RNA binding motif protein, Y chromosome, family 1, member A1 (RBM1A1) mRNA
1690	10902		2.24	0.0E+00	S94400.1	NT	Homo sapiens WAVE2 mRNA for WASP-family protein, complete cds
1699	10911	20098	1.48	0.0E+00	4557538	NT	TCR zeta [human, Genomic/mRNA, 365 nt, segment 1 of 8]
1718	10930	20115	2.88	0.0E+00	AF273841.1	NT	Homo sapiens solute carrier family 28 (sulfate transporter), member 2 (SLC28A2) mRNA
1755	12001		57.99	0.0E+00	4506718	NT	Homo sapiens SMCY (SMCY) gene, complete cds
1759	10970	20155	1.64	0.0E+00	4557556	NT	Homo sapiens ribosomal protein S2 (RPS2) mRNA
1759	10970	20158	1.64	0.0E+00	4557556	NT	Homo sapiens E1A binding protein p300 (EP300) mRNA
1761	10972	20159	2.04	0.0E+00	U63863.1	NT	Homo sapiens E1A binding protein p300 (EP300) mRNA
1764	12002	20163	5.71	0.0E+00	4505332	NT	Human CSF-1 receptor (FMS) gene, complete cds, and (SMF) gene, partial cds
							Homo sapiens nuclear autoantigenic sperm protein (histone-binding) (NASP) mRNA

Page 342 of 382  
Table 4  
Single Exon Probes Expressed in HELA Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1765	10975	20164	1.37	0.0E+00	AA113030.1	EST_HUMAN	zr65c08.s1 Stratagene HeLa cell s3 837218 Homo sapiens cDNA clone IMAGE:563056 3'
1776	10988	20178	19.75	0.0E+00	U14967.1	NT	Human ribosomal protein L21 mRNA, complete cds
1778	10988	20181	16.16	0.0E+00	AB002331.1	NT	Human mRNA for KIAA0333 gene, partial cds
1779	10989	20182	14.46	0.0E+00	4502284	NT	Homo sapiens activating transcription factor 4 (tax-responsive enhancer element B87) (ATF4) mRNA
1778	10989	20183	14.46	0.0E+00	4502284	NT	Homo sapiens activating transcription factor 4 (tax-responsive enhancer element B87) (ATF4) mRNA
1779	10989	20184	14.46	0.0E+00	4502284	NT	Homo sapiens activating transcription factor 4 (tax-responsive enhancer element B87) (ATF4) mRNA
1802	11011	20203	7.64	0.0E+00	6005855	NT	Homo sapiens Retina-derived POU-domain factor-1 (RPF-1), mRNA
1802	11011	20204	7.64	0.0E+00	6005855	NT	Homo sapiens Retina-derived POU-domain factor-1 (RPF-1), mRNA
1811	11020	20212	1.4	0.0E+00	AB032978.1	NT	Homo sapiens mRNA for KIAA1152 protein, partial cds
1811	11020	20213	1.4	0.0E+00	AB032978.1	NT	Homo sapiens mRNA for KIAA1152 protein, partial cds
1815	11023	20216	3.22	0.0E+00	4826783	NT	Homo sapiens potassium voltage-gated channel, Shab-related subfamily, member 1 (KCNB1) mRNA
1815	11023	20216	3.22	0.0E+00	4826783	NT	Homo sapiens potassium voltage-gated channel, Shab-related subfamily, member 1 (KCNB1) mRNA
1816	11024	20217	7.42	0.0E+00	U07147.1	NT	Homo sapiens potassium voltage-gated channel, Shab-related subfamily, member 1 (KCNB1) mRNA
1816	11024	20218	7.42	0.0E+00	U07147.1	NT	Human retinal degeneration slow (RDS) gene, exon 1
1819	11027	20221	1.23	0.0E+00	AW207280.1	EST_HUMAN	UI-H-B11-afn-f-07-Q-UI.st NCI CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2722333 3'
1819	11027	20222	1.23	0.0E+00	AW207280.1	EST_HUMAN	UI-H-B11-afn-f-07-Q-UI.st NCI CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2722333 3'
1841	11049	20239	2.69	0.0E+00	BE277465.1	EST_HUMAN	601179164F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3547239 5'
1841	11049	20240	2.69	0.0E+00	BE277465.1	EST_HUMAN	601179164F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3547239 5'
1859	11066	20257	1.73	0.0E+00	BE06292.1	EST_HUMAN	RC2-BN0126-200300-012-504 BN0126 Homo sapiens cDNA
1888	11095	20285	1.4	0.0E+00	7657390	NT	Homo sapiens nuclear protein (NP220), mRNA
1888	11095	20286	1.4	0.0E+00	7657390	NT	Homo sapiens nuclear protein (NP220), mRNA
1891	11098	20288	3.1	0.0E+00	4506384	NT	Homo sapiens RAD1 (S. pombe) homolog (RAD1) mRNA, and translated products
1891	11098	20289	3.1	0.0E+00	4506384	NT	Homo sapiens RAD1 (S. pombe) homolog (RAD1) mRNA, and translated products
1896	11103	20295	7.07	0.0E+00	AB037788.1	NT	Homo sapiens mRNA for KIAA1367 protein, partial cds
1900	11107		1.45	0.0E+00	AF157478.1	NT	Homo sapiens DNA polymerase zeta catalytic subunit (REV3) mRNA, complete cds
1901	12006	20299	1.73	0.0E+00	M98478.1	NT	Human transglutaminase mRNA, complete cds
1901	12005	20300	1.73	0.0E+00	M98478.1	NT	Human transglutaminase mRNA, complete cds
1906	11112	20307	1.52	0.0E+00	4507464	NT	Homo sapiens transforming growth factor, beta 3 (TGFB3), mRNA
1906	11112	20308	1.52	0.0E+00	4507464	NT	Homo sapiens transforming growth factor, beta 3 (TGFB3), mRNA

Page 343 of 382  
Table 4  
Single Exon Probes Expressed in HELA Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1909	11114	20310	1.16	0.0E+00	7657038	NT	Homo sapiens death receptor 6 (DR6), mRNA
1911	11116		8.63	0.0E+00	AF240786.1	NT	Homo sapiens glutathione S-transferase theta 2 (GSTT2) and glutathione S-transferase theta 1 (GSTT1) genes, complete cds
1916	11121		3.42	0.0E+00	M55632.1	NT	Human topoisomerase I pseudogene 1
1918	12006	20317	1.66	0.0E+00	5901905	EST	Homo sapiens butyrophilin, subfamily 3, member A2 (BTN3A2), mRNA
1920	11124	20319	1.35	0.0E+00	BE018068.1	EST_HUMAN	bb73f11.y1 NIH_MGC_12 Homo sapiens cDNA clone IMAGE:3048045 5'
1926	11130	20324	1.24	0.0E+00	4809282	NT	Homo sapiens histidine aminotriase (HAL), mRNA
1928	11130	20325	1.24	0.0E+00	4809282	NT	Homo sapiens histidine aminotriase (HAL), mRNA
1936	11140		1.01	0.0E+00	AL163252.2	NT	Homo sapiens chromosome 21 segment HS21C052
1938	11142	20338	1.12	0.0E+00	8400716	NT	Homo sapiens nebulin (NEB), mRNA
1938	11142	20339	1.12	0.0E+00	8400716	NT	Homo sapiens nebulin (NEB), mRNA
1938	11143	20341	7	0.0E+00	4826638	NT	Homo sapiens actinin, alpha 4 (ACTN4), mRNA
1939	11143	20341	7	0.0E+00	4826638	NT	Homo sapiens actinin, alpha 4 (ACTN4), mRNA
1949	11153	20355	1.05	0.0E+00	AB018333.1	NT	Homo sapiens mRNA for KIAA0790 protein, partial cds
1949	11153	20356	1.05	0.0E+00	AB018333.1	NT	Homo sapiens mRNA for KIAA0790 protein, partial cds
1955	11159	20360	1.34	0.0E+00	M33782.1	NT	Human TFEB protein mRNA, partial cds
1955	11159	20361	1.34	0.0E+00	M33782.1	NT	Human TFEB protein mRNA, partial cds
1957	11161	20362	1.72	0.0E+00	AW193024.1	EST_HUMAN	AB018333.1 NCI_CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2679813 3'
1957	11161	20363	1.72	0.0E+00	AW193024.1	EST_HUMAN	AB018333.1 NCI_CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2679813 3'
1958	11162	20364	9.82	0.0E+00	6812457	NT	Homo sapiens calcineurin binding protein 1 (KIAA0330), mRNA
1958	11162	20365	9.82	0.0E+00	6812457	NT	Homo sapiens calcineurin binding protein 1 (KIAA0330), mRNA
1958	11162	20366	12.58	0.0E+00	7662095	NT	Homo sapiens KIAA0408 gene product (KIAA0408), mRNA
1960	11164	20367	1.95	0.0E+00	AB011149.1	NT	Homo sapiens mRNA for KIAA0577 protein, complete cds
1961	11165	20368	1.04	0.0E+00	Z47556.1	NT	H. sapiens genes for semenogelin I and semenogelin II
1962	11166	20369	1.04	0.0E+00	Z47556.1	NT	H. sapiens genes for semenogelin I and semenogelin II
1962	11166	20370	1.04	0.0E+00	Z47556.1	NT	H. sapiens genes for semenogelin I and semenogelin II
1963	11173	20379	4.4	0.0E+00	AB040946.1	NT	Homo sapiens mRNA for KIAA1513 protein, partial cds
1969	11183	20402	1.15	0.0E+00	AF273841.1	NT	Homo sapiens SMCY (SMCY) gene, complete cds
1980	11183	20403	1.15	0.0E+00	AF273841.1	NT	Homo sapiens SMCY (SMCY) gene, complete cds
1980	11183	20403	1.15	0.0E+00	AF273841.1	NT	Homo sapiens SMCY (SMCY) gene, complete cds
2020	11221	20429	1.36	0.0E+00	7708742	NT	Homo sapiens TP53TG3a (TP53TG3a), mRNA
2024	11225	20433	28.23	0.0E+00	BE743215.1	EST_HUMAN	601573895F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3835198 5'
2024	11225	20434	28.23	0.0E+00	BE743215.1	EST_HUMAN	601573895F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3835198 5'
2026	11227	20435	0.95	0.0E+00	4503948	NT	Homo sapiens coagulation factor IX (plasma thromboplastic component, Christmas disease, hemophilia B) (F9) mRNA
2027	11228	20436	1.44	0.0E+00	BF207688.1	EST_HUMAN	601881974F1 NIH_MGC_53 Homo sapiens cDNA clone IMAGE:4081483 5'

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2028	11229	20437	6.57	0.0E+00	AU140831.1	EST_HUMAN	AU140831 PLACE4 Homo sapiens cDNA clone PLACE4000321 5'
2030	11231	20439	1.7	0.0E+00	AA077589.1	EST_HUMAN	7B22E10 Chromosome 7 Fetal Brain cDNA Library Homo sapiens cDNA clone 7B22E10
2030	11231	20440	1.7	0.0E+00	AA077589.1	EST_HUMAN	7B22E10 Chromosome 7 Fetal Brain cDNA Library Homo sapiens cDNA clone 7B22E10
2032	11233		4.04	0.0E+00	7657468	NT	Homo sapiens similar to rat integral membrane glycoprotein POM121 (POM121L1), mRNA
2034	11235		2.43	0.0E+00	4585963	NT	Homo sapiens phosphodiesterase 6A, cGMP-specific, rod, alpha (PDE6A), mRNA
2035	11236	20443	2.31	0.0E+00	Z42399.1	EST_HUMAN	HSC01C021 normalized infant brain cDNA Homo sapiens cDNA clone c-0k02
2037	11238		2.23	0.0E+00	A1244247.1	EST_HUMAN	q96f08.x1 NCI_CGAP_U2 Homo sapiens cDNA clone IMAGE:1988871 3' similar to contains Alu repetitive element
2042	11243	20452	7.59	0.0E+00	BE877225.1	EST_HUMAN	601485148F1 NIH_MGC_69 Homo sapiens cDNA clone IMAGE:3887747 5'
2044	11245	20454	4.44	0.0E+00	BF315325.1	EST_HUMAN	601902604F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4135320 5'
2044	11245	20455	4.44	0.0E+00	BF315325.1	EST_HUMAN	601902604F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4135320 5'
2050	11251	20463	4.16	0.0E+00	BE697125.1	EST_HUMAN	RC3-CT0413-270700-022-410 CT0413 Homo sapiens cDNA
2050	11251	20464	4.16	0.0E+00	BE697125.1	EST_HUMAN	RC3-CT0413-270700-022-410 CT0413 Homo sapiens cDNA
2056	11257	20471	2.15	0.0E+00	L06620.1	NT	Human plasma membrane calcium ATPase isoform 2 (APT2B2) mRNA, complete cds
2058	11257	20472	2.15	0.0E+00	L06620.1	NT	Human plasma membrane calcium ATPase isoform 2 (APT2B2) mRNA, complete cds
2061	11262	20476	1.54	0.0E+00	4758489	NT	Homo sapiens GTP binding protein 1 (GTPBP1) mRNA
2065	11266	20479	1.28	0.0E+00	BE500995.1	EST_HUMAN	7a34c02.x1 NCI_CGAP_G08 Homo sapiens cDNA clone IMAGE:3220810 3' similar to SW:DTD_HUMAN
2084	11284		4.59	0.0E+00	BE767964.1	EST_HUMAN	P50443 SULFATE TRANSPORTER ;
2085	11285		1.21	0.0E+00	AF018963.1	NT	QV1-GN0065-140800-318-g10 GN0065 Homo sapiens cDNA
2087	11287	20500	8.37	0.0E+00	BF027562.1	EST_HUMAN	Homo sapiens X-linked juvenile retinoschisis protein (XLRST) gene, exon 8 and complete cds
2088	11288	20501	1.73	0.0E+00	BE072624.1	EST_HUMAN	601672068F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3954785 5'
2090	11290	20502	4.32	0.0E+00	AF240786.1	NT	PMO-BT0547-210300-004-F04 BT0547 Homo sapiens cDNA
2092	11292	20504	4.24	0.0E+00	AW752708.1	EST_HUMAN	Homo sapiens glutathione S-transferase theta 2 (GSTT2) and glutathione S-transferase theta 1 (GSTT1) genes, complete cds
2093	11293	20505	4.83	0.0E+00	A1904640.1	EST_HUMAN	IL3-CT0219-271099-022-G10 CT0219 Homo sapiens cDNA
2093	11293	20506	4.83	0.0E+00	A1904640.1	EST_HUMAN	QV-BT065-020399-092 BT065 Homo sapiens cDNA
2146	11344		4.65	0.0E+00	L14787.1	NT	QV-BT065-020399-092 BT065 Homo sapiens cDNA
2152	11350	20566	1.31	0.0E+00	BE274696.1	EST_HUMAN	Human DNA-binding protein mRNA, 3' end
2154	11352	20569	1.28	0.0E+00	D87685.1	NT	601122338F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3346688 5'
2155	11353	20570	78.41	0.0E+00	AV738288.1	EST_HUMAN	Human mRNA for KIAA0244 gene, partial cds
2155	11353	20571	78.41	0.0E+00	AV738288.1	EST_HUMAN	AV738288 CB Homo sapiens cDNA clone CBNBDE08 5'
2157	11355	20573	4.48	0.0E+00	AA931691.1	EST_HUMAN	AV738288 CB Homo sapiens cDNA clone CBNBDE08 5'
2161	11359	20577	47.03	0.0E+00	BF344434.1	EST_HUMAN	cc32a01.s1 NCI_CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1567888 3'
							602014828F1 NCI_CGAP_Bm64 Homo sapiens cDNA clone IMAGE:4150734 5'

Page 345 of 382  
Table 4  
Single Exon Probes Expressed in HELA Cells

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2182	11360	20578	100.43	0.0E+00	BE748899.1	EST_HUMAN	601572188T1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:38390123'
2185	11363	20581	7.65	0.0E+00	BF377897.1	EST_HUMAN	CM1-TN0141-250900-439-608 TN0141 Homo sapiens cDNA
2185	11363	20582	7.55	0.0E+00	BF377897.1	EST_HUMAN	CM1-TN0141-250900-439-608 TN0141 Homo sapiens cDNA
2189	12012	20587	5.54	0.0E+00	BF313817.1	EST_HUMAN	601900261F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4129622 5'
2172	11368	20590	4.03	0.0E+00	BE018750.1	EST_HUMAN	601900261F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3049082 5' similar to TR:Q15170 Q15170 TRANSCRIPTION FACTOR S-II-RELATED PROTEIN;
2174	11371	20592	33.41	0.0E+00	AA042813.1	EST_HUMAN	zK53c07.s1 Soares_pregnant_uterus_NbHPU Homo sapiens cDNA clone IMAGE:486540 3' similar to gb:X65857_cds1 OLFATORY RECEPTOR-LIKE PROTEIN HGMP07E (HUMAN);
2174	11371	20593	33.41	0.0E+00	AA042813.1	EST_HUMAN	zK53c07.s1 Soares_pregnant_uterus_NbHPU Homo sapiens cDNA clone IMAGE:486540 3' similar to gb:X65857_cds1 OLFATORY RECEPTOR-LIKE PROTEIN HGMP07E (HUMAN);
2181	11378	20600	4.19	0.0E+00	AL163204.2	NT	Homo sapiens chromosome 21 segment HS21C004
2181	11378	20601	4.19	0.0E+00	AL163204.2	NT	Homo sapiens chromosome 21 segment HS21C004
2182	11379	20602	11.03	0.0E+00	7662401	NT	Homo sapiens KIAA0952 protein (KIAA0952), mRNA
2182	11379	20603	11.03	0.0E+00	7662401	NT	Homo sapiens KIAA0952 protein (KIAA0952), mRNA
2187	11384		2.34	0.0E+00	U36284.1	NT	Human beta-prime-adaptin (BAM22) gene, exon 16
2188	11385	20608	1.94	0.0E+00	AA282281.1	EST_HUMAN	z12b10.r1 NCL_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:712891 5'
2195	11392	20614	3.49	0.0E+00	BE897487.1	EST_HUMAN	601432317F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3917453 5'
2205	11402	20627	5.93	0.0E+00	4557568	NT	Homo sapiens E1A binding protein p300 (EP300) mRNA
2211	11408	20632	11.03	0.0E+00	7662401	NT	Homo sapiens KIAA0952 protein (KIAA0952), mRNA
2217	11414	20639	17.25	0.0E+00	BE895281.1	EST_HUMAN	601433525F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3918607 5'
2221	11418	20643	6.39	0.0E+00	BE905563.1	EST_HUMAN	601495208F1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3897457 5'
2221	11418	20644	6.39	0.0E+00	BE905563.1	EST_HUMAN	601495208F1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3897457 5'
2224	11420	20646	3.52	0.0E+00	AB037784.1	NT	Homo sapiens mRNA for KIAA1363 protein, partial cds
2263	11458	20676	2.23	0.0E+00	BF344756.1	EST_HUMAN	6020714009F1 NCL_CGAP_Bm64 Homo sapiens cDNA clone IMAGE:4149770 5'
2263	11458	20677	2.23	0.0E+00	BF344756.1	EST_HUMAN	6020714009F1 NCL_CGAP_Bm64 Homo sapiens cDNA clone IMAGE:4149770 5'
2265	11460	20679	4.51	0.0E+00	11545748	NT	Homo sapiens differentially expressed in FDCP (mouse homolog) 6 (DEF6), mRNA
2265	11460	20680	4.51	0.0E+00	11545748	NT	Homo sapiens differentially expressed in FDCP (mouse homolog) 6 (DEF6), mRNA
2266	11461	20681	3.23	0.0E+00	A1076404.1	EST_HUMAN	6020714009F1 NCL_CGAP_Bm64 Homo sapiens cDNA clone IMAGE:4149770 5'
2269	11464	20684	3.65	0.0E+00	AA429001.1	EST_HUMAN	z778a11.r1 Soares_total_fetus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:759740 5'
2269	11464	20685	3.65	0.0E+00	AA429001.1	EST_HUMAN	z778a11.r1 Soares_total_fetus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:759740 5'
2271	11466	20687	2.65	0.0E+00	AA680367.1	EST_HUMAN	z11e12.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:430510 3'
2272	11487	20688	3.24	0.0E+00	BF3447039.1	EST_HUMAN	602021846F1 NCL_CGAP_Bm67 Homo sapiens cDNA clone IMAGE:4157339 5'
2277	11472	20694	1.47	0.0E+00	AB020717.1	NT	Homo sapiens mRNA for KIAA0910 protein, partial cds
2277	11472	20695	1.47	0.0E+00	AB020717.1	NT	Homo sapiens mRNA for KIAA0910 protein, partial cds

Table 4

## Single Exon Probes Expressed in HELA Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2278	11473	20698	1.81	0.0E+00	6325468	NT	Homo sapiens flavin containing monooxygenase 3 (FMO3), mRNA
2285	11480	20702	3.99	0.0E+00	BE876095.1	EST_HUMAN	7f2a02.x1 NCI_CGAP_CLL1 Homo sapiens cDNA clone IMAGE:3295370 3' similar to TR:O94939 O94939 KIAA0957 PROTEIN ;
2288	11483	20704	8.5	0.0E+00	AF044571.1	NT	Homo sapiens phosphatase kinase alpha subunit (PHKA2) gene, exon 32
2289	11484	20705	2.07	0.0E+00	AI625542.1	EST_HUMAN	y67c08.x1 NCI_CGAP_U12 Homo sapiens cDNA clone IMAGE:2283182 3'
2291	11488	20708	2.04	0.0E+00	AB011399.1	NT	Homo sapiens gene for AF-6, complete cds
2294	11489	20708	19.82	0.0E+00	7662401	NT	Homo sapiens KIAA0952 protein (KIAA0952), mRNA
2294	11489	20709	19.82	0.0E+00	7662401	NT	Homo sapiens KIAA0952 protein (KIAA0952), mRNA
2297	11492	20712	7.86	0.0E+00	5803178	NT	Homo sapiens sperm specific antigen 2 (SSFA2), mRNA
2297	11492	20713	7.86	0.0E+00	5803178	NT	Homo sapiens sperm specific antigen 2 (SSFA2), mRNA
2303	11497	20718	3.58	0.0E+00	7662007	NT	Homo sapiens KIAA0218 gene product (KIAA0218), mRNA
2303	11497	20717	3.58	0.0E+00	7662007	NT	Homo sapiens KIAA0218 gene product (KIAA0218), mRNA
2307	11501	20722	2.32	0.0E+00	D83778.1	NT	Human mRNA for KIAA0194 gene, partial cds
2307	11501	20723	2.32	0.0E+00	D83778.1	NT	Human mRNA for KIAA0194 gene, partial cds
2317	11511	20731	2.36	0.0E+00	5174678	NT	Homo sapiens signal regulatory protein, beta, 1 (SIRP-BETA-1) mRNA
2321	11514	20735	3.85	0.0E+00	AU131142.1	EST_HUMAN	AU131142 NT2RP3 Homo sapiens cDNA clone NT2RP3002084 5'
2322	11515	20738	65.13	0.0E+00	BE794028.1	EST_HUMAN	601586843F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3941003 5'
2323	11516	20738	17.63	0.0E+00	7662017	NT	Homo sapiens KIAA0244 protein (KIAA0244), mRNA
2324	11517	20737	1.62	0.0E+00	4758497	NT	Homo sapiens hexose-6-phosphate dehydrogenase (glucose 1-dehydrogenase) (H6PD), mRNA
2324	11517	20738	1.62	0.0E+00	4758497	NT	Homo sapiens hexose-6-phosphate dehydrogenase (glucose 1-dehydrogenase) (H6PD), mRNA
2325	11518		18.2	0.0E+00	AF280107.1	NT	Homo sapiens cytochrome P450 polypeptide 43 (CYP3A43) gene, partial cds; cytochrome P450 polypeptide 4 (CYP3A4) and cytochrome P450 polypeptide 7 (CYP3A7) genes, complete cds; and cytochrome P450 polypeptide 5 (CYP3A5) gene, partial cds
2327	11520	20740	16.28	0.0E+00	AU118082.1	EST_HUMAN	AU118082 HEMBA1 Homo sapiens cDNA clone HEMBA1002839 5'
2327	11520	20741	16.28	0.0E+00	AU118082.1	EST_HUMAN	AU118082 HEMBA1 Homo sapiens cDNA clone HEMBA1002839 5'
2327	11520	20742	16.28	0.0E+00	AU118082.1	EST_HUMAN	AU118082 HEMBA1 Homo sapiens cDNA clone HEMBA1002839 5'
2328	11521	20743	1.72	0.0E+00	8923089	NT	Homo sapiens hypothetical protein FLJ20081 (FLJ20081), mRNA
2345	11536		4.01	0.0E+00	BE814424.1	EST_HUMAN	MR0-BN0070-060600-028-d12 BN0070 Homo sapiens cDNA
2377	11570	20780	1.95	0.0E+00	AU118582.1	EST_HUMAN	AU118582 HEMBA1 Homo sapiens cDNA clone HEMBA1008155 5'
2379	11572		3.76	0.0E+00	AID42035.1	EST_HUMAN	ox60d02.x1 Soares_NHMPu_S1 Homo sapiens cDNA clone IMAGE:1680583 3' similar to TR:O08662 O08662 230KDA PHOSPHATIDYLINOSITOL 4-KINASE ;
2381	11574	20793	4.62	0.0E+00	8923620	NT	Homo sapiens hypothetical protein FLJ20893 (FLJ20893), mRNA
2383	11578	20784	1.68	0.0E+00	AW303988.1	EST_HUMAN	xy1507.x1 Soares_NFL_I_GBC_S1 Homo sapiens cDNA clone IMAGE:2813221 3' similar to TR:O54924 O54924 EXO84 ;

Table 4

## Single Exon Probes Expressed in HELA Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2385	11578		1.46	0.0E+00	BE895605.1	EST_HUMAN	601432608F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3918168 5'
2386	11589		30.25	0.0E+00	AB005622.1	EST_HUMAN	AB005622 HeLa cDNA (T.Noma) Homo sapiens cDNA similar to adenylate kinase isozyme 2
2399	11592	20810	4.93	0.0E+00	6006002	NT	Homo sapiens glutamate receptor, ionotropic, N-methyl D-aspartate 2A (GRIN2A) mRNA
2403	11595	20814	1.61	0.0E+00	D85606.1	NT	Homo sapiens gene for cholecystikinin type-A receptor, complete cds
2403	11595	20815	1.61	0.0E+00	D85606.1	NT	Homo sapiens gene for cholecystikinin type-A receptor, complete cds
2411	11603	20824	2.27	0.0E+00	AF106275.1	NT	Homo sapiens gene for cholecystikinin type-A receptor, complete cds
2415	11606	20828	2.38	0.0E+00	BF345274.1	EST_HUMAN	Homo sapiens immunoglobulin-like transcript 1c variant 4 (LT1c) gene, exon 6
2422	11613	20836	4.9	0.0E+00	5729777	NT	602018058F1 NCI_CGAP_Brn67 Homo sapiens cDNA clone IMAGE:4153670 5'
2430	11621	20842	1.25	0.0E+00	U13666.1	NT	Homo sapiens collagen, type XII, alpha 1 (COL12A1), mRNA
2430	11621	20843	1.25	0.0E+00	U13666.1	NT	Human G protein-coupled receptor (GPR1) gene, complete cds
2431	11622	20844	131.32	0.0E+00	BF569144.1	EST_HUMAN	Human G protein-coupled receptor (GPR1) gene, complete cds
2440	11631	20852	2.9	0.0E+00	AW 466922.1	EST_HUMAN	602184558T1 NIH_MGC_42 Homo sapiens cDNA clone IMAGE:4300383 3'
2442	11633	20853	5.63	0.0E+00	AW 501010.1	EST_HUMAN	h604h04.x1 NCI_CGAP_K1412 Homo sapiens cDNA clone IMAGE:2872759 3'
							UI-HF-BP0p-sis-c-07-Q-JL1 NIH_MGC_61 Homo sapiens cDNA clone IMAGE:3072780 5'
							q23f06.x1 NCI_CGAP_Lym6 Homo sapiens cDNA clone IMAGE:1862435 3' similar to contains element
2451	11642		1.22	0.0E+00	AI287878.1	EST_HUMAN	MIR repetitive element
2457	11648	20869	1.84	0.0E+00	5453965	NT	Homo sapiens protein kinase, AMP-activated, alpha 2 catalytic subunit (PRKAA2) mRNA
2457	11648	20870	1.84	0.0E+00	5453965	NT	Homo sapiens protein kinase, AMP-activated, alpha 2 catalytic subunit (PRKAA2) mRNA
2470	11661		2.3	0.0E+00	AW813853.1	EST_HUMAN	RC3-ST0197-300300-016-c04 ST0197 Homo sapiens cDNA
2475	11666	20885	70.13	0.0E+00	BE795542.1	EST_HUMAN	601592530F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3946518 5'
2476	11114	20310	3.28	0.0E+00	7657038	NT	Homo sapiens death receptor 8 (DR6), mRNA
2477	11667	20886	2.58	0.0E+00	BF609482.1	EST_HUMAN	UI-H-B14-eez-b-08-Q-JL1.s1 NCI_CGAP_Sub8 Homo sapiens cDNA clone IMAGE:3086535 3'
2480	11670	20888	2.03	0.0E+00	Z32684.2	NT	Homo sapiens mRNA for membrane transport protein (XK gene)
2482	11672		3.62	0.0E+00	5453871	NT	Homo sapiens platelet-derived growth factor receptor-like (PDGFR) mRNA
2485	11675	20892	2.44	0.0E+00	BE110378.1	EST_HUMAN	Homo sapiens platelet-derived growth factor receptor-like (PDGFR) mRNA
2486	11676	20893	6.81	0.0E+00	7657468	NT	Homo sapiens similar to rat integral membrane glycoprotein POM121 (POM121L1), mRNA
2487	11677	20894	2.18	0.0E+00	8023340	NT	Homo sapiens hypothetical protein FLJ20368 (FLJ20368), mRNA
2488	11678	20895	8.81	0.0E+00	U93239.1	NT	Human Sec62 (Sec62) mRNA, complete cds
2494	11684	20901	14.6	0.0E+00	BE806490.1	EST_HUMAN	601508211F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3909866 5'
2498	11687	20906	5.8	0.0E+00	BE875511.1	EST_HUMAN	601489241F1 NIH_MGC_69 Homo sapiens cDNA clone IMAGE:3891371 5'
2498	11687	20907	5.8	0.0E+00	BE875511.1	EST_HUMAN	601489241F1 NIH_MGC_69 Homo sapiens cDNA clone IMAGE:3891371 5'
2499	11688	20908	2.84	0.0E+00	AF114027.1	EST_HUMAN	AF114027 Homo sapiens lung fetus Homo sapiens cDNA clone EST6
2516	11705	20918	1.66	0.0E+00	BE536921.1	EST_HUMAN	601064738F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3451161 5'
2522	11710	20926	56.3	0.0E+00	AU143277.1	EST_HUMAN	AU143277 Y78AA1 Homo sapiens cDNA clone Y78AA1001673 5'
2522	11710	20927	56.3	0.0E+00	AU143277.1	EST_HUMAN	AU143277 Y78AA1 Homo sapiens cDNA clone Y78AA1001673 5'



Single Exon Probes Expressed in HELA Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2523	11711	20928	35.33	0.0E+00	BE292896.1	EST_HUMAN	601105312F1 NIH_MGC_15 Homo sapiens cDNA clone IMAGE:2887955 5'
2523	11711	20929	35.33	0.0E+00	BE292896.1	EST_HUMAN	601105312F1 NIH_MGC_15 Homo sapiens cDNA clone IMAGE:2887955 5'
2524	11712	20930	1.33	0.0E+00	BF223041.1	EST_HUMAN	7q27h12.x1 NCI_CGAP_GC8 Homo sapiens cDNA clone IMAGE:3' similar to TR:000248 000246
2527	11715	20932	8.27	0.0E+00	AF245505.1	NT	HYPOTHETICAL 9.3 KD PROTEIN;
2558	11954	20984	1.76	0.0E+00	AB037836.1	NT	Homo sapiens adiclin mRNA, complete cds
2558	11954	20985	1.78	0.0E+00	AB037836.1	NT	Homo sapiens mRNA for KIAA1415 protein, partial cds
2559	11745	20970	3.26	0.0E+00	BF513835.1	EST_HUMAN	Homo sapiens mRNA for KIAA1415 protein, partial cds
2564	11750	20970	1.78	0.0E+00	BF672818.1	EST_HUMAN	UI-H-BW1-amp-f-12-Q-UI s1 NCI_CGAP_Sub7 Homo sapiens cDNA clone IMAGE:3070631 3'
2566	11752	20975	2.67	0.0E+00	BE16695.1	EST_HUMAN	602152653F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4283812 5'
2570	11755	20978	0.91	0.0E+00	BF204131.1	EST_HUMAN	601279873F1 NIH_MGC_39 Homo sapiens cDNA clone IMAGE:3621768 5'
2570	11755	20978	0.91	0.0E+00	BF204131.1	EST_HUMAN	601279873F1 NIH_MGC_39 Homo sapiens cDNA clone IMAGE:4111411 5'
2574	11759	20979	3.98	0.0E+00	AB037742.1	NT	601869073F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4111411 5'
2575	11760	20980	2.79	0.0E+00	5032150	NT	601869073F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4111411 5'
2578	11764	20985	6.28	0.0E+00	AB037659.1	NT	Homo sapiens mRNA for KIAA1438 protein, partial cds
2579	11765	20986	2.28	0.0E+00	BE795445.1	EST_HUMAN	Homo sapiens mRNA for KIAA1438 protein, partial cds
2579	11765	20987	2.28	0.0E+00	BE795445.1	EST_HUMAN	601590108F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3944304 5'
2582	11768	20988	1.03	0.0E+00	BE293328.1	EST_HUMAN	601590108F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3944304 5'
2589	11775	20986	11.88	0.0E+00	BE792472.1	EST_HUMAN	601143722F1 NIH_MGC_15 Homo sapiens cDNA clone IMAGE:3051389 5'
2591	11777	20986	0.91	0.0E+00	AB020710.1	NT	601584930F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3939222 5'
2598	11784	21004	3.6	0.0E+00	AF173227.1	NT	Homo sapiens mRNA for KIAA0903 protein, partial cds
2608	11792	21011	4.33	0.0E+00	AF173227.1	NT	Homo sapiens IMP (inosine monophosphate) dehydrogenase 1 (IMPDH1) mRNA
2612	11798	21012	1.91	0.0E+00	AB011108.1	NT	Homo sapiens guanylate cyclase-activating protein 2 (GUCY1B) gene, exon 1
2613	11797	21013	2.06	0.0E+00	AJ133385.1	EST_HUMAN	Homo sapiens mRNA for KIAA0536 protein, partial cds
2614	11798	21014	0.92	0.0E+00	M69225.1	NT	AU133385 NT2RP4 Homo sapiens cDNA clone NT2RP4001884 5'
2617	11801	21017	3.04	0.0E+00	AU130403.1	EST_HUMAN	Human bullous pemphigoid antigen (BPAG1) mRNA, complete cds
2620	11804	21021	1.65	0.0E+00	AW887015.1	EST_HUMAN	AU130403 NT2RP3 Homo sapiens cDNA clone NT2RP3000779 5'
2623	11807	21024	1.42	0.0E+00	BF000018.1	EST_HUMAN	AU130403 NT2RP3 Homo sapiens cDNA clone NT2RP3000779 5'
2624	11808	21025	14.04	0.0E+00	BE383165.1	EST_HUMAN	RC1-OT0088-220300-011-d07 OT0088 Homo sapiens cDNA
2625	11809		2.6	0.0E+00	BE531263.1	EST_HUMAN	7n15h05.x1 NCI_CGAP_Co16 Homo sapiens cDNA clone IMAGE:3316089 3'
2649	11832	21046	0.9	0.0E+00	8922843	NT	601288714F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3628923 5'
2656	11840	21054	1.28	0.0E+00	AB037732.1	NT	601278373F1 NIH_MGC_39 Homo sapiens cDNA clone IMAGE:3610287 5'
							Homo sapiens hypothetical protein FLJ11052 (FLJ11052), mRNA
							Homo sapiens mRNA for KIAA1311 protein, partial cds

Page 349 of 382  
Table 4  
Single Exon Probes Expressed in HELA Cells

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2681	11863		33.03	0.0E+00	AA316723.1	EST_HUMAN	EST188414 HCC cell line (metastasis to liver in mouse) II Homo sapiens cDNA 5' end similar to ribosomal protein L29
2682	11864	21076	30.31	0.0E+00	BE794884.1	EST_HUMAN	601589625F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3943591 5'
2687	11868	21082	4.57	0.0E+00	U36253.1	NT	Human beta-prime-adaptin (BAM22) gene, exon 5
2689	11870	21084	1.69	0.0E+00	AF110763.1	NT	Homo sapiens skeletal muscle LIM-protein 1 (FHL-1) gene, complete cds
2694	11874	21088	60.93	0.0E+00	BE796376.1	EST_HUMAN	601581091F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3945983 5'
2695	11875	21089	1.08	0.0E+00	BF680632.1	EST_HUMAN	602155923F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4297132 5'
2698	12025	21093	28.45	0.0E+00	BE563433.1	EST_HUMAN	601335485F1 NIH_MGC_39 Homo sapiens cDNA clone IMAGE:3889564 5'
2699	11878		3.2	0.0E+00	AV721647.1	EST_HUMAN	AV721647 HTB Homo sapiens cDNA clone HTBBYE09 5'
2701	11880	21096	2.18	0.0E+00	5174486	NT	Homo sapiens spermatogenesis associated PDI (KIAA0757) mRNA
2701	11880	21097	2.18	0.0E+00	5174486	NT	Homo sapiens spermatogenesis associated PDI (KIAA0757) mRNA
2702	11881	21098	1.13	0.0E+00	8923441	NT	Homo sapiens hypothetical protein FLJ20477 (FLJ20477), mRNA
2702	11881	21099	1.13	0.0E+00	8923441	NT	Homo sapiens hypothetical protein FLJ20477 (FLJ20477), mRNA
2703	11882	21100	2.55	0.0E+00	AF280195.1	NT	Homo sapiens hypertension-related calcium-regulated gene mRNA, complete cds
2704	11883		83.21	0.0E+00	AV651066.1	EST_HUMAN	AV651066 GLC Homo sapiens cDNA clone GLCCLD07 3'
2705	11884	21101	5.42	0.0E+00	BF377897.1	EST_HUMAN	CM1-TN0141-250900-439-508 TN0141 Homo sapiens cDNA
2705	11884	21102	5.42	0.0E+00	BF377897.1	EST_HUMAN	CM1-TN0141-250900-439-508 TN0141 Homo sapiens cDNA
2712	11891	21109	14.18	0.0E+00	BE747193.1	EST_HUMAN	601580903F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3929472 5'
2724	11903		1.33	0.0E+00	AL163201.2	NT	Homo sapiens chromosome 21 segment HS21C001
2725	11904	21120	4.31	0.0E+00	BF614110.1	EST_HUMAN	ULH-BW1-amw-e-07-QJLs1 NCI_CGAP_Sub7 Homo sapiens cDNA clone IMAGE:3071340 3'
2736	11915	21128	4.15	0.0E+00	BF677694.1	EST_HUMAN	602085579F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4249915 5'
2741	11920	21135	1.04	0.0E+00	7427522	NT	Homo sapiens protein tyrosine phosphatase, receptor type, T (PTPRT), mRNA
2744	11923	21137	18.85	0.0E+00	AV725534.1	EST_HUMAN	AV725534 HTC Homo sapiens cDNA clone HTCCCA03 5'
2744	11923	21138	18.85	0.0E+00	AV725534.1	EST_HUMAN	AV725534 HTC Homo sapiens cDNA clone HTCCCA03 5'
2746	11925		13.22	0.0E+00	AI879163.1	EST_HUMAN	au55404.Y1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2518663 5' similar to SW:R13A_HUMAN P40429 60S RIBOSOMAL PROTEIN L13A ;
2749	11928	21143	2.75	0.0E+00	BF530661.1	EST_HUMAN	602071067F1 NCI_CGAP_Bm87 Homo sapiens cDNA clone IMAGE:4214679 5'
2750	11929	21144	43.65	0.0E+00	BE872768.1	EST_HUMAN	601450912F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3854642 5'
2752	11931	21145	3.13	0.0E+00	AU131494.1	EST_HUMAN	AU131494 NT2RP3 Homo sapiens cDNA clone NT2RP3002672 5'
2752	11931	21146	3.13	0.0E+00	AU131494.1	EST_HUMAN	AU131494 NT2RP3 Homo sapiens cDNA clone NT2RP3002672 5'
2753	11932	21147	94.45	0.0E+00	BE300344.1	EST_HUMAN	600944794F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:2980806 5'
2753	11932	21148	94.45	0.0E+00	BE300344.1	EST_HUMAN	600944794F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:2980806 5'
2758	9472	18603	2.6	0.0E+00	S76830.1	NT	glycoprotein D=Duffy group antigen [human, blood, Genomic DNA, 3088 nt]
2761	11938		3.13	0.0E+00	AB033281.1	NT	Homo sapiens BTRCP2 mRNA for F-box and WD-repeats protein isoform C, complete cds

Page 350 of 382  
Table 4  
Single Exon Probes Expressed in HELA Cells

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2767	9982	19125	2.16	0.0E+00	AF264750.1	NT	Homo sapiens ALR-like protein mRNA, partial cds
2767	9982	19126	2.16	0.0E+00	AF264750.1	NT	Homo sapiens ALR-like protein mRNA, partial cds
2771	10272	19423	5.49	0.0E+00	4503202	NT	Homo sapiens cytochrome P450, subfamily 1 (dioxin-inducible), polypeptide 1 (glaucoma 3, primary infantile) (CYP1B1) mRNA
2771	10272	19424	5.49	0.0E+00	4503202	NT	Homo sapiens cytochrome P450, subfamily 1 (dioxin-inducible), polypeptide 1 (glaucoma 3, primary infantile) (CYP1B1) mRNA
2789	12026	21156	4.21	0.0E+00	X85980.1	NT	H. sapiens serine hydroxymethyltransferase pseudogene
2780	12030		1.26	0.0E+00	AF068824.1	NT	Homo sapiens 5-aminolevulinic acid synthase 2 (ALAS2) gene, complete cds
2791	12031		1.42	0.0E+00	AB040960.1	NT	Homo sapiens mRNA for KIAA1527 protein, partial cds
2797	12037		1.15	0.0E+00	AJ238852.1	NT	Homo sapiens partial rp13 gene for ribosomal protein L3, U82 snRNA, U83a snRNA and U83b snRNA genes
2798	12038	21160	2.34	0.0E+00	AL163201.2	NT	Homo sapiens chromosome 21 segment HS21C001
2802	12042	21163	2.17	0.0E+00	M80902.1	NT	Human AHNK nucleoprotein mRNA, 5' end
2804	12044	21165	1.42	0.0E+00	BE154504.1	EST_HUMAN	PMO-HT0343-281298-003-e02 HT0343 Homo sapiens cDNA
2804	12044	21166	1.42	0.0E+00	BE154504.1	EST_HUMAN	PMO-HT0343-281298-003-e02 HT0343 Homo sapiens cDNA
2808	12046		1.59	0.0E+00	X73428.1	NT	H. sapiens l33 gene for HLH type transcription factor
2808	12048		2.79	0.0E+00	AL163288.2	NT	Homo sapiens chromosome 21 segment HS21C068
2809	12049	21169	1.22	0.0E+00	7019584	NT	Homo sapiens zinc finger protein 221 (ZNF221), mRNA
2809	12049	21170	1.22	0.0E+00	7019584	NT	Homo sapiens zinc finger protein 221 (ZNF221), mRNA
2809	12049	21171	1.22	0.0E+00	7019584	NT	Homo sapiens zinc finger protein 221 (ZNF221), mRNA
2811	12051	21172	1.03	0.0E+00	M88478.1	NT	Human transglutaminase mRNA, complete cds
2813	12054	21177	25.36	0.0E+00	D50657.1	NT	Homo sapiens gamma-cytoplasmic actin (ACTGP3) pseudogene
2815	12054	21178	25.36	0.0E+00	D50657.1	NT	Homo sapiens gamma-cytoplasmic actin (ACTGP3) pseudogene
2818	12057	21181	3.87	0.0E+00	AL096857.1	NT	Novel human mRNA from chromosome 1, which has similarities to BAT2 genes
2819	12058		10.77	0.0E+00	Y10658.1	NT	H. sapiens mRNA for nuclear DNA helicase II
2820	12059		1.01	0.0E+00	AF152303.1	NT	Homo sapiens protocadherin alpha C1 (PCDH-alpha-C1) mRNA, complete cds
2821	12060	21182	125.82	0.0E+00	4503470	NT	Homo sapiens eukaryotic translation elongation factor 1 alpha 1 (EEF1A1) mRNA
2821	12060	21183	125.82	0.0E+00	4503470	NT	Homo sapiens eukaryotic translation elongation factor 1 alpha 1 (EEF1A1) mRNA
2833	12072	21194	2.66	0.0E+00	4507280	NT	Homo sapiens serine/threonine kinase 9 (STK9) mRNA
2838	12075	21198	1.36	0.0E+00	AL047599.1	EST_HUMAN	DKFZp586G0621_r1 586 (synonym: hute1) Homo sapiens cDNA clone DKFZp586G0621
2837	12076	21199	1.1	0.0E+00	7661883	NT	Homo sapiens KIAA0054 gene product, Helicase (KIAA0054), mRNA
2837	12078	21200	1.1	0.0E+00	7661883	NT	Homo sapiens KIAA0054 gene product, Helicase (KIAA0054), mRNA
2838	12077		1.88	0.0E+00	4503098	NT	Homo sapiens chondroitin sulfate proteoglycan 4 (melanoma-associated) (CSPG4), mRNA
2840	12079	21202	6.06	0.0E+00	BE081896.1	EST_HUMAN	QV2-BT0636-130400-138-H03 BT0636 Homo sapiens cDNA

Page 351 of 382  
Table 4  
Single Exon Probes Expressed in HELA Cells

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2840	12079	21203	6.06	0.0E+00	BE081896.1	EST_HUMAN	QV2-BT0636-130400-138-h03 BT0636 Homo sapiens cDNA
2845	12084	21211	1.41	0.0E+00	6808918	NT	Homo sapiens low density lipoprotein-related protein 2 (LRP2), mRNA
2845	12084	21212	1.41	0.0E+00	6808918	NT	Homo sapiens low density lipoprotein-related protein 2 (LRP2), mRNA
2848	12087	21216	2.94	0.0E+00	AL163206.2	NT	Homo sapiens chromosome 21 segment HS21C006
2848	12087	21217	2.94	0.0E+00	AL163206.2	NT	Homo sapiens chromosome 21 segment HS21C006
2849	12088	21218	1.07	0.0E+00	AA215578.1	EST_HUMAN	z88b11.s1 NCL_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:683517 3' similar to contains Alu repetitive element;
2856	12094		4.27	0.0E+00	Y18210.1	NT	Homo sapiens HHB5 gene for hair keratin, exons 1 to 9
2859	12097	21227	1.07	0.0E+00	4758279	NT	Homo sapiens EphA4 (EPHA4) mRNA
2860	12098	21228	47.89	0.0E+00	4503470	NT	Homo sapiens eukaryotic translation elongation factor 1 alpha 1 (EEF1A1) mRNA
2861	12099	21229	2.25	0.0E+00	AI561002.1	EST_HUMAN	tn18d07.x1 NCL_CGAP_Bm25 Homo sapiens cDNA clone IMAGE:2167981 3' similar to TR:O16247
2861	12099	21230	2.25	0.0E+00	AI561002.1	EST_HUMAN	tn18d07.x1 NCL_CGAP_Bm25 Homo sapiens cDNA clone IMAGE:2167981 3' similar to TR:O16247
2863	12101	21232	1.52	0.0E+00	P52740	SWISSPROT	O16247 F44E7.2 PROTEIN.;
2864	12102	21233	1.33	0.0E+00	AF152338.1	NT	ZINC FINGER PROTEIN 132
2878	12116	21245	2.8	0.0E+00	AB033093.1	NT	Homo sapiens protocadherin gamma C4 (PCDH-gamma-C4) mRNA, complete cds
2878	12116	21246	2.8	0.0E+00	AB033093.1	NT	Homo sapiens mRNA for KIAA1267 protein, partial cds
2879	12117	21247	5.69	0.0E+00	AB040941.1	NT	Homo sapiens mRNA for KIAA1267 protein, partial cds
2879	12117	21248	5.69	0.0E+00	AB040941.1	NT	Homo sapiens mRNA for KIAA1508 protein, partial cds
2882	12120	21251	6.56	0.0E+00		NT	Homo sapiens mRNA for KIAA1508 protein, partial cds
2882	12120	21252	6.56	0.0E+00		NT	Homo sapiens KIAA0100 gene product (KIAA0100), mRNA
2883	12121	21253	3.32	0.0E+00		NT	Homo sapiens KIAA0100 gene product (KIAA0100), mRNA
2883	12121	21254	3.32	0.0E+00	5174574	NT	Homo sapiens myeloid/lymphoid or mixed-lineage leukemia (trithorax (Drosophila) homolog); translocated to, 4 (MLL T4) mRNA
2888	12125	21258	1.33	0.0E+00	5174574	NT	Homo sapiens myeloid/lymphoid or mixed-lineage leukemia (trithorax (Drosophila) homolog); translocated to, 4 (MLL T4) mRNA
2888	12125	21259	1.33	0.0E+00	BF110702.1	EST_HUMAN	7n40d03.x1 NCL_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3567028 3' similar to TR:Q9VLN1
2896	12134	21270	2.63	0.0E+00	BF110702.1	EST_HUMAN	Q9VLN1 CG17283 PROTEIN.;
2896	12134	21271	2.63	0.0E+00	4505084	NT	7n40d03.x1 NCL_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3567028 3' similar to TR:Q9VLN1
2896	12134	21271	2.63	0.0E+00	4505084	NT	Q9VLN1 CG17283 PROTEIN.;
2898	12136	21273	1.31	0.0E+00	4885214	NT	Homo sapiens melanoma antigen, family B, 4 (MAGEB4), mRNA
2898	12136	21273	1.31	0.0E+00	4885214	NT	Homo sapiens melanoma antigen, family B, 4 (MAGEB4), mRNA
2898	12136	21274	1.31	0.0E+00	4885214	NT	Homo sapiens v-erb-a avian erythroblastic leukemia viral oncogene homolog-like 4 (ERBB4) mRNA
2898	12136	21274	1.31	0.0E+00	4885214	NT	Homo sapiens v-erb-a avian erythroblastic leukemia viral oncogene homolog-like 4 (ERBB4) mRNA

Page 352 of 382  
Table 4  
Single Exon Probes Expressed in HELA Cells

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2802	12140	21277	1.23	0.0E+00	AB011083.1	NT	Homo sapiens mRNA for KIAA0511 protein, partial cds
2806	12144	21280	1.94	0.0E+00	4758827	NT	Homo sapiens neuroxin III (NRXN3) mRNA
2807	12145		0.96	0.0E+00	X98494.1	NT	H. sapiens mRNA for M phase phosphoprotein 10
2910	12148	21283	1.37	0.0E+00	AB030304.1	NT	Homo sapiens mRNA for KIAA1208 protein, partial cds
2912	12150	21284	1.32	0.0E+00	X15309.1	NT	H. sapiens NF-H gene, exon 4
2912	12150	21285	1.32	0.0E+00	X15309.1	NT	H. sapiens NF-H gene, exon 4
2914	12152	21287	10.32	0.0E+00	AF106275.1	NT	Homo sapiens immunoglobulin-like transcript 1c variant 4 (ILT1c) gene, exon 6
2928	12166		1.27	0.0E+00	AI149880.1	EST_HUMAN	qf43f09.x1 Soares_testis NHT Homo sapiens cDNA clone IMAGE:1752809 3'
2938	12176	21310	0.91	0.0E+00	AF281074.1	NT	Homo sapiens neuropilin 2 (NRP2) gene, complete cds, alternatively spliced
2938	12176	21311	0.91	0.0E+00	AF281074.1	NT	Homo sapiens neuropilin 2 (NRP2) gene, complete cds, alternatively spliced
2939	12177	21312	3.26	0.0E+00	AB004894.1	NT	Homo sapiens mRNA for PKU-alpha, partial cds
2951	12189	21322	1.83	0.0E+00	7662273	NT	Homo sapiens KIAA0737 gene product (KIAA0737), mRNA
2952	12190	21323	2.25	0.0E+00	5729755	NT	Homo sapiens calcium channel, voltage-dependent, gamma subunit 3 (CACNG3), mRNA
2952	12190	21324	2.25	0.0E+00	5729755	NT	Homo sapiens calcium channel, voltage-dependent, gamma subunit 3 (CACNG3), mRNA
2963	12201	21335	2.39	0.0E+00	AF114488.1	NT	Homo sapiens intersectin short isoform (ITSN) mRNA, complete cds
2963	12201	21336	2.39	0.0E+00	AF114488.1	NT	Homo sapiens intersectin short isoform (ITSN) mRNA, complete cds
2991	12228		0.66	0.0E+00	AL163246.2	NT	Homo sapiens chromosome 21 segment HS21C046
2993	12230	21392	1.2	0.0E+00	M74086.1	NT	Human displacement protein (GCAAT) mRNA
3002	12238	21388	0.65	0.0E+00	4508882	NT	Homo sapiens semenogelin I (SEMG1) mRNA
3004	12240	21370	1.08	0.0E+00	AW976268.1	EST_HUMAN	EST388375 MAGE resequences, MAGN Homo sapiens cDNA
3008	12245		4.68	0.0E+00	AF185953.1	NT	Homo sapiens membrane-bound aminopeptidase P (XNPEP2) gene, complete cds
3012	12248	21378	10.7	0.0E+00	5579469	NT	Homo sapiens heat shock 70kD protein 1 (HSPA1A), mRNA
3012	12248	21379	10.7	0.0E+00	5579469	NT	Homo sapiens heat shock 70kD protein 1 (HSPA1A), mRNA
3014	12250		7.18	0.0E+00	AL359403.1	NT	Isoform 2 of a novel human mRNA from chromosome 22
3018	12254	21383	3.07	0.0E+00	AF017433.1	NT	Homo sapiens putative transcription factor CR53 (CR53) mRNA, partial cds
							Homo sapiens transcription factor IG-HM enhancer 3, JM11 protein, JM4 protein, JM5 protein, T54 protein, JM10 protein, A4 differentiation-dependent protein, triple LIM domain protein 6, and synaptophysin genes, complete cds; and L-type calcium channel a2
3021	12257		2.58	0.0E+00	AF198779.1	NT	Human germline gene 16.1 for Ig lambda L-chain C region (IgL-C18.1)
3042	12279	21407	3.54	0.0E+00	X03528.1	NT	Homo sapiens F-box protein FBL5 (FBL5) mRNA, complete cds
3047	12283		1.69	0.0E+00	AF198355.1	NT	Homo sapiens melanoma-associated antigen (MAGE-C1) gene, complete cds
3051	12287	21413	1.89	0.0E+00	AF064589.1	NT	Homo sapiens melanoma-associated antigen (MAGE-C1) gene, complete cds
3070	12306	21428	4.81	0.0E+00	AF265208.1	NT	Homo sapiens SWI-SNF complex protein p270 mRNA, partial cds
3071	12307	21429	10.45	0.0E+00	AF149773.1	NT	Homo sapiens NOD1 protein (NOD1) gene, exons 1, 2, and 3
3076	12312	21433	4.31	0.0E+00	7662139	NT	Homo sapiens KIAA0469 gene product (KIAA0469), mRNA

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## Single Exon Probes Expressed in HELA Cells

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3077	12313	21434	1.49	0.0E+00	AF042075.1	NT	Homo sapiens olfactory receptor-like protein (OLFR 42B) gene, OLFR 42B-8110 allele, partial cds
3106	12341	21469	2.95	0.0E+00	4826783	NT	Homo sapiens potassium voltage-gated channel, Shab-related subfamily, member 1 (KCNB1) mRNA
3113	12348	21476	54.11	0.0E+00	L20941.1	NT	Human ferritin heavy chain mRNA, complete cds
3117	12352	21480	1.3	0.0E+00	AB011121.1	NT	Homo sapiens mRNA for KIAA0549 protein, partial cds
3117	12352	21481	1.3	0.0E+00	AB011121.1	NT	Homo sapiens mRNA for KIAA0549 protein, partial cds
3124	12359	21488	36.75	0.0E+00	T94870.1	EST_HUMAN	y63203.s1 Stragene lung (#37210) Homo sapiens cDNA clone IMAGE:119453 3' similar to SP:526639
3140	12375	21508	1.17	0.0E+00	BF243336.1	EST_HUMAN	S29539 BASIC PROTEIN, 23k -
3142	12377	21507	1.02	0.0E+00	AI968088.1	EST_HUMAN	601878507F1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:4107433 5'
3147	12382	21514	4.69	0.0E+00	X98922.1	NT	wu12h10.x1 NCI_GCAP_GC6 Homo sapiens cDNA clone IMAGE:2516803 3'
3147	12382	21515	4.69	0.0E+00	X98922.1	NT	H. sapiens mRNA for gamma-glutamyltransferase
3156	12391	21525	1.61	0.0E+00	4758827	NT	H. sapiens mRNA for gamma-glutamyltransferase
3156	12391	21526	1.61	0.0E+00	4758827	NT	Homo sapiens neuroxin III (NRXN3) mRNA
3164	12399	21534	10.06	0.0E+00	4504658	NT	Homo sapiens neuroxin III (NRXN3) mRNA
3163	12418	21552	10.77	0.0E+00	M28699.1	NT	Homo sapiens interleukin 1 receptor, type I (IL1R1) mRNA
3186	12421	21554	7.27	0.0E+00	4502098	NT	Homo sapiens nucleolar phosphoprotein B23 (NPM1) mRNA, complete cds
3192	12427	21562	0.97	0.0E+00	4758055	NT	Homo sapiens solute carrier family 25 (mitochondrial carrier; adenine nucleotide translocator), member 5 (SLC25A5), nuclear gene encoding mitochondrial protein, mRNA
3192	12427	21563	0.97	0.0E+00	4758055	NT	Homo sapiens CREB binding protein (Rubinstein-Taybi syndrome) (CREBBP) mRNA
3194	12428	21564	7.38	0.0E+00	AA774783.1	EST_HUMAN	Homo sapiens CREB binding protein (Rubinstein-Taybi syndrome) (CREBBP) mRNA
3202	12437	21572	5.8	0.0E+00	AF286598.1	NT	aa87b11.s1 Stragene schizo brain S11 Homo sapiens cDNA clone IMAGE:971133 3'
3202	12437	21573	5.8	0.0E+00	AF286598.1	NT	Homo sapiens angiotensin binding protein 1 mRNA, complete cds
3215	12449	21581	1.45	0.0E+00	4557590	NT	Homo sapiens angiotensin binding protein 1 mRNA, complete cds
3220	12454	21587	0.96	0.0E+00	4507720	NT	Homo sapiens fibrillin 1 (Marfan syndrome) (FBN1) mRNA
							Homo sapiens titin (TTN) mRNA
							Homo sapiens HLA class III region containing tenascin X (tenascin-X) gene, partial cds; cyclochrome P450 21-hydroxylase (CYP21B), complement component C4 (C4B) G11, helicase (SKI2W), RD, complement factor B (BF), and complement component C2 (C2) genes, >
3228	12462	21594	1.77	0.0E+00	AF019413.1	NT	Homo sapiens very large G-protein coupled receptor-1 (VLGR1) mRNA, complete cds
3231	12465	21597	4.91	0.0E+00	AF055084.1	NT	Homo sapiens KIAA0440 protein (KIAA0440), mRNA
3234	12468	21599	1.25	0.0E+00	7662125	NT	Homo sapiens KIAA0440 protein (KIAA0440), mRNA
3234	12468	21600	1.25	0.0E+00	7662125	NT	Homo sapiens A kinase (PRKA) anchor protein 1 (AKAP1), mRNA
3242	14485	21607	3.5	0.0E+00	4502014	NT	Homo sapiens A kinase (PRKA) anchor protein 1 (AKAP1), mRNA
3242	14485	21608	3.5	0.0E+00	4502014	NT	Homo sapiens A kinase (PRKA) anchor protein 1 (AKAP1), mRNA
3259	12492	21623	3.47	0.0E+00	AF285208.1	NT	Homo sapiens SWI-SNF complex protein p270 mRNA, partial cds

Page 354 of 382  
Table 4  
Single Exon Probes Expressed in HELA Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3260	12493	21624	1.11	0.0E+00	8823624	NT	Homo sapiens hypothetical protein FLJ20695 (FLJ20695), mRNA
3274	12507	21638	1.28	0.0E+00	7657038	NT	Homo sapiens death receptor 6 (DR6), mRNA
3285	12516	21647	0.74	0.0E+00	4885312	NT	Homo sapiens G protein-coupled receptor 24 (GPR24), mRNA
3298	12527	21658	8.17	0.0E+00	AI589294.1	EST_HUMAN	t5808.x2 NCI_CGAP_Pan1 Homo sapiens cDNA clone IMAGE:222535 3' similar to SW:RL11_RAT
3308	12536	21668	3.01	0.0E+00	AF128893.1	NT	P25121 60S RIBOSOMAL PROTEIN L11; contains Alu repetitive element,
3308	12536	21669	3.01	0.0E+00	AF128893.1	NT	Homo sapiens G protein-coupled receptor 24 (GPR24), mRNA
3307	12537	21670	0.98	0.0E+00	7657213	NT	Homo sapiens telomerase reverse transcriptase (TERT) gene, exons 1-6
3307	12537	21671	0.98	0.0E+00	7657213	NT	Homo sapiens telomerase reverse transcriptase (TERT) gene, exons 1-6
3309	12539	21673	1.61	0.0E+00	4502582	NT	Homo sapiens hormonally upregulated neu tumor-associated kinase (HUNK), mRNA
3309	12539	21674	1.61	0.0E+00	4502582	NT	Homo sapiens caspase 8, apoptosis-related cysteine protease (CASP8) mRNA
3312	12542	21678	12.9	0.0E+00	AF111183.1	NT	Homo sapiens caspase 8, apoptosis-related cysteine protease (CASP8) mRNA
3314	12544	21678	0.93	0.0E+00	AB040940.1	NT	Homo sapiens pyrin (MEFV) gene, complete cds
3321	12550	21684	0.79	0.0E+00	BE79039.1	EST_HUMAN	Homo sapiens mRNA for KIAA1507 protein, partial cds
3333	12562	21700	0.85	0.0E+00	AI82569.1	EST_HUMAN	601484955F1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3868246 5'
3374	12602	21738	2.97	0.0E+00	AU123664.1	EST_HUMAN	wb1004.x1 NCI_CGAP_G06 Homo sapiens cDNA clone IMAGE:2306279 3' similar to TR:091929 Q81929
3381	12608	21741	0.94	0.0E+00	7363436	NT	ZINC FINGER PROTEIN;
3381	12608	21742	0.94	0.0E+00	7363436	NT	AU123664 NT2RM2 Homo sapiens cDNA clone NT2RM2000735 5'
3384	12611	21744	1.38	0.0E+00	7708239	NT	Homo sapiens olfactory receptor, family 10, subfamily C, member 1 (OR10C1), mRNA
3385	12612	21745	1.16	0.0E+00	AF211189.1	NT	Homo sapiens olfactory receptor, family 10, subfamily C, member 1 (OR10C1), mRNA
3389	12616		1.19	0.0E+00	AW867015.1	EST_HUMAN	Homo sapiens neuroblastoma-amplified protein (LOC51594), mRNA
3403	12628	21759	3.18	0.0E+00	7682401	NT	Homo sapiens T-type calcium channel alpha1 subunit Alpha1I-a isoform (CACNA1I) mRNA, complete cds
3403	12628	21760	3.18	0.0E+00	7682401	NT	MR1-SN0033-100400-001 -08 SN0033 Homo sapiens cDNA
3404	12630	21761	0.98	0.0E+00	4502398	NT	Homo sapiens KIAA0952 protein (KIAA0952), mRNA
3406	12632	21762	2.09	0.0E+00	5803067	NT	Homo sapiens KIAA0952 protein (KIAA0952), mRNA
3415	11870	21084	3.07	0.0E+00	AF110763.1	NT	Homo sapiens beaded filament structural protein 1, filensin (BFSP1) mRNA
3419	12644	21773	2.84	0.0E+00	7657038	NT	Homo sapiens leukocyte immunoglobulin-like receptor, subfamily A (with TM domain), member 2 (LILRA2), mRNA
3422	12847	21777	6.12	0.0E+00	K02380.1	NT	Homo sapiens skeletal muscle LIM-protein 1 (FHL1) gene, complete cds
3424	12849	21779	0.95	0.0E+00	7427522	NT	Homo sapiens skeletal muscle LIM-protein 1 (FHL1) gene, complete cds
3427	12852	21782	2.08	0.0E+00	4557748	NT	Homo sapiens death receptor 6 (DR6), mRNA
							Bacteriophage P1 replication region including repA, parA, and parB genes and incA, incB, and incC
							incompatibility determinants
							Homo sapiens protein tyrosine phosphatase, receptor type, T (PTPRT), mRNA
							Homo sapiens met proto-oncogene (hepatocyte growth factor receptor) (MET) mRNA

Page 355 of 382  
Table 4  
Single Exon Probes Expressed in HELA Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3432	12657	21787	4.07	0.0E+00	AI935159.1	EST_HUMAN	wp14d10.x1 NCI_CGAP_Lu19 Homo sapiens cDNA clone IMAGE:2484819 3' similar to TR:O73634 O73634 NEURAL CELL ADHESION MOLECULE.;
3432	12657	21788	4.07	0.0E+00	AI935159.1	EST_HUMAN	wp14d10.x1 NCI_CGAP_Lu19 Homo sapiens cDNA clone IMAGE:2484819 3' similar to TR:O73634 O73634 NEURAL CELL ADHESION MOLECULE.;
3436	12661	21783	2.57	0.0E+00	AJ278120.1	NT	Homo sapiens mRNA for putative ankyrin-repeat containing protein (ORF1)
3442	12667	21801	2.8	0.0E+00	6552332	NT	Homo sapiens v-fos FBJ murine osteosarcoma viral oncogene homolog (FOS), mRNA
3442	12667	21802	2.8	0.0E+00	6552332	NT	Homo sapiens v-fos FBJ murine osteosarcoma viral oncogene homolog (FOS), mRNA
3448	12673	21808	1.89	0.0E+00	M14123.1	NT	Human endogenous retrovirus HERV-K10
3452	12677	21812	7.14	0.0E+00	U43293.1	NT	Human MDS1A (AML1/MDS1 fusion) mRNA, partial cds
3460	12685	21820	2.98	0.0E+00	AF045452.1	NT	Homo sapiens cell-line KG1 transcriptional regulatory protein p54 mRNA, complete cds
3460	12685	21821	2.98	0.0E+00	AF045452.1	NT	Homo sapiens cell-line KG1 transcriptional regulatory protein p54 mRNA, complete cds
3468	12683	21830	1.05	0.0E+00	AF231922.1	NT	Homo sapiens chromosome 21 unknown mRNA
3476	12700	21836	1.23	0.0E+00	4508028	NT	Homo sapiens zinc finger protein 45 (a Kruppel-associated box (KRAB) domain polypeptide) (ZNF45) mRNA
3479	12703	21838	1.95	0.0E+00	BE304791.1	EST_HUMAN	601143853F1 NIH_MGC_15 Homo sapiens cDNA clone IMAGE:3051373 5'
3479	12703	21839	1.95	0.0E+00	BE304791.1	EST_HUMAN	601143853F1 NIH_MGC_15 Homo sapiens cDNA clone IMAGE:3051373 5'
3482	12706	21842	1.24	0.0E+00	4826795	NT	Homo sapiens potassium voltage-gated channel, Isk-related family, member 2 (KONE2) mRNA
3484	12708	21845	1.98	0.0E+00	O14867	SWISSPROT	TRANSCRIPTION REGULATOR PROTEIN BACH1 (BTB AND CNC HOMOLOG-1) (HA2303)
3488	12712	21848	0.74	0.0E+00	AI384007.1	EST_HUMAN	t835g12.x1 Soares_NHMPu_S1 Homo sapiens cDNA clone IMAGE:2088742 3' similar to TR:O00498
3508	12730	21867	0.61	0.0E+00	AB032979.1	NT	O00498 MYASTHENIA GRAVIS AUTOANTIGEN GRAVIN ;
3508	12730	21868	0.61	0.0E+00	AB032979.1	NT	Homo sapiens mRNA for KIAA1153 protein, partial cds
3514	12738	21876	0.95	0.0E+00	AB029019.1	NT	Homo sapiens mRNA for KIAA1153 protein, partial cds
3516	12740	21877	0.89	0.0E+00	AV701869.1	EST_HUMAN	Homo sapiens mRNA for KIAA1096 protein, partial cds
3517	12741	21878	5.33	0.0E+00	4508884	NT	AV701869 ADB Homo sapiens cDNA clone ADBDAH08 5'
3518	12742		2.19	0.0E+00	AF078868.1	NT	Homo sapiens semaphorin II (SEMG2) mRNA
3526	12750	21882	1.74	0.0E+00	AL133204.1	NT	Homo sapiens homologous yeast-44.2 protein mRNA, complete cds
3528	12752	21885	0.84	0.0E+00	AB040909.1	NT	Novel human gene mapping to chromosome X
3540	12763	21894	0.9	0.0E+00	8823087	NT	Homo sapiens mRNA for KIAA1476 protein, partial cds
3548	12772	21900	0.98	0.0E+00	6997248	NT	Homo sapiens hypothetical protein FLJ20080 (FLJ20080), mRNA
3549	12772	21901	0.96	0.0E+00	6997248	NT	Homo sapiens sal (Drosophila)-like 1 (SALL1), mRNA
						NT	Homo sapiens sal (Drosophila)-like 1 (SALL1), mRNA
3550	12773		1.1	0.0E+00	AI081807.1	EST_HUMAN	ox77c11.x1 Soares_NHMPu_S1 Homo sapiens cDNA clone IMAGE:1682356 3' similar to WP:119B4.4 CE13742 ;
3552	12775	21804	1.13	0.0E+00	6325463	NT	Homo sapiens butyrophilin, subfamily 3, member A3 (BTN3A3), mRNA



Table 4

## Single Exon Probes Expressed in HELA Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3558	12781		5.31	0.0E+00	AW852217.1	EST_HUMAN	QV0-CT0225-230300-168-e01 CT0225 Homo sapiens cDNA
3562	12785	21915	1.05	0.0E+00	4504294	NT	Homo sapiens H3 histone family, member K (H3FK), mRNA
3566	12789		0.8	0.0E+00	AF118846.1	NT	Homo sapiens gamma-glutamylcysteine synthetase (GLCLC) gene, partial cds
3567	12790	21916	8.26	0.0E+00	BF676393.1	EST_HUMAN	602084583F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4248596 5'
3571	12794		1.08	0.0E+00	AA988715.1	EST_HUMAN	cc94h08.s1 NCI_CGAP_Kid6 Homo sapiens cDNA clone IMAGE:1594043 3' similar to contains MER28.b2
3581	12803	21929	0.72	0.0E+00	AW937677.1	EST_HUMAN	MER29 repetitive element
3584	12815		1.18	0.0E+00	4826967	NT	QV0-DT0047-170200-123-g01 DT0047 Homo sapiens cDNA
3586	12817	21937	0.7	0.0E+00	AW664693.1	EST_HUMAN	Homo sapiens retinoblastoma-binding protein 2 (RBBP2) mRNA
3596	12817	21938	0.7	0.0E+00	AW664693.1	EST_HUMAN	hi84g01.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2978024 3'
3601	12822	21944	0.82	0.0E+00	7682319	NT	hi84g01.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2978024 3'
3608	12828	21949	1.13	0.0E+00	4557752	NT	Homo sapiens KIAA0808 gene product (KIAA0808), mRNA
3608	12828	21950	1.13	0.0E+00	4557752	NT	Homo sapiens midline 1 (Opitz/BBB syndrome) (MID1) mRNA
3626	12847	21965	1.9	0.0E+00	D87327.1	NT	Homo sapiens midline 1 (Opitz/BBB syndrome) (MID1) mRNA
3630	12851		30.7	0.0E+00	7689491	NT	Homo sapiens mRNA for G protein-coupled inward rectifier potassium channel, complete cds
3648	12869	21986	2.32	0.0E+00	AB026542.1	NT	Homo sapiens glyceraldehyde-3-phosphate dehydrogenase (GAPD), mRNA
3650	12871	21988	2.49	0.0E+00	AB007896.2	NT	Homo sapiens WAVE2 mRNA for WASP-family protein, complete cds
3651	12872	21989	3.61	0.0E+00	AF124250.1	NT	Homo sapiens mRNA for KIAA0406 protein, partial cds
3651	12872	21990	3.61	0.0E+00	AF124250.1	NT	Homo sapiens SH2-containing protein Nsp2 mRNA, complete cds
3659	12880	21999	1.62	0.0E+00	AL163204.2	NT	Homo sapiens SH2-containing protein Nsp2 mRNA, complete cds
3659	12880	21999	1.62	0.0E+00	AL163204.2	NT	Homo sapiens chromosome 21 segment HS21C004
3659	12880	22000	1.62	0.0E+00	AL163204.2	NT	Homo sapiens chromosome 21 segment HS21C004
3660	12881	22001	1.03	0.0E+00	AB002331.1	NT	Homo sapiens chromosome 21 segment HS21C004
3660	12881	22002	1.03	0.0E+00	AB002331.1	NT	Human mRNA for KIAA0333 gene, partial cds
3663	12884	22005	1.57	0.0E+00	AW851714.1	EST_HUMAN	Human mRNA for KIAA0333 gene, partial cds
3665	12886	22007	1.6	0.0E+00	5729928	NT	MR2-CT0222-281099-005-e05 CT0222 Homo sapiens cDNA
3667	12888	22009	1.54	0.0E+00	AB018339.1	NT	Homo sapiens matrix metalloproteinase 24 (membrane-inserted) (MMP24), mRNA
3669	12890	22011	1.67	0.0E+00	O14867	SWISSPROT	Homo sapiens mRNA for KIAA0796 protein, partial cds
3680	12901	22021	1.01	0.0E+00	5729733	NT	Homo sapiens activator of S phase kinase (ASK) mRNA
3680	12901	22022	1.01	0.0E+00	5729733	NT	TRANSCRIPTION REGULATOR PROTEIN BACH1 (BTB AND CNC HOMOLOG 1) (HA2303)
3684	12905	22024	5.05	0.0E+00	AW288134.1	EST_HUMAN	Homo sapiens activator of S phase kinase (ASK) mRNA
3684	12905	22025	5.05	0.0E+00	AW288134.1	EST_HUMAN	Homo sapiens activator of S phase kinase (ASK) mRNA
3710	12930	22048	1.27	0.0E+00	AB004630.1	NT	UIH-BW0-aj-s-e-12-Q-U1.s1 NCI_CGAP_Sub6 Homo sapiens cDNA clone IMAGE:2733022 3'
3711	12931	22049	1.11	0.0E+00	AA463659.1	EST_HUMAN	Human gene for Type XIX collagen a1 chain, exon 6
							aa06g01.r1 Soares_NHMPu_S1 Homo sapiens cDNA clone IMAGE:812498 5' similar to
							SW-KRB4_SHEEP P02445 KERATIN, HIGH-SULFUR MATRIX PROTEIN, IIIB4, [1]:

Table 4

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3715	12835	22053	0.9	0.0E+00	AB020710.1	NT	Homo sapiens mRNA for KIAA0893 protein, partial cds
3718	12938	22055	4.28	0.0E+00	7657468	NT	Homo sapiens similar to rat integral membrane glycoprotein POM121 (POM121L1), mRNA
3728	12947	22065	1.04	0.0E+00	AB037835.1	NT	Homo sapiens mRNA for KIAA1414 protein, partial cds
3742	12962	22077	11.29	0.0E+00	7662183	NT	Homo sapiens KIAA0568 gene product (KIAA0568), mRNA
3745	12965	22080	33.84	0.0E+00	4506718	NT	Homo sapiens ribosomal protein S2 (RPS2) mRNA
3810	13028		0.68	0.0E+00	AF195658.1	NT	Homo sapiens DNA mismatch repair protein (MLH3) gene, complete cds
3811	13029	22138	2.52	0.0E+00	AF179733.1	NT	Pan troglodytes olfactory receptor (PTR208) gene, partial cds
3814	13032	22142	2.35	0.0E+00	7657468	NT	Homo sapiens similar to rat integral membrane glycoprotein POM121 (POM121L1), mRNA
3814	13032	22143	2.35	0.0E+00	7657468	NT	Homo sapiens similar to rat integral membrane glycoprotein POM121 (POM121L1), mRNA
3818	13036	22149	2.12	0.0E+00	4756011	NT	Homo sapiens RAB9, member RAS oncogene family (RAB9) mRNA
3819	13037	22149	0.99	0.0E+00	10181139	NT	Mus musculus junctophilin 1 (Jp1-pending), mRNA
3820	13038	22150	1.18	0.0E+00	AF127851.1	NT	Gorilla gorilla olfactory receptor (GGOT1) gene, partial cds
3820	13038	22151	1.18	0.0E+00	AF127851.1	NT	Gorilla gorilla olfactory receptor (GGOT1) gene, partial cds
3821	13039	22152	1.3	0.0E+00	AI377696.1	EST_HUMAN	ta2210.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2091307 3'
3822	13040		1.15	0.0E+00	AF152498.1	NT	Homo sapiens protocadherin beta 3 (PCDH-beta3) mRNA, complete cds
3823	13041	22153	3.87	0.0E+00	4758199	NT	Homo sapiens desmoplakin (DPI, DPII) (DSP) mRNA
3825	13043	22154	15.35	0.0E+00	S78685.1	NT	Homo sapiens ATP-sensitive inwardly rectifying K-channel subunit (KCNJ8/BIR1) gene, complete cds
3828	13044	22155	2.43	0.0E+00	7710149	NT	Homo sapiens methyl CpG binding protein 2 (MECP2), mRNA
3827	13045	22156	1.87	0.0E+00	7662183	NT	Homo sapiens KIAA0568 gene product (KIAA0568), mRNA
3833	13050	22160	1.08	0.0E+00	6912735	NT	Homo sapiens transient receptor potential channel 5 (TRPC5), mRNA
3837	13054	22167	6.52	0.0E+00	4503178	NT	Homo sapiens chromosome X open reading frame 5 (CXORF5) mRNA
3837	13054	22168	6.52	0.0E+00	4503178	NT	Homo sapiens chromosome X open reading frame 5 (CXORF5) mRNA
3839	13056	22171	3.62	0.0E+00	U09412.1	NT	Human zinc finger protein ZNF134 mRNA, complete cds
3840	13057	22172	0.92	0.0E+00	AF114488.1	NT	Homo sapiens intersectin short isoform (ITSN) mRNA, complete cds
3843	13060	22174	1.29	0.0E+00	4826783	NT	Homo sapiens potassium voltage-gated channel, Shab-related subfamily, member 1 (KCNB1) mRNA
3845	13062	22176	2.63	0.0E+00	4759171	NT	Homo sapiens SC35-interacting protein 1 (SRRP129), mRNA
3847	13064	22178	0.8	0.0E+00	AF096117.1	NT	Homo sapiens amphiphysin gene, partial cds
3856	13072	22187	2.52	0.0E+00	AI884727.1	EST_HUMAN	wk01f01.x1 NCJ_CGAP_Lym12 Homo sapiens cDNA clone IMAGE:2411065 3' similar to TR-O43340
3857	13073	22188	1.05	0.0E+00	AL163248.2	NT	O43340 R28830.2, contains element PTR7 repetitive element ;
3860	13076	22192	15.3	0.0E+00	4506742	NT	Homo sapiens chromosome 21 segment HS21C048
3862	13078	22194	1.81	0.0E+00	AL040338.1	EST_HUMAN	Homo sapiens ribosomal protein S8 (RPS8), mRNA
							DKFZp434N0413_t1 434 (synonym: hba3) Homo sapiens cDNA clone DKFZp434N0413 5'

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3867	13083	22200	0.98	0.0E+00	6005887	NT	Homo sapiens AP1 gamma subunit binding protein 1 (AP1GBP1), mRNA
3867	13083	22201	0.98	0.0E+00	6005887	NT	Homo sapiens AP1 gamma subunit binding protein 1 (AP1GBP1), mRNA
3868	13084	22202	2.93	0.0E+00	4504138	NT	Homo sapiens glutamate receptor, metabotropic 3 (GRM3), mRNA
3869	13085		1.91	0.0E+00	4505078	NT	Homo sapiens melanoma antigen, family B, 1 (MAGEB1), mRNA
3873	13089	22205	1.28	0.0E+00	AF149412.1	NT	Homo sapiens HBP17 heparin-binding and FGF-binding protein gene, complete cds
3882	13098	22215	1.08	0.0E+00	4508758	NT	Homo sapiens tyrosine receptor 3 (RYR3), mRNA
3886	13102	22219	2.28	0.0E+00	4585842	NT	Homo sapiens zinc finger protein (KIAA0412), mRNA
3893	13109	22227	4	0.0E+00	BF355295.1	EST_HUMAN	RC3-HIT0860-170800-011-a12 HIT0860 Homo sapiens cDNA
3899	13115	22232	2.47	0.0E+00	AF129533.1	NT	Homo sapiens F-box protein Fbl3b (FBL3B), mRNA, partial cds
3902	13118	22235	1	0.0E+00	U86281.1	NT	Homo sapiens olfactory receptor (OR7-141) gene, partial cds
3902	13118	22236	1	0.0E+00	U86281.1	NT	Homo sapiens olfactory receptor (OR7-141) gene, partial cds
3906	13122	22240	4.33	0.0E+00	BE378602.1	EST_HUMAN	Homo sapiens olfactory receptor (OR7-141) gene, partial cds
3914	13130	22247	0.91	0.0E+00	AW580740.1	EST_HUMAN	Homo sapiens olfactory receptor (OR7-141) gene, partial cds
3915	13131	22248	1.01	0.0E+00	BE284998.1	EST_HUMAN	PM3-LT0031-100100-003-H09 LT0031 Homo sapiens cDNA
3915	13131	22248	1.01	0.0E+00	BE284998.1	EST_HUMAN	PM3-LT0031-100100-003-H09 LT0031 Homo sapiens cDNA clone IMAGE:3537774 5'
3915	13131	22248	1.01	0.0E+00	BE284998.1	EST_HUMAN	601193927F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3537774 5'
3953	13188	22281	5.67	0.0E+00	AF116195.1	NT	601193927F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3537774 5'
3953	13188	22282	5.67	0.0E+00	AF116195.1	NT	Homo sapiens cancer-testis antigen CT10 (CT10) gene, complete cds
3963	13178		4.8	0.0E+00	M23910.1	NT	Homo sapiens cancer-testis antigen CT10 (CT10) gene, complete cds
3965	13180		5.59	0.0E+00	AL163303.2	NT	Homo sapiens class II lymphocyte antigen DPw4-beta-2 pseudogene, exon 2
3974	13188	22286	3.74	0.0E+00	AL163284.2	NT	Homo sapiens chromosome 21 segment HS21C103
3982	13196	22304	1.95	0.0E+00	AL163288.2	NT	Homo sapiens chromosome 21 segment HS21C084
3994	13208		82.28	0.0E+00	4503470	NT	Homo sapiens chromosome 21 segment HS21C008
4002	13215		1.09	0.0E+00	AF657076.1	EST_HUMAN	Homo sapiens eukaryotic translation elongation factor 1 alpha 1 (EEF1A1), mRNA
4005	13217	22321	1.97	0.0E+00	U09366.1	NT	tt55g08.x1 NCL_CGAP_GC6 Homo sapiens cDNA clone IMAGE:2244734 3' similar to TR:060309 O60309
4023	13234	22339	15.84	0.0E+00	AB015610.1	NT	KIAA0563 PROTEIN ;
4032	13242		3.9	0.0E+00	AJ238617.1	NT	Human zinc finger protein ZNF133
4042	13252	22353	1.88	0.0E+00	AL163203.2	NT	Chlorocebus aethiops mRNA for ribosomal protein S4X, complete cds
4043	13253	22354	3.29	0.0E+00	AJ277276.1	NT	Homo sapiens mRNA for UGA suppressor tRNA-associated antigenic protein (tRNA48 gene)
4043	13253	22355	3.29	0.0E+00	AJ277276.1	NT	Homo sapiens mRNA for rps-2 (rps gene)
4050	13260	22362	11.29	0.0E+00	5032026	NT	Homo sapiens retinoblastoma-binding protein 4 (RBBP4), mRNA
4050	13260	22363	11.29	0.0E+00	5032026	NT	Homo sapiens retinoblastoma-binding protein 4 (RBBP4), mRNA
4080	13271	22373	1.03	0.0E+00	4503914	NT	Homo sapiens phosphoribosylglycinamide formyltransferase, phosphoribosylglycinamide synthetase, phosphoribosylaminimidazole synthetase (GART), mRNA

Page 359 of 382  
Table 4  
Single Exon Probes Expressed in HELA Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4066	13278	22377	5.4	0.0E+00	4885308	NT	Homo sapiens G protein-coupled receptor 21 (GPR21), mRNA
4067	13277	22378	1.63	0.0E+00	AB006625.1	NT	Homo sapiens mRNA for KIAA0287 gene, partial cds
4070	13280	22379	0.59	0.0E+00	4759807	NT	Homo sapiens ras GTPase activating protein-like (NGAP) mRNA
4071	13281	22380	9.39	0.0E+00	11419297	NT	Homo sapiens IMP (inosine monophosphate) dehydrogenase 1 (IMPDH1), mRNA
4072	13282	22381	5.92	0.0E+00	AL088657.1	NT	Novel human mRNA from chromosome 1, which has similarities to BAT2 genes
4080	13290	22389	4.73	0.0E+00	AF165527.1	NT	Homo sapiens DGOR8 (DGOR8) mRNA, complete cds
4089	10363	19513	1.01	0.0E+00	4826047	NT	Homo sapiens protein kinase, X-linked (PRKX) mRNA
4089	10363	19514	1.01	0.0E+00	4826047	NT	Homo sapiens protein kinase, X-linked (PRKX) mRNA
4086	13304	22403	0.99	0.0E+00	5801805	NT	Homo sapiens butyrophilin, subfamily 3, member A2 (BTN3A2), mRNA
4087	13305	22404	1.08	0.0E+00	4503854	NT	Homo sapiens GA-binding protein transcription factor, alpha subunit (60kD) (GABPA), mRNA
4097	13305	22405	1.08	0.0E+00	4503854	NT	Homo sapiens GA-binding protein transcription factor, alpha subunit (60kD) (GABPA), mRNA
4100	12741	21878	0.59	0.0E+00	4508884	NT	Homo sapiens semorogelin II (SEMG2) mRNA
4102	13309	22408	0.68	0.0E+00	8922391	NT	Homo sapiens hypothetical protein FLJ10379 (FLJ10379), mRNA
4108	13309	22409	0.68	0.0E+00	8922391	NT	Homo sapiens hypothetical protein FLJ10379 (FLJ10379), mRNA
4115	13322	22422	0.81	0.0E+00	AB020702.1	NT	Homo sapiens mRNA for KIAA0895 protein, partial cds
4115	13322	22422	6.13	0.0E+00	AI982597.1	EST_HUMAN	wu04d04.x1 NCJ CGAP GC8 Homo sapiens cDNA clone IMAGE:2515975 3'
4115	13322	22423	6.13	0.0E+00	AI982597.1	EST_HUMAN	wu04d04.x1 NCJ CGAP GC8 Homo sapiens cDNA clone IMAGE:2515975 3'
4118	13324	22425	1.2	0.0E+00	BE184856.1	EST_HUMAN	MR1-HT0707-100500-001-a02 HT0707 Homo sapiens cDNA
4118	13324	22426	1.2	0.0E+00	BE184856.1	EST_HUMAN	MR1-HT0707-100500-001-a02 HT0707 Homo sapiens cDNA
4122	13328		5.85	0.0E+00	BE274217.1	EST_HUMAN	601120778F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:2867690 5'
4128	13334	22432	0.96	0.0E+00	AB032851.1	NT	Homo sapiens mRNA for KIAA1125 protein, partial cds
4128	13334	22433	0.96	0.0E+00	AB032851.1	NT	Homo sapiens mRNA for KIAA1125 protein, partial cds
4130	13336	22435	2.13	0.0E+00	5729726	NT	Homo sapiens nuclear receptor coactivator 3 (NCOA3), mRNA
4138	13344		6.07	0.0E+00	AW675599.1	EST_HUMAN	ba511f04.x1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:2800085 3' similar to SW:TH12_BOVIN
4143	13349	22449	1.61	0.0E+00	AW408788.1	EST_HUMAN	Q95108 MITOCHONDRIAL THIOREDOXIN PRECURSOR ;
4145	13351	22452	1.52	0.0E+00	8922468	NT	UI-HF-BMD-adv-c-02 Q-U1.1 NIH_MGC_38 Homo sapiens cDNA clone IMAGE:3063147 5'
4145	13351	22453	1.52	0.0E+00	8922468	NT	Homo sapiens hypothetical protein FLJ10498 (FLJ10498), mRNA
4154	13360		2.25	0.0E+00	5174632	NT	Homo sapiens polycystic kidney disease (polycystin) and REJ (sperm receptor for egg jelly, sea urchin homolog)-like (PKDREJ) mRNA
4185	13368	22468	1.08	0.0E+00	AB037739.1	NT	Homo sapiens mRNA for KIAA1318 protein, partial cds
4174	13378	22477	10.79	0.0E+00	AA401438.1	EST_HUMAN	zu68107.g1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:743197 3' similar to contains Alu repetitive element; contains element MER35 repetitive element;

Table 4

## Single Exon Probes Expressed In HELA Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4174	13378	22478	10.79	0.0E+00	AA401438.1	EST_HUMAN	z168h07.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:743197 3' similar to contains Alu repetitive element; contains element MER35 repetitive element;
4177	13381	22482	1.36	0.0E+00	AF157476.1	NT	Homo sapiens DNA polymerase zeta catalytic subunit (REV3) mRNA, complete cds
4191	13395	22495	1.6	0.0E+00	7662125	NT	Homo sapiens KIAA0440 protein (KIAA0440), mRNA
4201	8301	18403	6.72	0.0E+00	AA228126.1	EST_HUMAN	z158c04.r1 Soares_NHTMPu_S1 Homo sapiens cDNA clone IMAGE:667560 5' similar to TR:G222811
4201	9301	18404	6.72	0.0E+00	AA228126.1	EST_HUMAN	G222811 ALPHA 1 CHAIN OF TYPE XII COLLAGEN.;
4208	13409	22502	4.97	0.0E+00	4758199	NT	Homo sapiens desmoplakin (DPI, DPII) (DSP) mRNA
4208	13409	22503	4.97	0.0E+00	4758199	NT	Homo sapiens desmoplakin (DPI, DPII) (DSP) mRNA
4215	13418	22540	0.92	0.0E+00	AL163303.2	NT	Homo sapiens chromosome 21 segment HS21C103
4246	13449	22540	0.98	0.0E+00	AJ010770.1	NT	Homo sapiens hypericin gene, exons 1-50
4259	13462	22554	2.79	0.0E+00	J02610.1	NT	Human apolipoprotein B-100 mRNA, complete cds
4273	13476	22573	0.84	0.0E+00	AW936889.1	EST_HUMAN	PM2-DT0023-080300-004-g08 DT0023 Homo sapiens cDNA
4281	13484	22582	0.83	0.0E+00	4829827	NT	Homo sapiens myelodysplasia syndrome 1 (MDST) mRNA
4281	13484	22583	0.83	0.0E+00	4829827	NT	Homo sapiens myelodysplasia syndrome 1 (MDST) mRNA
4283	13486	22585	3.57	0.0E+00	AF174590.1	NT	Homo sapiens F-box protein Fbl4 (FBL4) mRNA, partial cds
4289	13491	22589	1.36	0.0E+00	6809918	NT	Homo sapiens low density lipoprotein-related protein 2 (LRP2) mRNA
4289	13491	22590	1.36	0.0E+00	6809918	NT	Homo sapiens low density lipoprotein-related protein 2 (LRP2) mRNA
4290	13492		2.48	0.0E+00	AI188844.1	EST_HUMAN	q123f06.x1 Soares_placenta_86c5weeks_2NbhP8tc9W Homo sapiens cDNA clone IMAGE:1724579 3' similar to contains MER20.b2 MER20 repetitive element;
4294	13495		4.58	0.0E+00	U14520.1	NT	Human CBFA3 (Cbfa3) gene, partial cds
4298	13498	22595	0.64	0.0E+00	5174574	NT	Homo sapiens myeloid/lymphoid or mixed-lineage leukemia (trithorax (Drosophila) homolog); translocated to, 4 (MLL T4) mRNA
4316	13517	22612	1.43	0.0E+00	6563384	NT	Homo sapiens protein kinase C, nu (PRKCN), mRNA
4316	13517	22613	1.43	0.0E+00	6563384	NT	Homo sapiens protein kinase C, nu (PRKCN), mRNA
4323	13524	22619	1.16	0.0E+00	U10991.1	NT	Human G2 protein mRNA, partial cds
4323	13524	22620	1.16	0.0E+00	U10991.1	NT	Human G2 protein mRNA, partial cds
4334	13535	22626	8.99	0.0E+00	6912281	NT	Homo sapiens COMPLEMENT COMPONENT C1q RECEPTOR (C1QR), mRNA
4354	13556		1.34	0.0E+00	AF153047.2	NT	Homo sapiens gap junction protein connexin-38 (Cx38) gene, complete cds
4364	13566	22681	4.84	0.0E+00	L14561.1	NT	Homo sapiens plasma membrane calcium ATPase isoform 1 (ATP2B1) gene, alternative splice products, partial cds
4368	13570	22686	6.52	0.0E+00	Z80780.1	NT	H.sapiens H2B/h gene
4368	13570	22687	6.52	0.0E+00	Z80780.1	NT	H.sapiens H2B/h gene

Page 361 of 382  
Table 4  
Single Exon Probes Expressed in HELA Cells

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4369	13571	22668	1.2	0.0E+00	AW168933.1	EST_HUMAN	xc68e10.x1 NCL CGAP_U4 Homo sapiens cDNA clone IMAGE:2633514 3' similar to TR:P97365 P97365
4375	13577	22674	1.54	0.0E+00	X60483.1	NT	ZINC FINGER PROTEIN 64 ;
4375	13577	22675	1.54	0.0E+00	X60483.1	NT	H. sapiens H4/d gene for H4 histone
4380	13581	22681	9.12	0.0E+00	7682091	NT	H. sapiens H4/d gene for H4 histone
4380	13581	22682	9.12	0.0E+00	7682091	NT	Homo sapiens KIAA0390 gene product (KIAA0390), mRNA
4388	13589	22691	1.03	0.0E+00	X82338.1	NT	Homo sapiens KIAA0390 gene product (KIAA0390), mRNA
4391	13592	22695	16.08	0.0E+00	4885126	NT	Homo sapiens Menkes disease gene, exon 4
4392	13593	22698	1.77	0.0E+00	AJ271736.1	NT	Homo sapiens caudal type homeo box transcription factor 4 (CDX4), mRNA
4393	13594	22702	0.99	0.0E+00	AL163207.2	NT	Homo sapiens Xq pseudautosomal region; segment 2/2
4396	13597	22698	4.78	0.0E+00	AB037781.1	NT	Homo sapiens chromosome 21 segment HS21C007
4424	13624	22719	1.16	0.0E+00	7019456	NT	Homo sapiens mRNA for KIAA1360 protein, partial cds
4435	13635	22733	8.37	0.0E+00	AF195953.1	NT	Homo sapiens myosin regulatory light chain interacting protein (MIR), mRNA
4442	13642	22733	26.88	0.0E+00	AJ248765.1	NT	Homo sapiens membrane-bound aminopeptidase P (XNPEP2) gene, complete cds
4442	13642	22734	26.88	0.0E+00	AJ248765.1	NT	Homo sapiens ACTN2 gene for alpha-Actinin 2, exon 10
4446	13645	22740	0.67	0.0E+00	W26179.1	EST_HUMAN	Homo sapiens ACTN2 gene for alpha-Actinin 2, exon 10
4446	13645	22741	0.67	0.0E+00	W26179.1	EST_HUMAN	24q7 Human retina cDNA randomly primed sublibrary Homo sapiens cDNA
4464	13662		2.27	0.0E+00	AF200628.1	NT	24q7 Human retina cDNA randomly primed sublibrary Homo sapiens cDNA
4487	13685		1.02	0.0E+00	M14123.1	NT	Homo sapiens HPS1 gene, intron 5
						NT	Human endogenous retrovirus HERV-K10
4488	13686	22778	0.72	0.0E+00	AA228128.1	EST_HUMAN	zr58c04.r1 Soares_NHMPu_S1 Homo sapiens cDNA clone IMAGE:667590 5' similar to TR:G222811
4488	13686	22777	0.72	0.0E+00	AA228128.1	EST_HUMAN	G222811 ALPHA 1 CHAIN OF TYPE XII COLLAGEN ;
						EST_HUMAN	zr58c04.r1 Soares_NHMPu_S1 Homo sapiens cDNA clone IMAGE:667590 5' similar to TR:G222811
						EST_HUMAN	G222811 ALPHA 1 CHAIN OF TYPE XII COLLAGEN ;
4504	13701	22795	13.33	0.0E+00	AW084984.1	EST_HUMAN	xc68e08.x1 NCL CGAP_Eso2 Homo sapiens cDNA clone IMAGE:2589446 3' similar to SW-AHNK_HUMAN
4506	14471		2.11	0.0E+00	8051619	NT	Q09666 NEUROBLAST DIFFERENTIATION ASSOCIATED PROTEIN AHNK ;
4510	13708		8.66	0.0E+00	AL163207.2	NT	Homo sapiens LIM domain kinase 2 (LIMK2), transcript variant 2a, mRNA
4512	13708	22801	3.69	0.0E+00	AW381570.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C007
4517	13713	22806	1.93	0.0E+00	AJ278120.1	NT	PM1-H70305-101199-002-403 HT0305 Homo sapiens cDNA
4517	13713	22807	1.93	0.0E+00	AJ278120.1	NT	Homo sapiens mRNA for putative ankyrin-repeat containing protein (ORF1)
4519	13715	22809	1.19	0.0E+00	4758487	NT	Homo sapiens mRNA for putative ankyrin-repeat containing protein (ORF1)
4520	13716	22810	1.72	0.0E+00	AF108830.1	NT	Homo sapiens G protein-coupled receptor 50 (GPR50) mRNA
4524	13720	22815	1.43	0.0E+00	Z66526.1	NT	Homo sapiens serine-threonine protein kinase (MNBH) mRNA, complete cds
4526	13724	22820	1.14	0.0E+00	AF111163.1	NT	H. sapiens pancreatic polypeptide receptor PP1 gene
						NT	Homo sapiens pyrin (MEFV) gene, complete cds

Page 362 of 382  
Table 4  
Single Exon Probes Expressed in HELA Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4528	13724	22821	1.14	0.0E+00	AF111163.1	NT	Homo sapiens pylin (MEFV) gene, complete cds
4536	14472	22829	4.41	0.0E+00	6005973	NT	Homo sapiens zinc finger protein 195 (ZNF195), mRNA
4541	13738	22834	7.2	0.0E+00	AF208161.1	NT	Homo sapiens synovial precursor, mRNA, complete cds
4546	13741	22841	1.23	0.0E+00	AF152337.1	NT	Homo sapiens protocadherin gamma C3 (PCDH-gamma-C3) mRNA, complete cds
4549	13744	22845	1.3	0.0E+00	5454175	NT	Homo sapiens zinc finger protein 211 (ZNF211), mRNA
4561	13755	22853	33.93	0.0E+00	4503470	NT	Homo sapiens eukaryotic translation elongation factor 1 alpha 1 (EEF1A1) mRNA
4568	13762	22858	16.96	0.0E+00	4505016	NT	Homo sapiens low density lipoprotein receptor-related protein 8 (LRP8) mRNA, and translated products
4572	13766	22861	1.1	0.0E+00	4503098	NT	Homo sapiens chondroitin sulfate proteoglycan 4 (melanoma-associated) (CSPG4), mRNA
4577	13771	22867	1.06	0.0E+00	4502556	NT	Homo sapiens calcium/calmodulin-dependent protein kinase IV (CAMK4) mRNA
4580	13774		1.11	0.0E+00	BE871908.1	EST_HUMAN	601447932F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3852127 5'
4583	13777		2.86	0.0E+00	L35485.1	NT	Homo sapiens iduronate sulphate sulphatase (IDS) gene, complete cds
4585	13779	22870	12.98	0.0E+00	7662091	NT	Homo sapiens KIAA0390 gene product (KIAA0390), mRNA
4585	13779	22871	12.86	0.0E+00	7662091	NT	Homo sapiens KIAA0390 gene product (KIAA0390), mRNA
4602	13796	22896	2.51	0.0E+00	AF143314.1	NT	Homo sapiens PTEN (PTEN) gene, exons 3 through 5
4605	13799	22899	11.6	0.0E+00	AJ245418.1	NT	Homo sapiens mRNA for G7c protein (G7c gene located in the class III region of the major histocompatibility complex)
4605	13799	22899	11.6	0.0E+00	AJ245418.1	NT	Homo sapiens mRNA for G7c protein (G7c gene located in the class III region of the major histocompatibility complex)
4607	13801	22891	0.73	0.0E+00	AB018338.1	NT	Homo sapiens mRNA for KIAA0795 protein, partial cds
4616	13808		0.64	0.0E+00	D87675.1	NT	Homo sapiens DNA for amyloid precursor protein, complete cds
4626	13820		1.54	0.0E+00	AA174072.1	EST_HUMAN	zp18g08.s1 Strategene fetal retina 937202 Homo sapiens cDNA clone IMAGE:609854 3'
4628	13822		1.75	0.0E+00	7657410	NT	Homo sapiens odz (odd Oz/ten-m, Drosophila) homolog 1 (ODZ1), mRNA
4630	13824		5.76	0.0E+00	AL163284.2	NT	Homo sapiens chromosome 21 segment HS21C084
4631	13825	22913	1.18	0.0E+00	H92741.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C100
4631	13825	22914	1.18	0.0E+00	H92741.1	EST_HUMAN	y92b01.s1 Soares_pineal_gland_N3HPG Homo sapiens cDNA clone IMAGE:231721 3'
4632	13826	22915	1.92	0.0E+00	AF184110.1	NT	y92b01.s1 Soares_pineal_gland_N3HPG Homo sapiens cDNA clone IMAGE:231721 3'
4633	13827	22916	5.71	0.0E+00	AL163300.2	NT	Homo sapiens cyclophilin-related protein (NKTTR) gene, complete cds
4634	13828		1.78	0.0E+00	AB037521.1	NT	Homo sapiens chromosome 21 segment HS21C100
4638	13832	22920	1.07	0.0E+00	AB007868.2	NT	Homo sapiens gene for natriuretic protein, partial cds
4643	13837	22926	36.33	0.0E+00	4557887	NT	Homo sapiens mRNA for KIAA0405 protein, partial cds
4643	13837	22927	36.33	0.0E+00	4557887	NT	Homo sapiens keratin 18 (KRT18) mRNA
4644	13838	22928	2.55	0.0E+00	AF167441.1	NT	Homo sapiens keratin 18 (KRT18) mRNA
4654	13848	22940	1.04	0.0E+00	L78810.1	NT	Mus musculus E-cadherin binding protein E7 mRNA, complete cds Homo sapiens ADP/ATP carrier protein (ANT-2) gene, complete cds

Page 363 of 382  
Table 4  
Single Exon Probes Expressed in HELA Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4654	13848	22941	1.04	0.0E+00	L78810.1	NT	Homo sapiens ADP/ATP carrier protein (ANT-2) gene, complete cds
4654	13848	22942	1.04	0.0E+00	L78810.1	NT	Homo sapiens ADP/ATP carrier protein (ANT-2) gene, complete cds
4655	13849	22943	1.88	0.0E+00	AB028970.1	NT	Homo sapiens mRNA for KIAA1047 protein, partial cds
4655	13849	22944	1.88	0.0E+00	AB028970.1	NT	Homo sapiens mRNA for KIAA1047 protein, partial cds
4655	13850	22954	7.88	0.0E+00	Y18890.1	NT	Human endogenous retrovirus type K (HERV-K), gag, pol and env genes
4658	13862	22963	2.3	0.0E+00	BE081527.1	EST_HUMAN	QV2-BT0635-160400-142-h05 BT0635 Homo sapiens cDNA
4659	13863	22964	1.23	0.0E+00	AA418246.1	EST_HUMAN	z66507.s1 Soares, NHMPU, S1 Homo sapiens cDNA clone IMAGE:767605 3'
4675	13869		2.11	0.0E+00	AF086641.1	NT	Homo sapiens truncated tenascin XB (TNXB) gene, partial cds and TNXA gene recombination breakpoint region
4683	13875	22975	1.02	0.0E+00	AL163278.2	NT	Homo sapiens chromosome 21 segment HS21C078
4683	13875	22976	1.02	0.0E+00	AL163278.2	NT	Homo sapiens chromosome 21 segment HS21C078
4684	13876	22977	2.48	0.0E+00	AB037820.1	NT	Homo sapiens mRNA for KIAA1399 protein, partial cds
4684	13876	22978	2.48	0.0E+00	AB037820.1	NT	Homo sapiens mRNA for KIAA1399 protein, partial cds
4685	13877	22979	2.47	0.0E+00	M74099.1	NT	Human displacement protein (CCAAT) mRNA
4687	13879	22981	1.63	0.0E+00	AW294800.1	EST_HUMAN	UI-H-B12-ah1-c-05-0-UI.s1 NCJ CGAP Sub4 Homo sapiens cDNA clone IMAGE:2726792 3'
4687	13879	22982	1.63	0.0E+00	AW294800.1	EST_HUMAN	UI-H-B12-ah1-c-05-0-UI.s1 NCJ CGAP Sub4 Homo sapiens cDNA clone IMAGE:2726792 3'
4689	13881	22983	2.61	0.0E+00	8453812	NT	Homo sapiens butyrophilin, subfamily 2, member A2 (BTN2A2), mRNA
4689	13881	22984	2.61	0.0E+00	8453812	NT	Homo sapiens butyrophilin, subfamily 2, member A2 (BTN2A2), mRNA
4690	9419	18553	0.78	0.0E+00	T56945.1	EST_HUMAN	Homo sapiens cDNA clone IMAGE:88310 5'
4690	9419	18554	0.78	0.0E+00	T56945.1	EST_HUMAN	Homo sapiens cDNA clone IMAGE:88310 5'
4693	13884	23016	1.01	0.0E+00	BE278730.1	EST_HUMAN	601158835F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3505521 5'
4724	13915	23016	12.07	0.0E+00	M80902.1	NT	Human AHNAK nucleoprotein mRNA, 5' end
4724	13915	23019	2.93	0.0E+00	M69197.1	NT	Human haptoglobin and haptoglobin-related protein (HP and HPR) genes, complete cds
4727	13918	23020	2.93	0.0E+00	M69197.1	NT	Human haptoglobin and haptoglobin-related protein (HP and HPR) genes, complete cds
4727	13918	23020	2.93	0.0E+00	M69197.1	NT	Human haptoglobin and haptoglobin-related protein (HP and HPR) genes, complete cds
4732	13923	23027	1.32	0.0E+00	AF184110.1	NT	Homo sapiens cyclophilin-related protein (NKTR) gene, complete cds
4733	13924	23028	0.61	0.0E+00	7662479	NT	Homo sapiens KIAA1084 protein (KIAA1084), mRNA
4735	13926	23029	1.65	0.0E+00	7662181	NT	Homo sapiens KIAA0563 gene product (KIAA0563), mRNA
4740	13931	23035	1.12	0.0E+00	U07563.1	NT	Human proto-oncogene tyrosine-protein kinase (ABL) gene, exon 1a and exons 2-10, complete cds
4745	13936	23040	0.99	0.0E+00	AL099857.1	NT	Novel human mRNA from chromosome 1, which has similarities to BAT2 genes
4753	13944	23060	0.95	0.0E+00	X58487.1	NT	Human CYP2D7AP pseudogene for cytochrome P450 2D6
4770	13959	23062	1.19	0.0E+00	AF026801.1	NT	Homo sapiens alpha-3 type IX collagen (COL9A3) gene, promoter region, and exons 1-26
4772	13961	23063	1.2	0.0E+00	6877700	NT	Homo sapiens G-protein coupled receptor (RE2), mRNA
4772	13961	23063	1.2	0.0E+00	6877700	NT	Homo sapiens G-protein coupled receptor (RE2), mRNA



Table 4

## Single Exon Probes Expressed in HELA Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4775	13984	23068	0.86	0.0E+00	7018320	NT	Homo sapiens proteinx0008 (AD013), mRNA
4775	13984	23067	0.86	0.0E+00	7018320	NT	Homo sapiens proteinx0008 (AD013), mRNA
4786	13985	23060	1.06	0.0E+00	AW444637.1	EST_HUMAN	UJH-BI3-qjw-c-04-0-UJ.s1 NCJ_CGAP_Sub5 Homo sapiens cDNA clone IMAGE:2733284 3'
4801	13990	23098	1.24	0.0E+00	AF303134.1	NT	Homo sapiens aldehyde dehydrogenase 12 (ALDH12) mRNA, complete cds
4804	13983		1.63	0.0E+00	AF083242.1	NT	Homo sapiens HSPC024-iso mRNA, complete cds
4853	14042	23135	0.67	0.0E+00	J00191.1	NT	Human MHC class I transplantation antigen (hla) gene
4853	14042	23136	0.67	0.0E+00	J00191.1	NT	Human MHC class I transplantation antigen (hla) gene
4860	14048		5.76	0.0E+00	AF240786.1	NT	Homo sapiens glutathione S-transferase theta 2 (GSTT2) and glutathione S-transferase theta 1 (GSTT1) genes, complete cds
4862	14050	23144	1.87	0.0E+00	X87205.1	NT	M.fascicularis mRNA for metalloproteinase-like, disintegrin-like protein, IVa
4864	14052	23146	2.5	0.0E+00	AF084478.1	NT	Homo sapiens Williams-Buren syndrome deletion transcript 9 (WBSR9) mRNA, complete cds
4865	14053	23147	1.79	0.0E+00	AF067416.1	NT	Mus musculus zinc finger transcription factor Kaiso mRNA, complete cds
4866	14054	23148	5.28	0.0E+00	4503768	NT	Homo sapiens fragile X mental retardation 2 (FMR2) mRNA
4868	14056	23150	17.49	0.0E+00	4885048	NT	Homo sapiens actin, alpha, cardiac muscle (ACTC), mRNA
4869	14057	23151	1.01	0.0E+00	P52740	SWISSPROT	ZINC FINGER PROTEIN 132
4871	14059	23153	1.92	0.0E+00	8922180	NT	Homo sapiens hypothetical protein DKFZp782E1312 (DKFZp782E1312), mRNA
4874	14062	23157	5.79	0.0E+00	8923080	NT	Homo sapiens hypothetical protein FLJ20073 (FLJ20073), mRNA
4878	14066	23161	1.05	0.0E+00	7661979	NT	Homo sapiens KIAA0187 gene product (KIAA0187), mRNA
4879	14067	23162	1.61	0.0E+00	M94081.1	NT	Human Tcr-C-delta gene, exons 1-4; Tcr-V-delta gene, exons 1-2; T-cell receptor alpha (Tcr-alpha) gene, J1-segments; and Tcr-C-alpha gene, exons 1-4
4879	14067	23163	1.61	0.0E+00	M94081.1	NT	Human Tcr-C-delta gene, exons 1-4; Tcr-V-delta gene, exons 1-2; T-cell receptor alpha (Tcr-alpha) gene, J1-segments; and Tcr-C-alpha gene, exons 1-4
4881	14069	23165	1.73	0.0E+00	X94628.1	NT	H.sapiens MeCP-2 gene
4881	14069	23166	1.73	0.0E+00	X94628.1	NT	H.sapiens MeCP-2 gene
4884	14072	23169	3.1	0.0E+00	AL163280.2	NT	Homo sapiens chromosome 21 segment HS21C080
4895	14083	23176	1.21	0.0E+00	5032150	NT	Homo sapiens TATA box binding protein (TBP)-associated factor, RNA polymerase II, 1, 28KD (TAF21)
4905	14093	23186	1.59	0.0E+00	6806918	NT	Homo sapiens low density lipoprotein-related protein 2 (LRP2), mRNA
4907	14095	23188	3.28	0.0E+00	X92841.1	NT	H.sapiens MICA gene
4909	14097	23180	2.44	0.0E+00	4585642	NT	Homo sapiens zinc finger protein (KIAA0412) mRNA
4910	14098	23191	0.64	0.0E+00	AB037864.1	NT	Homo sapiens mRNA for KIAA1443 protein, partial cds
4911	14099	23192	1.88	0.0E+00	AB014533.1	NT	Homo sapiens mRNA for KIAA0633 protein, partial cds
4912	14100	23193	2.45	0.0E+00	6677648	NT	Mus musculus zinc finger protein interacting with K protein 1 (Zik1): mRNA
4913	14101	23194	1.89	0.0E+00	5174560	NT	Homo sapiens meningioma expressed antigen 6 (colled-coil proline-rich) (MGEA6), mRNA

Page 365 of 382  
Table 4  
Single Exon Probes Expressed in HELA Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4815	14103	23198	6.44	0.0E+00	4758199	NT	Homo sapiens desmoplakin (DPI, DPII) (DSP) mRNA
4817	14105	23198	1.31	0.0E+00	5174560	NT	Homo sapiens meningioma expressed antigen 6 (coiled-coil proline-rich) (MGEA6), mRNA
4917	14105	23199	1.31	0.0E+00	5174560	NT	Homo sapiens meningioma expressed antigen 6 (coiled-coil proline-rich) (MGEA6), mRNA
4921	14109	23205	33.09	0.0E+00	AF05068.1	NT	Homo sapiens MHC class 1 region
4923	14111		3.19	0.0E+00	4505508	NT	Homo sapiens opioid receptor, delta 1 (OPRD1) mRNA
4924	14112	23208	3.02	0.0E+00	AF091711.1	NT	Homo sapiens splice variant AKAP350 mRNA, partial cds
4936	14123	23218	3.83	0.0E+00	4503884	NT	Homo sapiens farnesyl diphosphate synthase (farnesyl pyrophosphate synthetase, dimethylallyltransferase, geranyltransferase) (FDFS) mRNA
4938	14125	23220	8.87	0.0E+00	4557472	NT	Homo sapiens chloride channel 5 (nephrolithiasis 2, X-linked, Dent disease) (CLCN5) mRNA
4938	14125	23221	8.87	0.0E+00	4557472	NT	Homo sapiens chloride channel 5 (nephrolithiasis 2, X-linked, Dent disease) (CLCN5) mRNA
4946	14133		0.82	0.0E+00	AI281129.1	EST_HUMAN	q11605.x1 NCL CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1881921 3' similar to TR:Q61632 Q61632
4972	14159	23250	1.26	0.0E+00	AL163284.2	NT	EN-2/LACZ FUSION PROTEIN ;
4981	14168	23258	1.19	0.0E+00	AW452726.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C084
4989	14176	23267	0.98	0.0E+00	4502398	NT	UI-H-B13-ahv-f-02-Q-UJ.s1 NCL CGAP_Sub5 Homo sapiens cDNA clone IMAGE:3068691 3'
4992	14179		10.64	0.0E+00	U14967.1	NT	Homo sapiens beaded filament structural protein 1, filensin (BFSF1) mRNA
5003	14180	23280	1.06	0.0E+00	M10978.1	NT	Human ribosomal protein L21 mRNA, complete cds
5005	14192		3.04	0.0E+00	BE408803.1	EST_HUMAN	Human endogenous retroviral DNA (4-1), complete retroviral segment
5009	14198	23285	5.9	0.0E+00	4758199	NT	601303729F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3638118 5'
5016	14202	23289	1.97	0.0E+00	7662401	NT	Homo sapiens desmoplakin (DPI, DPII) (DSP) mRNA
5019	14206	23291	2.07	0.0E+00	AB028968.1	NT	Homo sapiens KIAA0952 protein (KIAA0952), mRNA
5032	14217	23301	2.25	0.0E+00	8923441	NT	Homo sapiens mRNA for KIAA1043 protein, partial cds
5032	14217	23302	2.25	0.0E+00	8923441	NT	Homo sapiens hypothetical protein FLJ20477 (FLJ20477), mRNA
5046	14229	23311	0.76	0.0E+00	AA601246.1	EST_HUMAN	Homo sapiens hypothetical protein FLJ20477 (FLJ20477), mRNA
5046	14229	23312	0.76	0.0E+00	AA601246.1	EST_HUMAN	no14g09.s1 NCL CGAP_Phe1 Homo sapiens cDNA clone IMAGE:1100704 3' similar to TR:E239140
5048	14229	23313	0.76	0.0E+00	AA601246.1	EST_HUMAN	E239140 SPALT PROTEIN ;
5049	14231	23315	1.68	0.0E+00	AF161463.1	NT	no14g09.s1 NCL CGAP_Phe1 Homo sapiens cDNA clone IMAGE:1100704 3' similar to TR:E239140
5049	14231	23316	1.68	0.0E+00	AF161463.1	NT	Homo sapiens HSPC114 mRNA, complete cds
						NT	Homo sapiens HSPC114 mRNA, complete cds
5051	14233	23318	3.31	0.0E+00	U82871.2	NT	Homo sapiens chromosome Xq28 melanoma antigen family A2a (MAGEA2A), melanoma antigen family A12 (MAGEA12), melanoma antigen family A2b (MAGEA2B), melanoma antigen family A3 (MAGEA3), caltactin (CALT), NAD(P)H dehydrogenase-like protein (NSDHL), and LI>

Page 366 of 382  
Table 4  
Single Exon Probes Expressed in HELA Cells

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5051	14233	23310	3.31	0.0E+00	U82671.2	NT	Homo sapiens chromosome Xq28 melanoma antigen family A2a (MAGEA2A), melanoma antigen family A12 (MAGEA12), melanoma antigen family A2b (MAGEA2B), melanoma antigen family A3 (MAGEA3), caltractin (CALT), NAD(P)H dehydrogenase-like protein (NSDHL), and LI>
5057	9496	18630	0.61	0.0E+00	AF196658.1	NT	Homo sapiens DNA mismatch repair protein (MLH3) gene, complete cds
5059	14239		1.1	0.0E+00	AL050253.1	NT	Human sapiens mRNA similar to D29763 mouse mRNA for seizure-related gene product 6. Shares domains with BMPs, Tollid, Sushi repeat proteins
5081	14241		1.06	0.0E+00	4758225	NT	Homo sapiens E2F transcription factor 2 (E2F2) mRNA
5073	14253	23336	1.24	0.0E+00	AF016705.1	NT	Homo sapiens E6-AP ubiquitin-protein ligase (UBE3A) gene, exon 3
5076	14256	23339	0.85	0.0E+00	U53588.1	NT	Homo sapiens MHC class 1 region
5087	14267		1.48	0.0E+00	AL163209.2	NT	Homo sapiens chromosome 21 segment HS21C009
5089	14269		33.47	0.0E+00	D50857.1	NT	Homo sapiens gamma-cytoplasmic actin (ACTGP3) pseudogene
5097	14277	23361	1.02	0.0E+00	AF207880.1	NT	Mus musculus teashirt 2 (Tsh2) gene, partial cds
5115	14295	23383	2.97	0.0E+00	X52388.1	NT	Bacillus amyloliquefaciens sacB gene for levansucrase (EC 2.4.1.10)
5116	14296	23384	0.68	0.0E+00	X72791.1	NT	Human endogenous retrovirus mRNA for gag protein
5128	14307	23398	0.69	0.0E+00	AF272663.1	NT	Homo sapiens gephyrin mRNA, complete cds
5133	14311	23402	0.89	0.0E+00	AF240835.1	NT	Homo sapiens vascular endothelial cadherin 2 mRNA, complete cds
5133	14311	23403	0.99	0.0E+00	AF240835.1	NT	Homo sapiens vascular endothelial cadherin 2 mRNA, complete cds
5134	14312	23404	1.22	0.0E+00	5454153	NT	Homo sapiens cyclophilin (USA-CYP) mRNA
5138	14316	23407	0.95	0.0E+00	AA683268.1	EST_HUMAN	aa62804.61 Strabagene schizo brain S11 Homo sapiens cDNA clone IMAGE:1020367 3'
5146	14325	23416	2.49	0.0E+00	11421001	NT	Homo sapiens HEF like Protein (HEFL), mRNA
5156	14335	23425	1.75	0.0E+00	Y12477.1	NT	Homo sapiens putative GPR37 gene, exon 2
5156	14335	23426	1.75	0.0E+00	Y12477.1	NT	Homo sapiens putative GPR37 gene, exon 2
5159	14338	23427	1.23	0.0E+00	Y08032.1	NT	Human endogenous retrovirus-K, LTR U5 and gag gene
5172	14351	23439	0.85	0.0E+00	5902091	NT	Homo sapiens solute carrier family 5 (hospital transporters), member 3 (SLC5A3), mRNA
5174	14352	23440	1.5	0.0E+00	AF124250.1	NT	Homo sapiens SH2-containing protein Nsp2 mRNA, complete cds
5187	14363	23450	0.63	0.0E+00	7708245	NT	Homo sapiens 4F2 light chain (LOC51597), mRNA
5187	14363	23451	0.63	0.0E+00	7708245	NT	Homo sapiens 4F2 light chain (LOC51597), mRNA
5188	14364	23452	1.06	0.0E+00	7662421	NT	Homo sapiens KIAA0971 protein (KIAA0971), mRNA
5189	14365	23453	0.98	0.0E+00	4828795	NT	Homo sapiens potassium voltage-gated channel, Isk-related family, member 2 (KCNE2) mRNA
5198	14374	23461	2.03	0.0E+00	U26555.1	NT	Human versican V2 core protein precursor splice-variant mRNA, complete cds
5202	14377	23464	0.94	0.0E+00	U71601.1	NT	Human zinc finger protein zfp47 (zfp47) mRNA, partial cds
5210	14385	23470	1.18	0.0E+00	4757889	NT	Homo sapiens chromosome 8 open reading frame 1 (C8ORF1) mRNA
5211	14386	23471	1.16	0.0E+00	AF196658.1	NT	Homo sapiens DNA mismatch repair protein (MLH3) gene, complete cds
5216	14473	23476	1.05	0.0E+00	AF167336.1	NT	Homo sapiens interleukin 1 receptor accessory protein (IL1RAP) gene, exon 4

Page 367 of 382  
Table 4  
Single Exon Probes Expressed in HELA Cells

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5219	14393	23476	0.75	0.0E+00	AF231922.1	NT	Homo sapiens chromosome 21 unknown mRNA
5220	14394	23479	1.22	0.0E+00	4826777	NT	Homo sapiens jumonji (mouse) homolog (JMU) mRNA
5230	14404	23487	1.66	0.0E+00	7657203	NT	Homo sapiens acidic 82 kDa protein mRNA (HSU15552), mRNA
5238	14412		1.31	0.0E+00	AB040946.1	NT	Homo sapiens mRNA for KIAA1513 protein, partial cds
5276	14448	23521	1.26	0.0E+00	7662108	NT	Homo sapiens KIAA0426 gene product (KIAA0426), mRNA
5280	14451		1.98	0.0E+00	AL163285.2	NT	Homo sapiens chromosome 21 segment HS21C085
5282	14453	23523	1.82	0.0E+00	4503764	NT	Homo sapiens flavin containing monooxygenase 1 (FMO1) mRNA
5287	14458	23526	23.87	0.0E+00	7662177	NT	Homo sapiens KIAA0555 gene product (KIAA0555), mRNA
5287	14458	23527	23.87	0.0E+00	7662177	NT	Homo sapiens KIAA0555 gene product (KIAA0555), mRNA
5298	14485		3.15	0.0E+00	AF063083.1	NT	Homo sapiens aconitase (ACO2) gene, nuclear gene encoding mitochondrial protein, exon 15
5302	14534	23537	2.19	0.0E+00	AF137286.1	NT	Homo sapiens keratin 12 (KRT12) gene, complete cds
5302	14534	23538	2.19	0.0E+00	AF137286.1	NT	Homo sapiens keratin 12 (KRT12) gene, complete cds
5313	14545	23614	1.76	0.0E+00	9256579	NT	Homo sapiens protodactherin alpha 13 (PCDHA13), mRNA
5321	14553	23623	3.91	0.0E+00	BE831080.1	EST_HUMAN	RC3-GN0076-310800-013-503 GN0076 Homo sapiens cDNA
5325	14557	23627	3.45	0.0E+00	AF182034.1	NT	Homo sapiens polycystic kidney disease-like 2 protein (PKDL2) mRNA, complete cds
5325	14557	23628	3.45	0.0E+00	AF182034.1	NT	Homo sapiens polycystic kidney disease-like 2 protein (PKDL2) mRNA, complete cds
5331	14562	23635	1.86	0.0E+00	X56183.1	NT	H. sapiens immunoglobulin heavy chain gene, variable region
5331	14562	23636	1.86	0.0E+00	X56183.1	NT	H. sapiens immunoglobulin heavy chain gene, variable region
5388	14617	23730	6.44	0.0E+00	BE575498.1	EST_HUMAN	7110008.x1 NCI_CGAP_CLL1 Homo sapiens cDNA clone IMAGE:3294250 3'
5389	14618	23731	1.72	0.0E+00	BE220753.1	EST_HUMAN	H99a02.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3165104 3' similar to SW:Y054_HUMAN
5390	14619	23732	1.68	0.0E+00	BE784412.1	EST_HUMAN	P42694 HYPOTHETICAL PROTEIN KIAA0084.
5390	14619	23733	1.68	0.0E+00	BE784412.1	EST_HUMAN	601589422F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3943804 5'
5392	14621	23735	5.3	0.0E+00	M29808.1	NT	601589422F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3943804 5'
5394	14623	23736	3.48	0.0E+00	A1791363.1	EST_HUMAN	Homo sapiens eosinophil peroxidase (EPP) gene, exon 7
5398	18053	23740	4.35	0.0E+00	11421038	NT	ch68a09.j6 NCI_CGAP_K145 Homo sapiens cDNA clone IMAGE:1472152 5' similar to gb:M18512.IG
5402	14630		2.86	0.0E+00	BF665962.1	EST_HUMAN	HEAVY CHAIN PRECURSOR V.I REGION (HUMAN);
5410	14638	23766	2.1	0.0E+00	BF526328.1	EST_HUMAN	Homo sapiens Sp4 transcription factor (SP4), mRNA
5410	14638	23767	2.1	0.0E+00	BF526328.1	EST_HUMAN	602118928F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4276254 5'
5421	15224	24643	2.57	0.0E+00	4557384	NT	602071372F1 NCI_CGAP_Bn64 Homo sapiens cDNA clone IMAGE:4214272 5'
5425	14652	23788	4.72	0.0E+00	AF257737.1	NT	602071372F1 NCI_CGAP_Bn64 Homo sapiens cDNA clone IMAGE:4214272 5'
5425	14652	23789	4.72	0.0E+00	AF257737.1	NT	Homo sapiens Bloom syndrome (BLM) mRNA
5436	14693	23810	1.92	0.0E+00	11420819	NT	Homo sapiens ciliary dynein heavy chain 9 (DNAH9) mRNA, complete cds
							Homo sapiens ciliary dynein heavy chain 9 (DNAH9) mRNA, complete cds
							Homo sapiens olfactory receptor, family 2, subfamily F, member 1 (OR2F1), mRNA

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Single Exon Probes Expressed in HELA Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5447	14673	23832	3.27	0.0E+00	BF529831.1	EST_HUMAN	602042322F1 NCI_CGAP_Bm67 Homo sapiens cDNA clone IMAGE:4179888 5'
5447	14673	23833	3.27	0.0E+00	BF529831.1	EST_HUMAN	602042322F1 NCI_CGAP_Bm67 Homo sapiens cDNA clone IMAGE:4179888 5'
5450	14676	23835	2.69	0.0E+00	BF313139.1	EST_HUMAN	601897658F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4128815 5'
5457	14683	24033	4.38	0.0E+00	11434382	NT	Homo sapiens calcium channel, voltage-dependent, alpha 1G subunit (CACNA1G), mRNA
5476	14703		3.14	0.0E+00	AW667316.1	EST_HUMAN	MRO-SN0037-030400-001-h07 SN0037 Homo sapiens cDNA
5485	14711	24067	1.95	0.0E+00	BE292889.1	EST_HUMAN	601105291F1 NIH_MGC_15 Homo sapiens cDNA clone IMAGE:2887903 5'
5485	14711	24068	1.95	0.0E+00	BE292889.1	EST_HUMAN	601105291F1 NIH_MGC_15 Homo sapiens cDNA clone IMAGE:2887903 5'
5495	14721	24078	1.84	0.0E+00	11420819	NT	Homo sapiens olfactory receptor, family 2, subfamily F, member 1 (OR2F1), mRNA
5495	14721	24079	1.84	0.0E+00	11420819	NT	Homo sapiens olfactory receptor, family 2, subfamily F, member 1 (OR2F1), mRNA
5498	14725	24084	4.29	0.0E+00	AF064254.1	NT	Homo sapiens very long-chain acyl-CoA synthetase homolog 1 mRNA, complete cds
5498	14725	24085	4.29	0.0E+00	AF064254.1	NT	Homo sapiens very long-chain acyl-CoA synthetase homolog 1 mRNA, complete cds
5502	14728	24089	3.04	0.0E+00	AJ224639.1	NT	Homo sapiens Surf-5 and Surf-6 genes
5502	14728	24090	3.04	0.0E+00	AJ224639.1	NT	Homo sapiens Surf-5 and Surf-6 genes
5513	14738	24103	7.42	0.0E+00	M85719.1	EST_HUMAN	EST02238 Fetal brain, Striatum (cat#363206) Homo sapiens cDNA clone HFBGM48
5518	14743	24110	5.68	0.0E+00	AW405472.1	EST_HUMAN	U1-HF-BLO-adj-d-02-Q-U11 NIH_MGC_37 Homo sapiens cDNA clone IMAGE:3081658 5'
5530	14754	24121	2.09	0.0E+00	AW361877.1	EST_HUMAN	PM3-CT0263-091299-007-h05 CT0263 Homo sapiens cDNA
5530	14754	24122	2.09	0.0E+00	AW361877.1	EST_HUMAN	PM3-CT0263-091299-007-h05 CT0263 Homo sapiens cDNA
5530	14754	24123	2.09	0.0E+00	AW361877.1	EST_HUMAN	PM3-CT0263-091299-007-h05 CT0263 Homo sapiens cDNA
5531	14755	24124	2.03	0.0E+00	U36281.1	NT	Human beta-prime-adaptin (BAM22) gene, exon 13
5565	14790	24161	1.72	0.0E+00	AJ006345.1	NT	Homo sapiens KVLQ1 gene
5565	14790	24162	1.72	0.0E+00	AJ006345.1	NT	Homo sapiens KVLQ1 gene
5575	14798	24172	5.12	0.0E+00	11416801	NT	Homo sapiens protocadherin beta 2 (PCDHB2), mRNA
5580	14804	24177	7.34	0.0E+00	BE560082.1	EST_HUMAN	601345141F1 NIH_MGC_8 Homo sapiens cDNA clone IMAGE:3677843 5'
5581	14805	24178	3.29	0.0E+00	U86981.1	NT	Human L-type calcium channel beta-1 subunit (CACNLB1) gene, exon 13B and isoform beta-1B, complete cds
5581	14805	24179	3.29	0.0E+00	U86981.1	NT	Human L-type calcium channel beta-1 subunit (CACNLB1) gene, exon 13B and isoform beta-1B, complete cds
5588	14812	24186	1.99	0.0E+00	BF338833.1	EST_HUMAN	602038272F1 NCI_CGAP_Bm64 Homo sapiens cDNA clone IMAGE:4184321 5'
5590	14814	24188	3.15	0.0E+00	BE273983.1	EST_HUMAN	601104462F1 NIH_MGC_14 Homo sapiens cDNA clone IMAGE:3347463 5'
5596	14820	24197	2.21	0.0E+00	BF569905.1	EST_HUMAN	602185852F1 NIH_MGC_45 Homo sapiens cDNA clone IMAGE:4310076 5'
5615	14838	24218	2.14	0.0E+00	AF217289.1	NT	Homo sapiens cadherin 20 (CDH20) mRNA, complete cds
5616	14839	24217	2.44	0.0E+00	BE828144.1	EST_HUMAN	RC5-ET0027-210600-022-G10 ET0027 Homo sapiens cDNA
5619	14842	24220	2.87	0.0E+00	BE958636.1	EST_HUMAN	601645287F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:3930453 5'
5640	14864		2.25	0.0E+00	AF012618.1	NT	Homo sapiens familial mental retardation protein 2 (FMR2) gene, exon 14

Page 369 of 382  
Table 4  
Single Exon Probes Expressed in HELA Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5642	14866	24249	3.34	0.0E+00	BE280197.1	EST_HUMAN	601158515F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3505323 5'
5645	14868	24253	2.69	0.0E+00	BE889810.1	EST_HUMAN	601512630F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3914238 5'
5663	18061	24275	10.36	0.0E+00	97899886	NT	Homo sapiens potassium voltage-gated channel, Shal-related subfamily, member 2 (KCND2), mRNA
5679	14899	24282	9.4	0.0E+00	U34825.1	NT	Human T cell surface glycoprotein CD-6 mRNA, complete cds
5679	14899	24283	9.4	0.0E+00	U34825.1	NT	Human T cell surface glycoprotein CD-6 mRNA, complete cds
5725	14943	24339	1.66	0.0E+00	BE378007.1	EST_HUMAN	601238276F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3608490 5'
5736	14955	24354	3.41	0.0E+00	U45982.1	NT	Human G protein-coupled receptor GPR-9-6 gene, complete cds
5748	14967	24368	4.14	0.0E+00	AA204740.1	EST_HUMAN	2qB1d03.r1 Stratiogene hNT neuron (#937233) Homo sapiens cDNA clone IMAGE:649005 5' similar to TR:G854195 G854195 LEUKOCYTE SURFACE PROTEIN ;
5749	14968	24367	3.86	0.0E+00	11545913	NT	Homo sapiens xylosyltransferase II (XT2), mRNA
5749	14968	24368	3.86	0.0E+00	11545913	NT	Homo sapiens xylosyltransferase II (XT2), mRNA
5763	14982	24381	4.66	0.0E+00	BE257173.1	EST_HUMAN	601109532F1 NIH_MGC_18 Homo sapiens cDNA clone IMAGE:3350822 5'
5779	14997	24399	1.73	0.0E+00	11435630	NT	Homo sapiens peptide transporter 3 (LOC51286), mRNA
5806	15023		8.8	0.0E+00	AV650020.1	EST_HUMAN	AV650020 GLC Homo sapiens cDNA clone GLCCAD09 3'
5810	15027	24428	3.35	0.0E+00	AW575598.1	EST_HUMAN	UI-HF-BLD-acc-g-12-Q-U1.s1 NIH_MGC_37 Homo sapiens cDNA clone IMAGE:3058751 3'
5812	15029	24430	3.9	0.0E+00	H01255.1	EST_HUMAN	y27b03.r1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:149933 5'
5817	15034	24435	1.7	0.0E+00	X15377.1	NT	Human gene for the light and heavy chains of myeloperoxidase
5821	15038	24438	4.44	0.0E+00	BE735989.1	EST_HUMAN	601305388F1 NIH_MGC_39 Homo sapiens cDNA clone IMAGE:3638618 5'
5821	15038	24440	4.44	0.0E+00	BE735989.1	EST_HUMAN	601305388F1 NIH_MGC_39 Homo sapiens cDNA clone IMAGE:3638618 5'
5823	15040	24442	23.06	0.0E+00	AU119245.1	EST_HUMAN	AU119245 HEMBA1 Homo sapiens cDNA clone HEMBA1005360 5'
5823	15040	24443	23.06	0.0E+00	AU119245.1	EST_HUMAN	AU119245 HEMBA1 Homo sapiens cDNA clone HEMBA1005360 5'
5831	15048	24452	4.25	0.0E+00	BE283153.1	EST_HUMAN	601105344F1 NIH_MGC_15 Homo sapiens cDNA clone IMAGE:2987863 5'
5831	15048	24453	4.25	0.0E+00	BE283153.1	EST_HUMAN	601105344F1 NIH_MGC_15 Homo sapiens cDNA clone IMAGE:2987863 5'
5887	15104	24515	2.57	0.0E+00	AF190860.1	NT	Homo sapiens low voltage-activated T-type calcium channel alpha 1G splice variant CavT.1a (CACNA1G) mRNA, complete cds
5893	15110	24521	3.97	0.0E+00	AW163640.1	EST_HUMAN	au86108.y1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2784159 5' similar to TR:O15390 O15390 GT24.[3] TR:O43840 TR:O43206 ;
5893	15110	24522	3.97	0.0E+00	AW163640.1	EST_HUMAN	au86108.y1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2784159 5' similar to TR:O15390 O15390 GT24.[3] TR:O43840 TR:O43206 ;
5908	15123	24532	5.08	0.0E+00	BE799873.1	EST_HUMAN	601587561F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3941847 5'
5908	15125	24533	7.6	0.0E+00	BE889813.1	EST_HUMAN	601512058F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3913311 5'
5908	15125	24534	7.6	0.0E+00	BE889813.1	EST_HUMAN	601512058F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3913311 5'
5914	15131	24540	4.33	0.0E+00	L24483.1	NT	Human antigen CD27 gene, exons 1-2



Page 371 of 382  
Table 4  
Single Exon Probes Expressed in HELA Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6098	15298	24730	5.25	0.0E+00	BF306996.1	EST_HUMAN	601889823F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4123948 5'
6101	15301	24733	2.33	0.0E+00	U41302.1	NT	Human chromosome 10 creatine transporter (SLC6A8) and (CDM) paralogous genes, complete cds
6137	15321	24756	2.26	0.0E+00	AU133213.1	EST_HUMAN	AU133213 NT2RP4 Homo sapiens cDNA clone NT2RP4001556 5'
6150	15334		2.53	0.0E+00	AU143706.1	EST_HUMAN	AU143706 Y79AA1 Homo sapiens cDNA clone Y79AA1002365 5'
6165	14534	23537	2.38	0.0E+00	AF137286.1	NT	Homo sapiens keratin 12 (KRT12) gene, complete cds
6165	14534	23538	2.38	0.0E+00	AF137286.1	NT	Homo sapiens keratin 12 (KRT12) gene, complete cds
6174	15356	24784	4.35	0.0E+00	11436689	NT	Homo sapiens vitamin D (1,25-dihydroxyvitamin D3) receptor (VDR), mRNA
6174	15356	24795	4.35	0.0E+00	11436689	NT	Homo sapiens vitamin D (1,25-dihydroxyvitamin D3) receptor (VDR), mRNA
							similar to SW:ARSD_HUMAN P61689 ARYL SULFATASE D PRECURSOR ; contains element HGR
6188	15370	24810	34.37	0.0E+00	A1128344.1	EST_HUMAN	repetitive element ;
							qc37a07.x1 Soares_placenta_8to9weeks_2NBHP8b9W Homo sapiens cDNA clone IMAGE:1714644 3'
							similar to SW:ARSD_HUMAN P61689 ARYL SULFATASE D PRECURSOR ; contains element HGR
6188	15370	24811	34.37	0.0E+00	A1128344.1	EST_HUMAN	repetitive element ;
6180	15372	24813	4.12	0.0E+00	11426392	NT	Homo sapiens myosin, heavy polypeptide 8, skeletal muscle, perinatal (MYH8), mRNA
6180	15372	24814	4.12	0.0E+00	11426392	NT	Homo sapiens myosin, heavy polypeptide 8, skeletal muscle, perinatal (MYH8), mRNA
6192	15374		14	0.0E+00	BF337376.1	EST_HUMAN	602035089F1 NCI_CGAP_Brm64 Homo sapiens cDNA clone IMAGE:4182839 5'
6194	15376	24816	2.36	0.0E+00	AA128453.1	EST_HUMAN	zr60f09.r1 Stratagene muscle 637209 Homo sapiens cDNA clone IMAGE:562601 5' similar to TR:G806562
6213	15394		2.23	0.0E+00	AU118607.1	EST_HUMAN	G808562 NEBULIN ;
6214	15395	24838	1.95	0.0E+00	AF005213.1	NT	AU118607 HEMBA1 Homo sapiens cDNA clone HEMBA1003969 5'
6214	15395	24839	1.95	0.0E+00	AF005213.1	NT	Homo sapiens ankyrin 1 (ANK1) mRNA, complete cds
6223	15404	24845	7.18	0.0E+00	X70172.1	NT	Homo sapiens ankyrin 1 (ANK1) mRNA, complete cds
6225	15406	24847	9.65	0.0E+00	U45448.1	NT	H. sapiens DNA for ZNGP2 pseudogene, exon 4
6225	15406	24848	9.65	0.0E+00	U45448.1	NT	Human P2x1 receptor mRNA, complete cds
6231	15412	24863	2.5	0.0E+00	AW050516.1	EST_HUMAN	Human P2x1 receptor mRNA, complete cds
6260	15441	24880	2.71	0.0E+00	AW239326.1	EST_HUMAN	EST362586 MAGE resequences, MAGE Homo sapiens cDNA
6270	15450	24889	4.1	0.0E+00	11427135	NT	xb39a05.y1 NCI_CGAP_Lu31 Homo sapiens cDNA clone IMAGE:2578640 5' similar to TR:Q08050 Q08050
6281	15461	24903	2.21	0.0E+00	AW405627.1	EST_HUMAN	HNFB3FH TRANSCRIPTION FACTOR GENESIS ;
							Homo sapiens glucagon-like peptide 2 receptor (GLP2R), mRNA
							UI-HF-BL0-abs-d-07-0-UI.r1 NIH_MGC_37 Homo sapiens cDNA clone IMAGE:3057469 5'
6317	15487	24941	4.45	0.0E+00	A1752561.1	EST_HUMAN	cn17d05.x1 Normal Human Trabecular Bone Cells Homo sapiens cDNA clone NHTBC_cn17d05 random



Page 372 of 382  
Table 4  
Single Exon Probes Expressed in HELA Cells

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6317	15487	24942	4.45	0.0E+00	AI752561.1	EST_HUMAN	cn17d05.x1 Normal Human Trabecular Bone Cells Homo sapiens cDNA clone NHTBC_cn17d05 random
6374	15554	25011	2.06	0.0E+00	6912735	NT	Homo sapiens transient receptor potential channel 5 (TRPC5), mRNA
6377	15557	25013	5.62	0.0E+00	BF217905.1	EST_HUMAN	601885465F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4103729 5'
6381	15561	25017	3.89	0.0E+00	AU128622.1	EST_HUMAN	AU128622 NT2RP2 Homo sapiens cDNA clone NT2RP2005913 5'
6392	15572	25028	6.75	0.0E+00	4501848	NT	Homo sapiens ATP-binding cassette, sub-family A (ABC1), member 3 (ABCA3), mRNA
6395	15575	25030	5.9	0.0E+00	BE739870.1	EST_HUMAN	601593156F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3947385 5'
6395	15575	25031	5.9	0.0E+00	BE739870.1	EST_HUMAN	601593156F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3947385 5'
6407	15588	25047	2.02	0.0E+00	BE787610.1	EST_HUMAN	601481713F1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3884258 5'
6407	15588	25048	2.02	0.0E+00	BE787610.1	EST_HUMAN	601481713F1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3884258 5'
6449	15646	25114	3.8	0.0E+00	BE736046.1	EST_HUMAN	601305658F1 NIH_MGC_39 Homo sapiens cDNA clone IMAGE:3839903 5'
6457	15654	25123	3.92	0.0E+00	M34872.1	NT	Human amyloid-beta protein (APP) gene, exon 11
6457	15654	25124	3.92	0.0E+00	M34872.1	NT	Human amyloid-beta protein (APP) gene, exon 11
6468	15665	25136	2.95	0.0E+00	AA397551.1	EST_HUMAN	z81b04.11 Striatum schizo brain S11 Homo sapiens cDNA clone IMAGE:728719 5' similar to TR:G300482
6471	15668	25137	6.84	0.0E+00	AU142402.1	EST_HUMAN	G300482 POL=REVERSE TRANSCRIPTASE HOMOLOG [RETROVIRAL ELEMENT];
6479	15678	25171	7.06	0.0E+00	BF673096.1	EST_HUMAN	AU142402 Y78AA1 Homo sapiens cDNA clone IMAGE:4294128 5'
6510	15706	25171	3.93	0.0E+00	AW500549.1	EST_HUMAN	602153008F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:3077496 5'
6514	15710	25174	12.31	0.0E+00	AW157233.1	EST_HUMAN	UI-HF-BN0-akj-01-0-UI.1 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:2783799 3' similar to
6556	15752	25214	2.38	0.0E+00	11427235	NT	au83b08.x1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2783799 3' similar to
6556	15752	25215	2.38	0.0E+00	11427235	NT	TR:O60463 O60463 TYPE-2 PHOSPHATIDIC ACID PHOSPHOHYDROLASE. [1];
6574	15770	25214	5.05	0.0E+00	AA398511.1	EST_HUMAN	Homo sapiens Chediak-Higashi syndrome 1 (CHS1), mRNA
6604	15800	25262	3.33	0.0E+00	BE690797.1	EST_HUMAN	Homo sapiens Chediak-Higashi syndrome 1 (CHS1), mRNA
6610	15806	25263	3.19	0.0E+00	4759695	NT	z73a08.s1 Soares testis_NHT Homo sapiens cDNA clone IMAGE:727958 3' similar to gb:S85655
6626	15822	25282	4.61	0.0E+00	X98922.1	NT	PROHIBITIN (HUMAN);
6626	15822	25283	4.61	0.0E+00	X98922.1	NT	Homo sapiens mitogen-activated protein kinase kinase 13 (MAP3K13), mRNA
6626	15822	25284	4.61	0.0E+00	X98922.1	NT	Homo sapiens mitogen-activated protein kinase kinase 13 (MAP3K13), mRNA
6650	15845	25308	2.28	0.0E+00	AW513513.1	EST_HUMAN	H. sapiens mRNA for gamma-glutamyltransferase
6652	15847	25308	9.98	0.0E+00	D52650.1	EST_HUMAN	H. sapiens mRNA for gamma-glutamyltransferase
							xa46a01.x1 NCI_CGAP_U11 Homo sapiens cDNA clone IMAGE:2707032 3' similar to gb:M14123_cd54
							RETROVIRUS-RELATED POL POLYPROTEIN (HUMAN);
							HUM084C02B Clontech human fetal brain polyA+ mRNA (#6535) Homo sapiens cDNA clone GEN:084C02

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6661	15856	25315	6.79	0.0E+00	BE378495.1	EST_HUMAN	601238488F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3608709 5'
6663	15858	25317	2.22	0.0E+00	AA410545.1	EST_HUMAN	z32e04.1 Scores ovary tumor NbHOT Homo sapiens cDNA clone IMAGE:724082 5'
6661	15896	25345	10.28	0.0E+00	AAB82527.1	EST_HUMAN	601238488F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3608709 5'
6694	15889	25349	5.08	0.0E+00	10947037	NT	601238488F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3608709 5'
6694	15889	25350	5.08	0.0E+00	10947037	NT	601238488F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3608709 5'
6708	15903	25365	2.95	0.0E+00	AV718377.1	EST_HUMAN	601238488F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3608709 5'
6711	15908	25365	2.28	0.0E+00	AU124051.1	EST_HUMAN	601238488F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3608709 5'
6739	15934	25393	8.1	0.0E+00	AW592233.1	EST_HUMAN	601238488F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3608709 5'
6739	15934	25394	8.1	0.0E+00	AW592233.1	EST_HUMAN	601238488F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3608709 5'
6762	15957	25412	6	0.0E+00	11422857	NT	601238488F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3608709 5'
6767	15962	25418	7.02	0.0E+00	AB020630.1	NT	601238488F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3608709 5'
6767	15962	25419	7.02	0.0E+00	AB020630.1	NT	601238488F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3608709 5'
6769	15984	25422	4.5	0.0E+00	7706638	NT	601238488F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3608709 5'
6783	15978	25436	3.18	0.0E+00	BE315402.1	EST_HUMAN	601238488F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3608709 5'
6783	15978	25437	3.18	0.0E+00	BE315402.1	EST_HUMAN	601238488F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3608709 5'
6790	15985	25445	2.37	0.0E+00	X14766.1	NT	601238488F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3608709 5'
6798	15994	25452	2.92	0.0E+00	AB954607.1	EST_HUMAN	601238488F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3608709 5'
6802	15997	25455	5.73	0.0E+00	9256595	NT	601238488F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3608709 5'
6807	16002	25462	2.77	0.0E+00	AW958311.1	EST_HUMAN	601238488F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3608709 5'
6822	16016	25481	3.11	0.0E+00	BE794823.1	EST_HUMAN	601238488F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3608709 5'
6865	16055	25522	2.65	0.0E+00	BE712515.1	EST_HUMAN	601238488F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3608709 5'
6889	15595	25057	3.59	0.0E+00	11560151	NT	601238488F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3608709 5'
6889	15595	25058	3.59	0.0E+00	11560151	NT	601238488F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3608709 5'
6891	15597	25061	12.21	0.0E+00	AL290909.1	EST_HUMAN	601238488F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3608709 5'
6891	15597	25062	12.21	0.0E+00	AL290909.1	EST_HUMAN	601238488F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3608709 5'
6902	16059	25527	4.68	0.0E+00	AF153468.1	NT	601238488F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3608709 5'
6907	16095	25562	15.37	0.0E+00	BE255829.1	EST_HUMAN	601238488F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3608709 5'
6908	16098	25562	24.85	0.0E+00	AW163779.1	EST_HUMAN	601238488F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3608709 5'
6925	16118	25584	6.68	0.0E+00	C08158.1	EST_HUMAN	601238488F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3608709 5'

Table 4

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6825	16118	25585	6.68	0.0E+00	C08158.1	EST_HUMAN	C08158 Human pancreatic islet Homo sapiens cDNA clone hbc5605
6927	16120	25588	5.28	0.0E+00	BE746215.1	EST_HUMAN	60157863F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3927548 5'
6942	16086	25554	2.48	0.0E+00	BE900549.1	EST_HUMAN	601673425F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3956238 5'
6955	16133	25602	3.1	0.0E+00	AF018084.1	NT	Homo sapiens keratin 2a (KRT2E) gene, complete cds
6955	16133	25603	3.1	0.0E+00	AF018084.1	NT	Homo sapiens keratin 2a (KRT2E) gene, complete cds
7001	16179	25650	2.7	0.0E+00	S78486.1	NT	AIGF=androgen-induced growth factor AIGF [human, placenta, Genomic/mRNA, 498 nt, segment 5 of 5]
7001	16179	25651	2.7	0.0E+00	S78486.1	NT	AIGF=androgen-induced growth factor AIGF [human, placenta, Genomic/mRNA, 498 nt, segment 5 of 5]
7002	16180	25652	3.47	0.0E+00	BE563320.1	EST_HUMAN	601334603F1 NIH_MGC_39 Homo sapiens cDNA clone IMAGE:3886680 5'
7017	16194	25668	2.39	0.0E+00	AU132349.1	EST_HUMAN	AU132349 NT2RP3 Homo sapiens cDNA clone NT2RP3004260 5'
7017	16194	25669	2.39	0.0E+00	AU132349.1	EST_HUMAN	AU132349 NT2RP3 Homo sapiens cDNA clone NT2RP3004260 5'
7020	16197	25673	16.33	0.0E+00	BE740490.1	EST_HUMAN	601595558F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3949383 5'
7020	16197	25674	16.33	0.0E+00	BE740490.1	EST_HUMAN	601595558F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3949383 5'
7023	16200	25678	2.71	0.0E+00	7662087	NT	Homo sapiens KIAA0345 gene product (KIAA0345), mRNA
7034	16211	25687	3.29	0.0E+00	AU132349.1	EST_HUMAN	AU132349 NT2RP3 Homo sapiens cDNA clone NT2RP3004260 5'
7056	16233	25708	3.33	0.0E+00	BE280793.1	EST_HUMAN	601155227F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3138788 5'
7059	16236	25709	9.74	0.0E+00	BE388700.1	EST_HUMAN	601286351F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3813045 5'
7059	16236	25710	9.74	0.0E+00	BE388700.1	EST_HUMAN	601286351F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3813045 5'
7082	16239	25712	6.83	0.0E+00	AW236289.1	EST_HUMAN	xn72b01.xt NCI CGAP_CML1 Homo sapiens cDNA clone IMAGE:2899977 3' similar to gb:X02152_cds1 L-LACTATE DEHYDROGENASE M CHAIN (HUMAN)
7078	16255	25728	3.3	0.0E+00	AU143673.1	EST_HUMAN	AU143673 Y78AA1 Homo sapiens cDNA clone Y78AA1002307 5'
7078	16255	25729	3.3	0.0E+00	AU143673.1	EST_HUMAN	AU143673 Y78AA1 Homo sapiens cDNA clone Y78AA1002307 5'
7079	16256	25730	3.59	0.0E+00	AF072408.1	NT	Homo sapiens killer cell inhibitory receptor KIRCI gene, exons 2, 3, and 4
7081	16258	25732	2.51	0.0E+00	11421001	NT	Homo sapiens HEF like Protein (HEFL), mRNA
7081	16258	25733	2.51	0.0E+00	11421001	NT	Homo sapiens HEF like Protein (HEFL), mRNA
7081	16268	25745	2.83	0.0E+00	AU136637.1	EST_HUMAN	AU136637 PLACE1 Homo sapiens cDNA clone PLACE1004737 5'
7091	16268	25746	2.83	0.0E+00	AU136637.1	EST_HUMAN	AU136637 PLACE1 Homo sapiens cDNA clone PLACE1004737 5'
7103	16280	25760	2.95	0.0E+00	AA198387.1	EST_HUMAN	zp97n1.1 Stratigene muscle 937209 Homo sapiens cDNA clone IMAGE:628197 5'
7125	16302	25783	2.32	0.0E+00	AF178308.1	NT	Homo sapiens KIF4 (KIF4) mRNA, complete cds
7139	16316	25797	12.52	0.0E+00	BE730772.1	EST_HUMAN	601570712F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3845403 5'
7139	16316	25798	12.52	0.0E+00	BE730772.1	EST_HUMAN	601570712F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3845403 5'
7167	16344	25822	4.03	0.0E+00	BF340331.1	EST_HUMAN	602037045F1 NCI CGAP_Bm64 Homo sapiens cDNA clone IMAGE:4184939 5'
7167	16344	25823	4.03	0.0E+00	BF340331.1	EST_HUMAN	602037045F1 NCI CGAP_Bm64 Homo sapiens cDNA clone IMAGE:4184939 5'

Page 375 of 382  
Table 4  
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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7108	16375	25857	2.47	0.0E+00	BF436218.1	EST_HUMAN	nab45012.x1 Soares_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:3265271 3'
7206	16383	25864	5.33	0.0E+00	AW517960.1	EST_HUMAN	ku74601.x1 NCI_CGAP_Kid8 Homo sapiens cDNA clone IMAGE:2807401 3' similar to gb:M89068 MOESIN (HUMAN);
7208	16385	25868	13.01	0.0E+00	BE549213.1	EST_HUMAN	601078764F1 NIH_MGC_12 Homo sapiens cDNA clone IMAGE:3464703 5'
7214	16391	25873	2.88	0.0E+00	BE781742.1	EST_HUMAN	601487419F1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3870700 5'
7216	16393	25876	2.52	0.0E+00	BE082720.1	EST_HUMAN	RC2-BT0642-150200-012-d03 BT0642 Homo sapiens cDNA
7216	16393	25877	2.52	0.0E+00	BE082720.1	EST_HUMAN	RC2-BT0642-150200-012-d03 BT0642 Homo sapiens cDNA
7219	16396	25880	5.18	0.0E+00	BE743215.1	EST_HUMAN	601573895F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3835198 5'
7219	16396	25881	5.18	0.0E+00	BE743215.1	EST_HUMAN	601573895F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3835198 5'
7230	16451	25940	2.86	0.0E+00	AV711075.1	EST_HUMAN	AV711075 Cu Homo sapiens cDNA clone CuAAKG05 5'
7230	16451	25941	2.86	0.0E+00	AV711075.1	EST_HUMAN	AV711075 Cu Homo sapiens cDNA clone CuAAKG05 5'
7232	16453		6.94	0.0E+00	AW813783.1	EST_HUMAN	RC3-ST0197-120200-015-g03 ST0197 Homo sapiens cDNA
7239	16459	25948	7.82	0.0E+00	AW963583.1	EST_HUMAN	EST375636 MAGE resequences; MAGH Homo sapiens cDNA
7252	16472	25983	2.36	0.0E+00	11431124	NT	Homo sapiens ATP-binding cassette, sub-family A (ABC1), member 3 (ABCA3), mRNA
7252	16472	25984	2.36	0.0E+00	11431124	NT	Homo sapiens ATP-binding cassette, sub-family A (ABC1), member 3 (ABCA3), mRNA
7254	16474	25988	2.16	0.0E+00	AW057621.1	EST_HUMAN	wy61f09.x1 Soares_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:2553085 3' similar to TR:Q60566 Q60566 VDX;
7262	16481	25973	2.11	0.0E+00	BE243270.1	EST_HUMAN	TCAAP3D0917 Pediatric acute myelogenous leukemia cell (FAB M1) Baylor-HGSC project=TCAA Homo sapiens cDNA clone TCAAP0917
7263	16482	25974	5.84	0.0E+00	AI652239.1	EST_HUMAN	wb28a12.x1 NCI_CGAP_GC6 Homo sapiens cDNA clone IMAGE:2306874 3' similar to contains element
7263	16482	25975	5.84	0.0E+00	AI652239.1	EST_HUMAN	MSR1 MSR1 repetitive element;
7273	16492	25983	4.32	0.0E+00	11545911	NT	MSR1 MSR1 repetitive element;
7273	16492	25984	4.32	0.0E+00	11545911	NT	Homo sapiens NOD2 protein (NOD2), mRNA
7287	16508	25997	2.37	0.0E+00	AW404795.1	EST_HUMAN	Homo sapiens NOD2 protein (NOD2), mRNA
7290	16509	26000	5.68	0.0E+00	11424829	NT	UI-HF-BL0-acm-d-04-0-UJ.1 NIH_MGC_37 Homo sapiens cDNA clone IMAGE:3059383 5'
7291	16510	26001	10.37	0.0E+00	4504538	NT	Homo sapiens hypothetical protein FLJ20079 (FLJ20079), mRNA
7291	16510	26002	10.37	0.0E+00	4504538	NT	Homo sapiens 5-hydroxytryptamine (serotonin) receptor 1E (HTR1E) mRNA
7292	16511	26003	2.78	0.0E+00	AI991827.1	EST_HUMAN	Homo sapiens 5-hydroxytryptamine (serotonin) receptor 1E (HTR1E) mRNA
7295	16514	26007	2.95	0.0E+00	BE862109.1	EST_HUMAN	wu32b06.x1 Soares_Dieckgreffe_colon_NHCD Homo sapiens cDNA clone IMAGE:2521715 3'
7299	16518	26009	14.1	0.0E+00	BE891830.1	EST_HUMAN	601505204F2 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3808865 5'
7301	16520	26010	1.93	0.0E+00	8923939	NT	601434522F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3918636 5'
7301	16520	26011	1.93	0.0E+00	8923939	NT	Homo sapiens myosin, heavy polypeptide 2, skeletal muscle, adult (MYH2), mRNA

Page 376 of 382  
Table 4  
Single Exon Probes Expressed in HELA Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7315	16533	26022	12.28	0.0E+00	BE003304.1	EST_HUMAN	601674332F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3957343 5'
7318	14789	24160	2.45	0.0E+00	AA195905.1	EST_HUMAN	zp95b11.11 Stragene muscle 837209 Homo sapiens cDNA clone IMAGE:627933 5' similar to gb:X03740
7337	16553	26042	6.57	0.0E+00	BE793498.1	EST_HUMAN	MYOSIN HEAVY CHAIN, SKELETAL MUSCLE (HUMAN);
7345	16561	26049	25.26	0.0E+00	AV727362.1	EST_HUMAN	601588828F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3943015 5'
7345	16561	26050	25.28	0.0E+00	AV727362.1	EST_HUMAN	AV727362 HTC Homo sapiens cDNA clone HTCAQH06 5'
7356	16572	26064	18.75	0.0E+00	AW516055.1	EST_HUMAN	AV727362 HTC Homo sapiens cDNA clone HTCAQH06 5'
7362	16578	26068	1.96	0.0E+00	AU135741.1	EST_HUMAN	xy04g10.x1 NCI_CGAP_Lym12 Homo sapiens cDNA clone IMAGE:2852226 3' similar to gb:M60854 40S RIBOSOMAL PROTEIN S16 (HUMAN);
7367	16583	26072	3.09	0.0E+00	AW593333.1	EST_HUMAN	AU135741 PLACE1 Homo sapiens cDNA clone PLACE1002794 5'
7367	16583	26073	3.09	0.0E+00	AW593333.1	EST_HUMAN	hg13d02.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2945475 3' similar to contains element MSR1 repetitive element;
7367	16583	26074	3.09	0.0E+00	AW593333.1	EST_HUMAN	hg13d02.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2945475 3' similar to contains element MSR1 repetitive element;
7368	16585	26075	1.79	0.0E+00	Z34897.1	NT	hg13d02.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2945475 3' similar to contains element MSR1 repetitive element;
7370	16586	26076	3.22	0.0E+00	F13069.1	EST_HUMAN	hg13d02.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2945475 3' similar to contains element MSR1 repetitive element;
7377	16593	26081	1.98	0.0E+00	D10083.1	NT	hg13d02.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2945475 3' similar to contains element MSR1 repetitive element;
7393	16607	26087	2.97	0.0E+00	AW338094.1	EST_HUMAN	H.sapiens mRNA for H1 histamine receptor
7394	16608	26098	5.93	0.0E+00	AW451230.1	EST_HUMAN	HSC3(CO3)1 normalized Infant brain cDNA Homo sapiens cDNA clone c-3ic03
7394	16608	26099	5.83	0.0E+00	AW451230.1	EST_HUMAN	Homo sapiens RGH1 gene, retrovirus-like element
7396	9498		16.35	0.0E+00	4508632	NT	Homo sapiens ribosomal protein L31 (RPL31) mRNA
7398	16611	26101	2.2	0.0E+00	AB014567.1	NT	Human sapiens mRNA for KIAA0687 protein, partial cds
7411	16623	26117	2.76	0.0E+00	BE298449.1	EST_HUMAN	601119248F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3028219 5'
7427	16637	26130	1.88	0.0E+00	AB011117.1	NT	Homo sapiens mRNA for KIAA0545 protein, partial cds
7443	16651	26143	2.8	0.0E+00	BE792155.1	EST_HUMAN	Homo sapiens mRNA for KIAA0545 protein, partial cds
7444	16652		62.57	0.0E+00	BF684061.1	EST_HUMAN	602141405F1 NIH_MGC_46 Homo sapiens cDNA clone IMAGE:3936539 5'
7447	16655	26146	5.83	0.0E+00	AU118368.1	EST_HUMAN	602141405F1 NIH_MGC_46 Homo sapiens cDNA clone IMAGE:4302492 5'
7448	16656		11.99	0.0E+00	AW236289.1	EST_HUMAN	AU118368 HEMBA1 Homo sapiens cDNA clone HEMBA1003486 5'
7453	16661	26150	8.59	0.0E+00	A1149808.1	EST_HUMAN	xn72b01.x1 NCI_CGAP_CML1 Homo sapiens cDNA clone IMAGE:2698977 3' similar to gb:X02152_cds1 L-LACTATE DEHYDROGENASE M CHAIN (HUMAN);
7453	16661	26151	8.59	0.0E+00	A1149808.1	EST_HUMAN	qf43c03.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1752772 3'
7454	16662	26152	4.17	0.0E+00	AW391937.1	EST_HUMAN	qf43c03.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1752772 3'
7454	16662	26152	4.17	0.0E+00	AW391937.1	EST_HUMAN	QV4-ST0234-121189-032-406 S70234 Homo sapiens cDNA

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7467	16875	26158	21.87	0.0E+00	11424726	NT	Homo sapiens insulin receptor (INSR), mRNA
7474	16882	26165	1.76	0.0E+00	BF340308.1	EST_HUMAN	602037014F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4184979 5'
7475	16883	26166	40.56	0.0E+00	BE261209.1	EST_HUMAN	601148357F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3163310 5'
7483	16892	26175	3.77	0.0E+00	U50326.1	NT	Human protein kinase C substrate 80K-H (PRKCSH) gene, exon 15-17
7489	16898	26180	2.19	0.0E+00	BE773038.1	EST_HUMAN	RC1-FT0134-170700-012-07 F10134 Homo sapiens cDNA
7489	16896	26181	2.19	0.0E+00	BE773038.1	EST_HUMAN	RC1-FT0134-170700-012-07 F10134 Homo sapiens cDNA
7510	16715	26203	19.32	0.0E+00	AA740782.1	EST_HUMAN	MSR1 repetitive element
7517	16722	26212	3.85	0.0E+00	AF252303.1	NT	Homo sapiens signaling lymphocytic activation molecule (SLAM) gene, exon 2
7530	16735	26225	6.93	0.0E+00	CO5089.1	EST_HUMAN	CO5089 Human heart cDNA (YNakamura) Homo sapiens cDNA clone 3NH4817
7537	16742	26233	2.19	0.0E+00	AA746375.1	EST_HUMAN	ae56h01.1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1308009 5'
7537	16742	26234	2.19	0.0E+00	AA746375.1	EST_HUMAN	ae56h01.1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1308009 5'
7547	16752	26246	2.05	0.0E+00	M78448.1	EST_HUMAN	EST00596 Fetal brain, Striatum (cat#9336206) Homo sapiens cDNA clone HFBCC28
7547	16752	26247	2.05	0.0E+00	M78448.1	EST_HUMAN	EST00596 Fetal brain, Striatum (cat#9336206) Homo sapiens cDNA clone HFBCC28
7550	16755	26248	7.75	0.0E+00	AL157608.1	EST_HUMAN	DKFZp761J2116.1 r1 761 (synonym: hamy2) Homo sapiens cDNA clone DKFZp761J2116 5'
7560	16765	26256	13.17	0.0E+00	AU116988.1	EST_HUMAN	AU116988 HEMBA1 Homo sapiens cDNA clone HEMBA1000424 5'
7572	16777	26270	2.02	0.0E+00	AV693658.1	EST_HUMAN	AV693658 GKC Homo sapiens cDNA clone GKCCNC03 5'
7580	16785	26279	2.07	0.0E+00	BF368563.1	EST_HUMAN	IL3-NT0104-200500-143-A07 NT0104 Homo sapiens cDNA
7603	16806	26302	3.42	0.0E+00	BE182360.1	EST_HUMAN	PMO-HT0845-060500-002-E05 HT0845 Homo sapiens cDNA
7603	16806	26303	3.42	0.0E+00	BE182360.1	EST_HUMAN	PMO-HT0845-060500-002-E05 HT0845 Homo sapiens cDNA
7605	16808		1.71	0.0E+00	AV701152.1	EST_HUMAN	AV701152 ADA Homo sapiens cDNA clone ADAAAD06 5'
7618	16821	26316	3.77	0.0E+00	BE898423.1	EST_HUMAN	601439092F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3924142 5'
7626	16828	26325	3.72	0.0E+00	BE018283.1	EST_HUMAN	bb78c04.y1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3048486 5' similar to gb:Y00345_cds1
7659	16859	26360	5.05	0.0E+00	BE897063.1	EST_HUMAN	POLYADENYLATE-BINDING PROTEIN (HUMAN); gb:X65553 M.musculus mRNA for poly(A) binding protein (MOUSE)
7660	16860	26361	1.88	0.0E+00	AI459545.1	EST_HUMAN	601440448F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3925403 5'
7680	16860	26362	1.88	0.0E+00	AI459545.1	EST_HUMAN	ae88g11.x1 Schiller meningioma Homo sapiens cDNA clone IMAGE:1952804 3'
7680	16860	26362	1.88	0.0E+00	AI459545.1	EST_HUMAN	ae88g11.x1 Schiller meningioma Homo sapiens cDNA clone IMAGE:1952804 3'
7698	16897	26406	4.25	0.0E+00	4758827	NT	Homo sapiens neuritin III (NRXN3) mRNA
7698	16898	26407	19.73	0.0E+00	BF208561.1	EST_HUMAN	601870902F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4101433 5'
7704	16903	26412	20.68	0.0E+00	AW207734.1	EST_HUMAN	UI-H-BI2-age-h-01-0-JL.s1 NCI_CGAP_Sub4 Homo sapiens cDNA clone IMAGE:2724312 3'
7708	16907	26415	6.88	0.0E+00	AB018260.1	NT	Homo sapiens mRNA for KIAA0717 protein, partial cds
7708	16907	26416	6.88	0.0E+00	AB018260.1	NT	Homo sapiens mRNA for KIAA0717 protein, partial cds

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## Single Exon Probes Expressed in HELA Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7709	16908	26417		3.24	BE206848.1	EST_HUMAN	ba04407.y1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2823373 5' similar to TR:O76022 O76022 E1B-55KDA-ASSOCIATED PROTEIN ;
7709	16908	26418		3.24	BE206848.1	EST_HUMAN	ba04407.y1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2823373 5' similar to TR:O76022 O76022 E1B-55KDA-ASSOCIATED PROTEIN ;
7731	15462	24904		2.19	L32832.1	NT	Homo sapiens zinc finger homeodomain protein (ATBF1-A) mRNA, complete cds
7734	16931	26438		2.97	BE148076.1	EST_HUMAN	RC3-H10230-040500-110-104 HT0230 Homo sapiens cDNA
7734	16931	26439		2.97	BE148076.1	EST_HUMAN	RC3-H10230-040500-110-104 HT0230 Homo sapiens cDNA
7734	16931	26439		2.97	BE148076.1	EST_HUMAN	UI-H-B14-ack-b-10-D-J1.s1 NCI CGAP Sub8 Homo sapiens cDNA clone IMAGE:3085026 3'
7767	16963	26475		4.64	BF507876.1	EST_HUMAN	UI-H-B14-ack-b-10-D-J1.s1 NCI CGAP Sub8 Homo sapiens cDNA clone IMAGE:3085026 3'
7767	16963	26476		4.64	BF507876.1	EST_HUMAN	UI-H-B14-ack-b-10-D-J1.s1 NCI CGAP Sub8 Homo sapiens cDNA clone IMAGE:3085026 3'
7775	16970	26483		2.28	BF507876.1	EST_HUMAN	UI-H-B14-ack-b-10-D-J1.s1 NCI CGAP Sub8 Homo sapiens cDNA clone IMAGE:3085026 3'
7775	16970	26483		2.28	BF507876.1	EST_HUMAN	UI-H-B14-ack-b-10-D-J1.s1 NCI CGAP Sub8 Homo sapiens cDNA clone IMAGE:3085026 3'
7780	16975	26488		10.51	BE76401.1	EST_HUMAN	UI-H-B14-ack-b-10-D-J1.s1 NCI CGAP Sub8 Homo sapiens cDNA clone IMAGE:3085026 3'
7780	16975	26488		10.51	BE76401.1	EST_HUMAN	UI-H-B14-ack-b-10-D-J1.s1 NCI CGAP Sub8 Homo sapiens cDNA clone IMAGE:3085026 3'
7786	16981	26494		4.77	BE76401.1	EST_HUMAN	UI-H-B14-ack-b-10-D-J1.s1 NCI CGAP Sub8 Homo sapiens cDNA clone IMAGE:3085026 3'
7786	16981	26494		4.77	BE76401.1	EST_HUMAN	UI-H-B14-ack-b-10-D-J1.s1 NCI CGAP Sub8 Homo sapiens cDNA clone IMAGE:3085026 3'
7792	16986	26510		3.35	AB037737.1	NT	Human mRNA for KIAA0241 gene, partial cds
7805	16998	26511		3.35	AB037737.1	NT	Human mRNA for KIAA0241 gene, partial cds
7805	16998	26511		3.35	AB037737.1	NT	Human mRNA for KIAA0241 gene, partial cds
7808	17002	26514		4.11	AB037737.1	NT	Human mRNA for KIAA0241 gene, partial cds
7808	17002	26514		4.11	AB037737.1	NT	Human mRNA for KIAA0241 gene, partial cds
7809	17002	26515		10.15	4503544	NT	Human mRNA for KIAA0241 gene, partial cds
7823	17015	26530		1.78	BF507876.1	EST_HUMAN	Human mRNA for KIAA0241 gene, partial cds
7831	17023	26538		7.53	AW328173.1	EST_HUMAN	Human gamma actin-like pseudogene, complete cds
7833	17025	26541		7.53	M55083.1	NT	Human gamma actin-like pseudogene, complete cds
7836	17028	26548		41.44	BF306996.1	EST_HUMAN	Human gamma actin-like pseudogene, complete cds
7841	17033	26549		3.52	BF306996.1	EST_HUMAN	Human gamma actin-like pseudogene, complete cds
7841	17033	26549		3.52	BF306996.1	EST_HUMAN	Human gamma actin-like pseudogene, complete cds
7848	17039	26558		26.43	BF306996.1	EST_HUMAN	Human gamma actin-like pseudogene, complete cds
7870	17060			4.97	BE887051.1	EST_HUMAN	Human gamma actin-like pseudogene, complete cds
7880	17068	26594		3.16	8923698	NT	Human gamma actin-like pseudogene, complete cds
7882	17070			3.22	BF207682.1	EST_HUMAN	Human gamma actin-like pseudogene, complete cds
7894	17110	26640		4.84	BE206848.1	EST_HUMAN	Human gamma actin-like pseudogene, complete cds
7894	17110	26641		4.84	BE206848.1	EST_HUMAN	Human gamma actin-like pseudogene, complete cds
7896	17112	26643		5.08	AW753028.1	EST_HUMAN	Human gamma actin-like pseudogene, complete cds

Table 4

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7901	17117		3.33	0.0E+00	AA558707.1	EST_HUMAN	h42c08.s1 NCI_CGAP_P14 Homo sapiens cDNA clone IMAGE:1043342 similar to gb:M95178 ALPHA-ACTININ 1, CYTOSKELETAL ISOFORM (HUMAN);
7902	14543	23612	3.76	0.0E+00	AI934954.1	EST_HUMAN	wp06g08.x1 NCI_CGAP_Kid12 Homo sapiens cDNA clone IMAGE:2464094 3'
7903	17118	26649	10.87	0.0E+00	AW327895.1	EST_HUMAN	dr02b08.x1 NIH_MGC_3 Homo sapiens cDNA clone IMAGE:2846919 5'
7921	18080	26667	1.71	0.0E+00	AW282776.1	EST_HUMAN	UI-H-BW0-aj-d-07-o-UI.s1 NCI_CGAP_Sub8 Homo sapiens cDNA clone IMAGE:2729509 3'
7934	17074	26601	2.83	0.0E+00	BE965909.2	EST_HUMAN	601659088R1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3895916 3'
7934	17074	26602	2.83	0.0E+00	BE965909.2	EST_HUMAN	601659088R1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3895916 3'
7935	17075	26603	4.9	0.0E+00	BE185656.1	EST_HUMAN	IL5-HT0731-020500-077-05 HT0731 Homo sapiens cDNA
7949	17088	26617	6.34	0.0E+00	AL046540.1	EST_HUMAN	DKFZp434G178_r1 434 (synonym: h1as3) Homo sapiens cDNA clone DKFZp434G178 5'
7949	17088	26618	6.34	0.0E+00	AL046540.1	EST_HUMAN	DKFZp434G178_r1 434 (synonym: h1as3) Homo sapiens cDNA clone DKFZp434G178 5'
7958	17097	26627	24.69	0.0E+00	AI923116.1	EST_HUMAN	wn83g03.x1 NCI_CGAP_U11 Homo sapiens cDNA clone IMAGE:2452468 3' similar to gb:S37431 LAMININ RECEPTOR (HUMAN);
7962	17141	26673	7.88	0.0E+00	AA760913.1	EST_HUMAN	nz11c07.s1 NCI_CGAP_GC81 Homo sapiens cDNA clone IMAGE:1287468 3' similar to TR:Q13686
7982	17141	26674	7.88	0.0E+00	AA760913.1	EST_HUMAN	nz11c07.s1 NCI_CGAP_GC81 Homo sapiens cDNA clone IMAGE:1287468 3' similar to TR:Q13686
7987	17148	26680	2.47	0.0E+00	BE910546.1	EST_HUMAN	Q13686 ALKB HOMOLOG PROTEIN. ;
7975	18410	25896	6.48	0.0E+00	BE676347.1	EST_HUMAN	7127112.x1 NCI_CGAP_QLL1 Homo sapiens cDNA clone IMAGE:3902626 5'
7978	18413	25899	1.65	0.0E+00	BE615686.1	EST_HUMAN	CHECKPOINT SUPPRESSOR 1. ;
7978	18413	25900	1.65	0.0E+00	BE615686.1	EST_HUMAN	601279335F1 NIH_MGC_39 Homo sapiens cDNA clone IMAGE:3811144 5'
8014	17153	26687	2.93	0.0E+00	L39891.1	NT	601279335F1 NIH_MGC_39 Homo sapiens cDNA clone IMAGE:3811144 5'
8014	17153	26688	2.93	0.0E+00	L39891.1	NT	Homo sapiens polycystic kidney disease-associated protein (PKD1) gene, complete cds
8027	17164	26701	4.05	0.0E+00	AU138211.1	EST_HUMAN	Homo sapiens polycystic kidney disease-associated protein (PKD1) gene, complete cds
8040	17176	26716	3.92	0.0E+00	BE622317.1	EST_HUMAN	AU138211 PLACE1 Homo sapiens cDNA clone PLACE1008077 5'
8073	17208	26741	26.14	0.0E+00	BE748899.1	EST_HUMAN	601441096F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3916270 5'
8073	17208	26742	26.14	0.0E+00	BE748899.1	EST_HUMAN	601572186T1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:3839012 3'
8084	17219	26754	3.94	0.0E+00	AU141892.1	EST_HUMAN	601572186T1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:3839012 3'
8084	17219	26755	3.94	0.0E+00	AU141892.1	EST_HUMAN	AU141892 THYRO1 Homo sapiens cDNA clone THYRO1001398 5'
8087	17222	26758	2.47	0.0E+00	AW006022.1	EST_HUMAN	AU141892 THYRO1 Homo sapiens cDNA clone THYRO1001398 5'
8091	18081	26762	4.52	0.0E+00	BF002333.1	EST_HUMAN	wz91h01.x1 NCI_CGAP_Brn25 Homo sapiens cDNA clone IMAGE:2566225 3' similar to WP:F63H10.2
8108	17242	26762	3.67	0.0E+00	AW387776.1	EST_HUMAN	CE11040 ZINC FINGER, C2H2 TYPE ;
							7h2b10.x1 NCI_CGAP_Cot16 Homo sapiens cDNA clone IMAGE:3316698 3' similar to TR:Q13458 Q13458 TRIO. ;
							MR4-ST0118-261099-012-b03 ST0118 Homo sapiens cDNA



Page 380 of 382  
Table 4  
Single Exon Probes Expressed in HELA Cells

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8108	17242	26783	3.67	0.0E+00	AW387776.1	EST_HUMAN	MR4-ST0118-261089-012-503 ST0118 Homo sapiens cDNA
8126	17282	26805	4.34	0.0E+00	11435244	NT	Homo sapiens KIAA0247 gene product (KIAA0247), mRNA
8128	17262	26808	4.34	0.0E+00	11435244	NT	Homo sapiens KIAA0247 gene product (KIAA0247), mRNA
8133	17266	26810	7.52	0.0E+00	U36253.1	NT	Human beta-prime-adaptin (BAM22) gene, exon 5
8135	17268	26812	17.97	0.0E+00	BE379254.1	EST_HUMAN	601237691F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3609623 5'
8135	17268	26813	17.97	0.0E+00	BE379254.1	EST_HUMAN	601237691F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3609623 5'
8149	17281	26826	2.37	0.0E+00	BE794758.1	EST_HUMAN	601590588F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3944708 5'
8150	17282	26827	96.17	0.0E+00	BE379254.1	EST_HUMAN	601590588F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3944708 5'
8160	17292	26833	9.23	0.0E+00	BE409993.1	EST_HUMAN	601491821F1 NIH_MGC_69 Homo sapiens cDNA clone IMAGE:3894220 5'
8161	17293	26834	1.7	0.0E+00	BE148650.1	EST_HUMAN	601491821F1 NIH_MGC_69 Homo sapiens cDNA clone IMAGE:3894220 5'
8162	17294	26835	1.74	0.0E+00	11427345	NT	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced
8162	17294	26836	1.74	0.0E+00	11427345	NT	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced
8162	17294	26837	1.74	0.0E+00	11427345	NT	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced
8163	17295	26838	2.96	0.0E+00	AF223391.1	NT	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced
8163	17295	26839	2.96	0.0E+00	AF223391.1	NT	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced
8170	17302	26847	2.12	0.0E+00	AU132940.1	EST_HUMAN	AU132940 NT2RP4 Homo sapiens cDNA clone NT2RP4000929 5'
8173	17305	26849	4.04	0.0E+00	BE603372.1	EST_HUMAN	601676357F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3958935 5'
8182	17314	26856	2.31	0.0E+00	BF312552.1	EST_HUMAN	601897524F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4127089 5'
8182	17314	26857	2.31	0.0E+00	BF312552.1	EST_HUMAN	601897524F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4127089 5'
8184	17316	26859	3.09	0.0E+00	X51755.1	NT	Human lambda-immunoglobulin constant region complex (germline)
8184	17316	26860	3.09	0.0E+00	X51755.1	NT	Human lambda-immunoglobulin constant region complex (germline)
8191	17323		1.98	0.0E+00	W88864.1	EST_HUMAN	z173405.s1 Soares_fetal_liver_spleen_1NF1S_S1 Homo sapiens cDNA clone IMAGE:417705 3'
8193	17325		2.05	0.0E+00	BE606402.1	EST_HUMAN	601498553F1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3900398 5'
8204	17335	26876	2.78	0.0E+00	9635487	NT	Human endogenous retrovirus, complete genome
8218	18082		15.82	0.0E+00	BF309120.1	EST_HUMAN	601890534F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4131416 5'
8224	17354	26891	75.29	0.0E+00	BE267175.1	EST_HUMAN	601177407F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3532988 5'
8254	15576	25032	2.25	0.0E+00		NT	Homo sapiens atrophin-1 interacting protein 1; activin receptor interacting protein 1 (KIAA0705), mRNA
8254	15576	25033	2.25	0.0E+00		NT	Homo sapiens atrophin-1 interacting protein 1; activin receptor interacting protein 1 (KIAA0705), mRNA
8265	17392	26922	2.1	0.0E+00	BE140795.1	EST_HUMAN	RCC-HT0022-090799-002-D01 HT0022 Homo sapiens cDNA
8279	18366	23590	1.91	0.0E+00	BE312542.1	EST_HUMAN	601150023F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3503020 5'

Page 381 of 382  
Table 4  
Single Exon Probes Expressed in HELA Cells

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8292	18208		1.39	0.0E+00	AL163246.2	NT	Homo sapiens chromosome 21, segment HS21C046
8294	18215		5.07	0.0E+00	AI190983.1	EST_HUMAN	q17b12.x1 Soares, fetal_lung_NHL19W Homo sapiens cDNA clone IMAGE:1739231 3'
8304	17411		2.71	0.0E+00	AB011399.1	NT	Homo sapiens gene for AF-8, complete cds
8325	17426		5.01	0.0E+00	AL163246.2	NT	Homo sapiens chromosome 21 segment HS21C046
8332	17431		3.24	0.0E+00	11417862	NT	Homo sapiens calcineurin binding protein 1 (KIAA0330), mRNA
8351	17445		4.53	0.0E+00	5802973	NT	Homo sapiens antioxidant protein 1 (AOP1), nuclear gene encoding mitochondrial protein, mRNA
8395	18174	23756	1.22	0.0E+00	AF240786.1	NT	Homo sapiens glutathione S-transferase theta 2 (GSTT2) and glutathione S-transferase theta 1 (GSTT1) genes, complete cds
8397	18184		3.55	0.0E+00	AL041931.1	EST_HUMAN	DKFZp434K0818_r1 434 (synonym: hhes3) Homo sapiens cDNA clone DKFZp434K0818 5'
8423	18334		3.8	0.0E+00	11418318	NT	Homo sapiens G-2 and S-phase expressed 1 (GTSE1), mRNA
8431	17497		4.18	0.0E+00	AL048544.1	EST_HUMAN	DKFZp434G218_r1 434 (synonym: hhes3) Homo sapiens cDNA clone DKFZp434G218 5'
8444	18219		1.87	0.0E+00	AI903497.1	EST_HUMAN	IL-BT030-271098-001 BT030 Homo sapiens cDNA
8498	18352		1.73	0.0E+00	N54484.1	EST_HUMAN	yw40e08.a1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:245222 3' similar to SW:POL_BAEVM P10272 POL POLYPROTEIN ;
8504	17543		4.14	0.0E+00	AF106658.1	NT	Homo sapiens adenylosuccinate lyase gene, complete cds
8507	10089	19250	3.7	0.0E+00	4507500	NT	Homo sapiens T-cell lymphoma invasion and metastasis 1 (TIAM1) mRNA
8507	10089	19251	3.7	0.0E+00	4507500	NT	Homo sapiens T-cell lymphoma invasion and metastasis 1 (TIAM1) mRNA
8516	18221		1.76	0.0E+00	10092587	NT	Homo sapiens nuclear factor of activated T-cells, cytoplasmic, calcineurin-dependent 2 (NFATC2), mRNA
8547	9805		3.58	0.0E+00	AF003528.1	NT	Homo sapiens X-linked anhidrotic ectodermal dysplasia protein gene (EDA), exon 2 and flanking repeat regions
8584	18031	23855	1.9	0.0E+00	11430460	NT	Homo sapiens low density lipoprotein-related protein 2 (LRP2), mRNA
8846	18155	23754	3.04	0.0E+00	AW590082.1	EST_HUMAN	hg31e06.x1 NCI_CGAP_G08 Homo sapiens cDNA clone IMAGE:2847234 3' similar to contains Alu repetitive element; contains element MER22 repetitive element ;
8677	18193		1.24	0.0E+00	L20493.1	NT	Human gamma-glutamyl transpeptidase mRNA, complete cds
8707	18217		2.42	0.0E+00	AF068757.1	NT	Homo sapiens somatostatin receptor subtype 3 (SSTR3) gene, 5' flanking region and partial cds
8744	17689		5.04	0.0E+00	9635487	NT	Human endogenous retrovirus, complete genome
8785	18209		2.02	0.0E+00	AI204914.1	EST_HUMAN	an05h04.x1 Strategene schizo brain S11 Homo sapiens cDNA clone IMAGE:1684759 3'
8817	17735		1.78	0.0E+00	AI904646.1	EST_HUMAN	QV-BT065-020399-103 BT065 Homo sapiens cDNA
8828	18207		1.56	0.0E+00	BE439792.1	EST_HUMAN	HTM1-854F HTM1 Homo sapiens cDNA
8839	11162	20364	1.69	0.0E+00	6912457	NT	Homo sapiens calcineurin binding protein 1 (KIAA0330), mRNA
8839	11162	20365	1.69	0.0E+00	6912457	NT	Homo sapiens calcineurin binding protein 1 (KIAA0330), mRNA
8858	17761	23934	1.41	0.0E+00	AF036365.1	NT	Homo sapiens caveolin-3 (CAV3) mRNA, complete cds

Page 382 of 382  
Table 4

## Single Exon Probes Expressed in HELA Cells

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8872	10873	20056	2.95	0.0E+00	H30132.1	EST_HUMAN	yc69a08.r1 Soares breast 3NBH8t Homo sapiens cDNA clone IMAGE:182248 5' similar to gb:M64089
							GAMMA-GLUTAMYL-TRANSEPTIDASE 5 PRECURSOR (HUMAN);
8872	10873	20057	2.95	0.0E+00	H30132.1	EST_HUMAN	yc69a08.r1 Soares breast 3NBH8t Homo sapiens cDNA clone IMAGE:182248 5' similar to gb:M64089
8886	17781		26.04	0.0E+00	D50659.1	NT	GAMMA-GLUTAMYL-TRANSEPTIDASE 5 PRECURSOR (HUMAN);
8888	17783	23916	5.39	0.0E+00	11418189	NT	Human gamma-cytoplasmic actin (ACTGPF8) pseudogene
8888	17783	23917	5.39	0.0E+00	11418189	NT	Homo sapiens thyroid autoantigen 70kD (Ku antigen) (G22P1), mRNA
							Homo sapiens thyroid autoantigen 70kD (Ku antigen) (G22P1), mRNA
							Homo sapiens DNA, DLEC1 to ORCTL4 gene region, section 1/2 (DLEC1, ORCTL3, ORCTL4 genes, complete cds)
8891	17788		1.74	0.0E+00	AB026898.1	NT	Homo sapiens GTP binding protein 1 (GTPBP1) mRNA
8909	11262	20476	1.55	0.0E+00	4758489	NT	Homo sapiens GTP binding protein 1 (GTPBP1) mRNA
8845	17822		1.37	0.0E+00	AW684999.1	EST_HUMAN	hi88a08.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2978154 3'
8853	17827	23908	1.34	0.0E+00	11430460	NT	Homo sapiens low density lipoprotein-related protein 2 (LRP2), mRNA
8957	17830	23908	1.31	0.0E+00	11430460	NT	Homo sapiens low density lipoprotein-related protein 2 (LRP2), mRNA
8890	10448	18604	1.62	0.0E+00	8922583	NT	Homo sapiens hypothetical protein FLJ10687 (FLJ10687), mRNA
8897	17858		2.87	0.0E+00	11526201	NT	Homo sapiens hypothetical protein FLJ20454 (FLJ20454), mRNA
9021	12516	21647	3.3	0.0E+00	4885312	NT	Homo sapiens G protein-coupled receptor 24 (GPR24), mRNA
9032	14093	23186	2.05	0.0E+00	6806918	NT	Homo sapiens low density lipoprotein-related protein 2 (LRP2), mRNA
9038	17881		1.78	0.0E+00	AB028900.1	NT	Homo sapiens CST gene for carboxylate sulfotransferase, exon 1, 2, 3, 4, 5
9078	17903	23902	2.37	0.0E+00	9558724	NT	Homo sapiens cleavage and polyadenylation specific factor 1, 160kD subunit (CPSF1), mRNA
9103	18377		6.14	0.0E+00	AL163248.2	NT	Homo sapiens chromosome 21 segment HS21CQ46
9110	9877	18998	2.2	0.0E+00	6806918	NT	Homo sapiens low density lipoprotein-related protein 2 (LRP2), mRNA
9157	10679	19852	1.39	0.0E+00	6912457	NT	Homo sapiens calcineurin binding protein 1 (KIAA0330), mRNA
9190	17878	23859	1.41	0.0E+00	11417862	NT	Homo sapiens calcineurin binding protein 1 (KIAA0330), mRNA
9196	17883		3.67	0.0E+00	7657020	NT	Homo sapiens DKFZP434P211 protein (DKFZP434P211), mRNA
							Homo sapiens DNA, DLEC1 to ORCTL4 gene region, section 1/2 (DLEC1, ORCTL3, ORCTL4 genes, complete cds)
9217	17896		1.3	0.0E+00	AB026898.1	NT	Homo sapiens period (Drosophila) homolog 3 (PER3), mRNA
9231	18007	23849	1.35	0.0E+00	8567387	NT	Homo sapiens period (Drosophila) homolog 3 (PER3), mRNA
							wu83c07.x1 NCI_CGAP_Kid3 Homo sapiens cDNA clone IMAGE:2527698 3' similar to TR:Q12844 Q12844
9257	18025	23853	2.2	0.0E+00	AW025032.1	EST_HUMAN	BREAKPOINT CLUSTER REGION PROTEIN :contains TAR1 t3 TAR1 repetitive element :
9260	18028		1.77	0.0E+00	AV656287.1	EST_HUMAN	AV656287 GLC Homo sapiens cDNA clone GLOCEPG06 3'
9276	10386	19537	3.04	0.0E+00	9968844	NT	Homo sapiens chromosome 12 open reading frame 3 (C12ORF3), mRNA

1/10

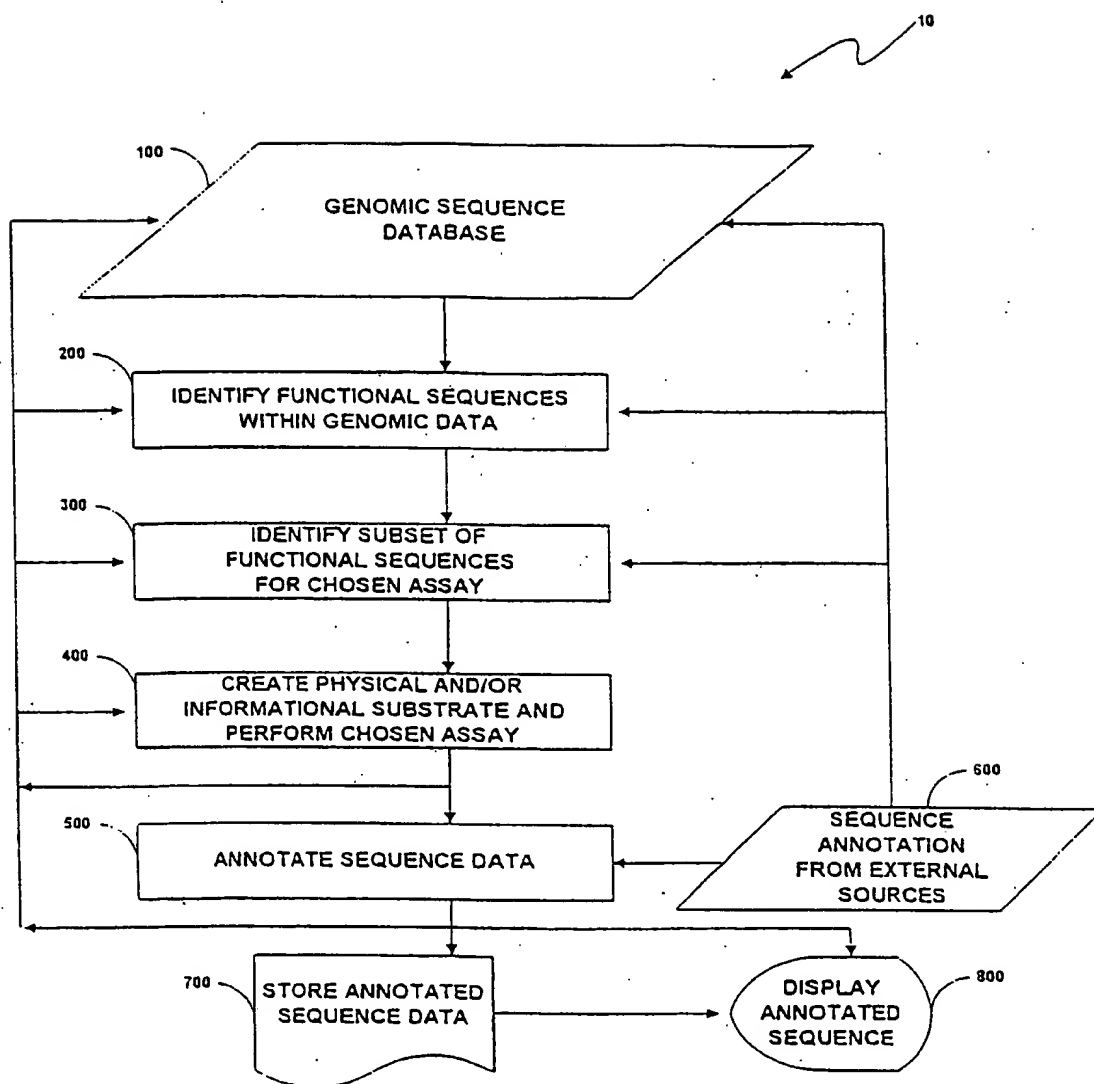


Fig. 1

2/10

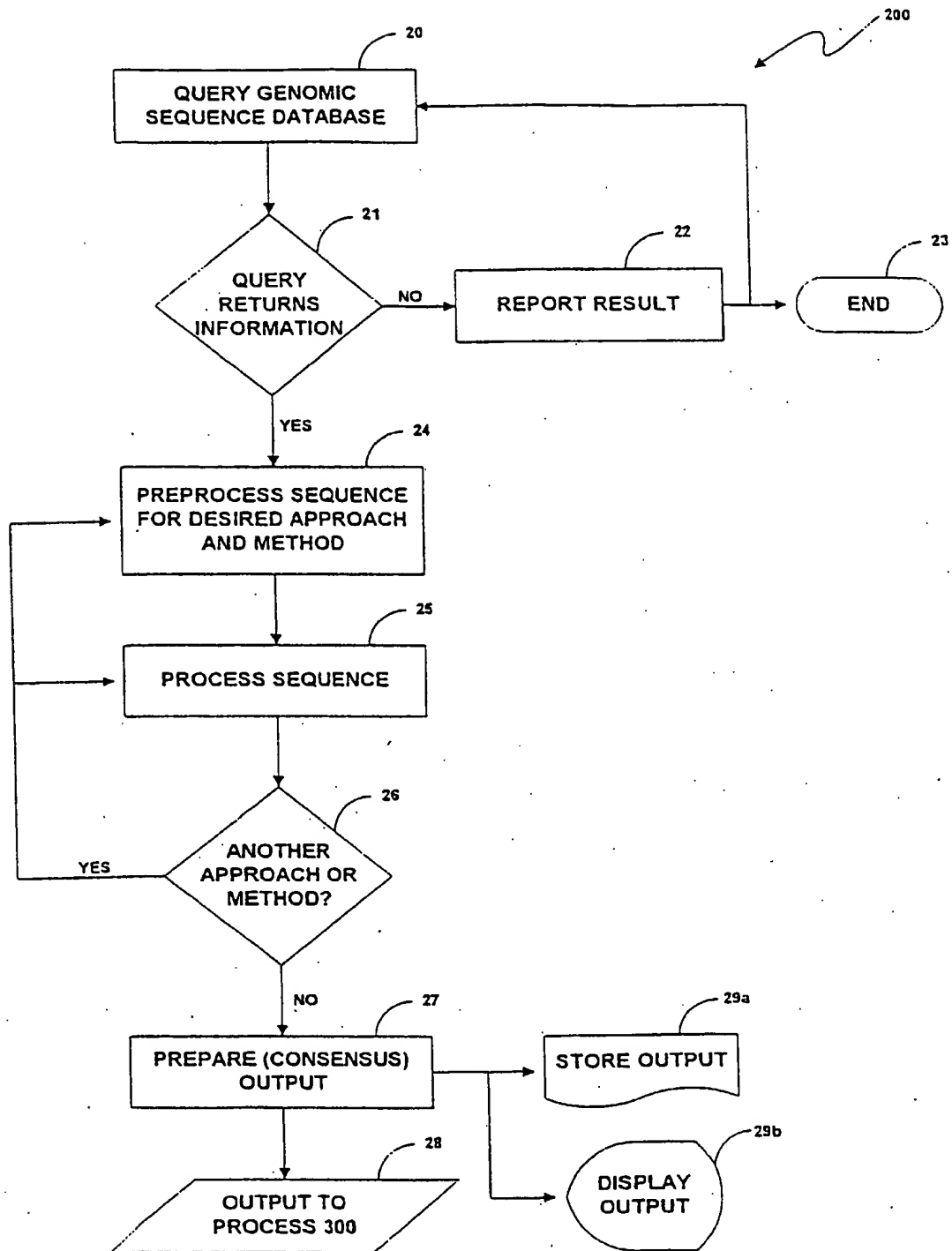


Fig. 2

3/10

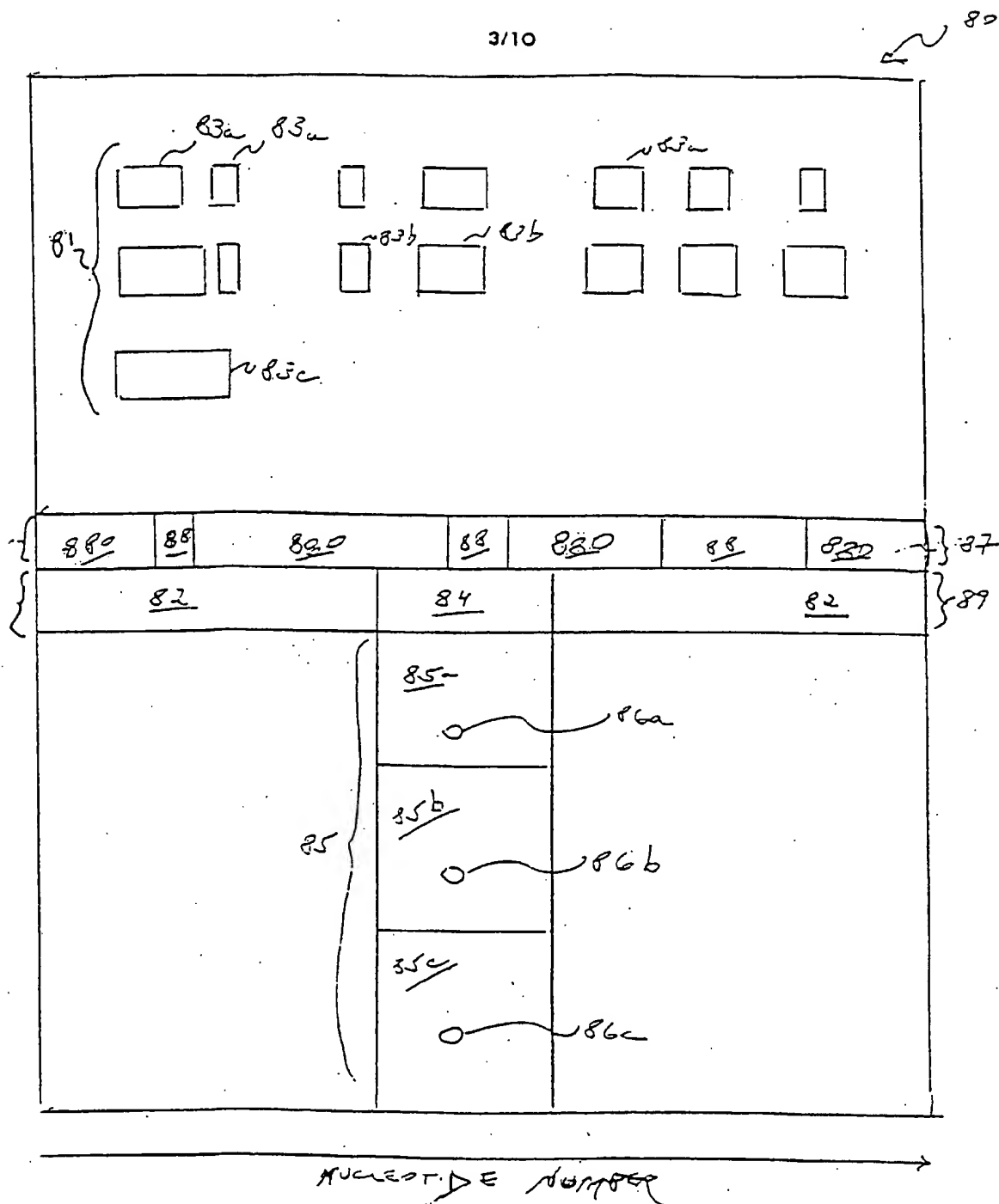


Fig. 3

4/10

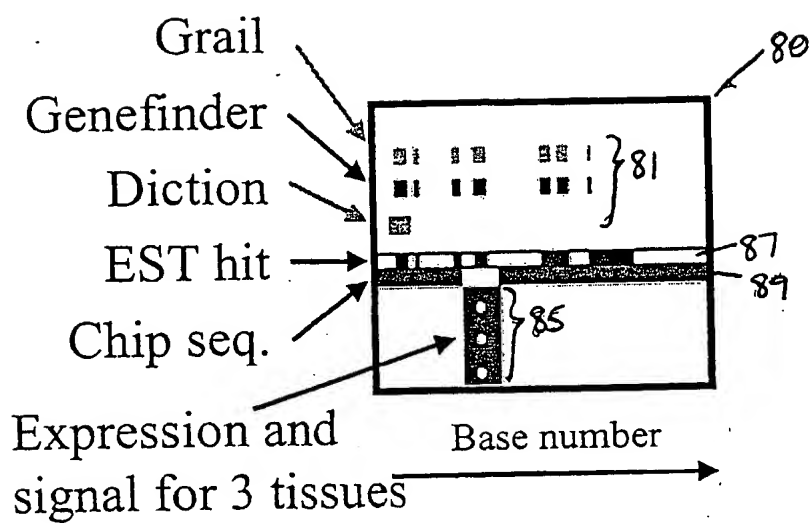


Fig. 4

5/10

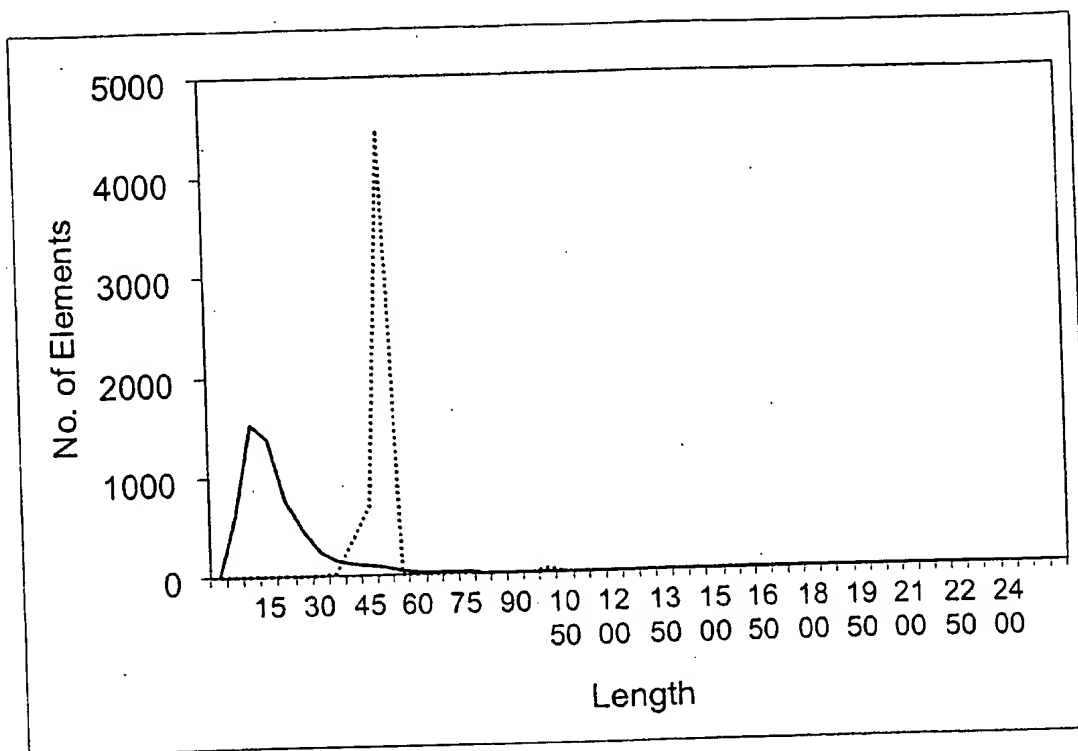


Fig. 5



6/10

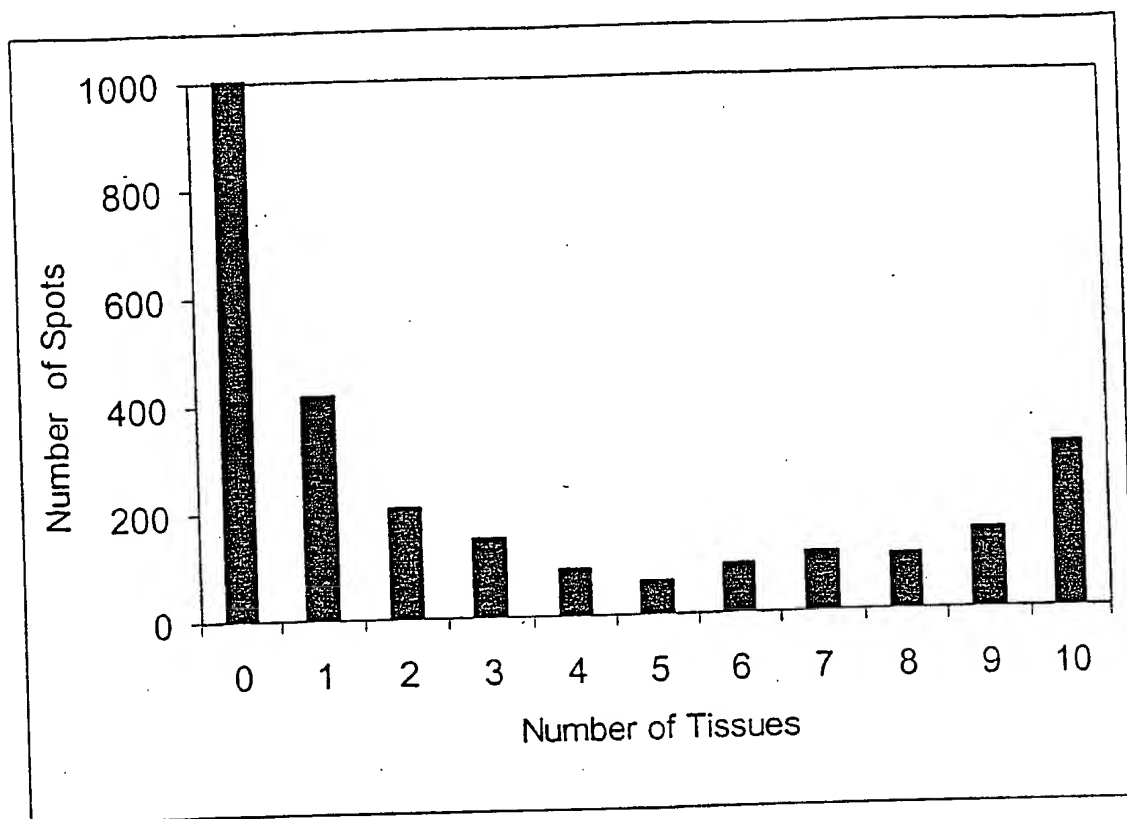


Fig. 6

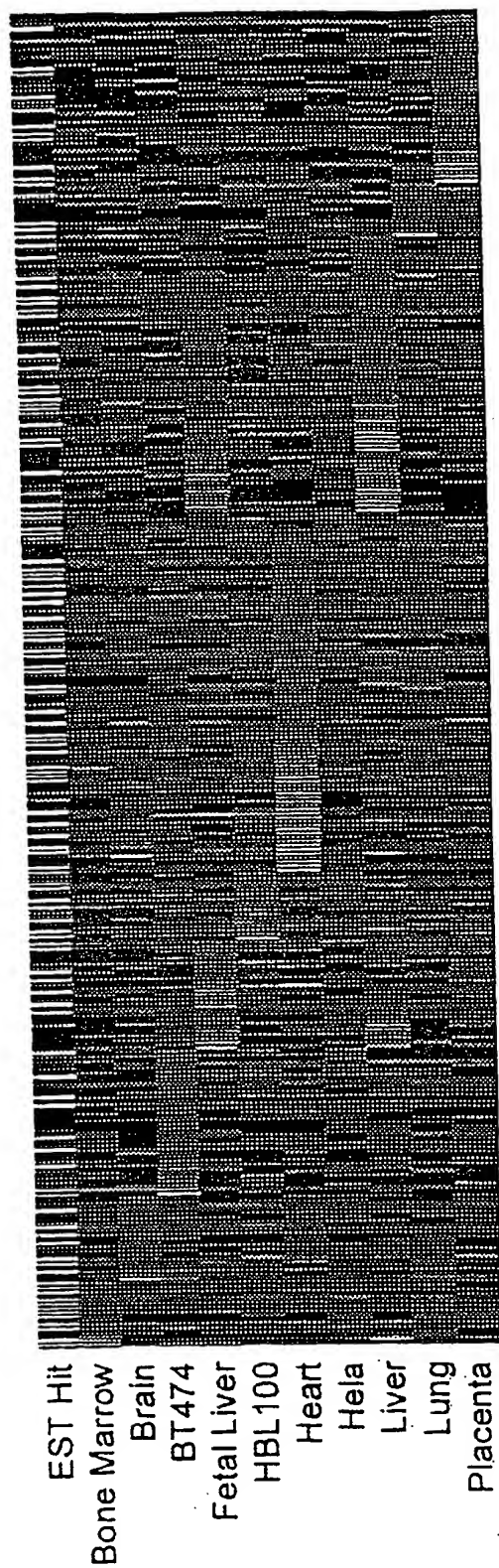


Fig. 7a

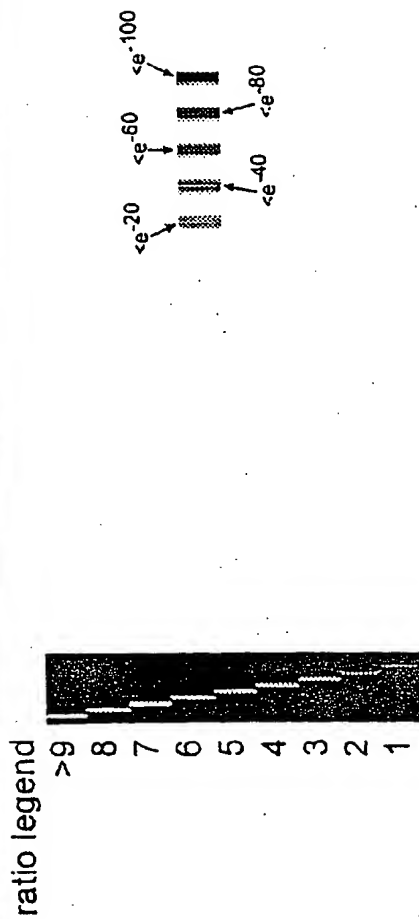


Fig. 7b

Fig. 7c

8/10

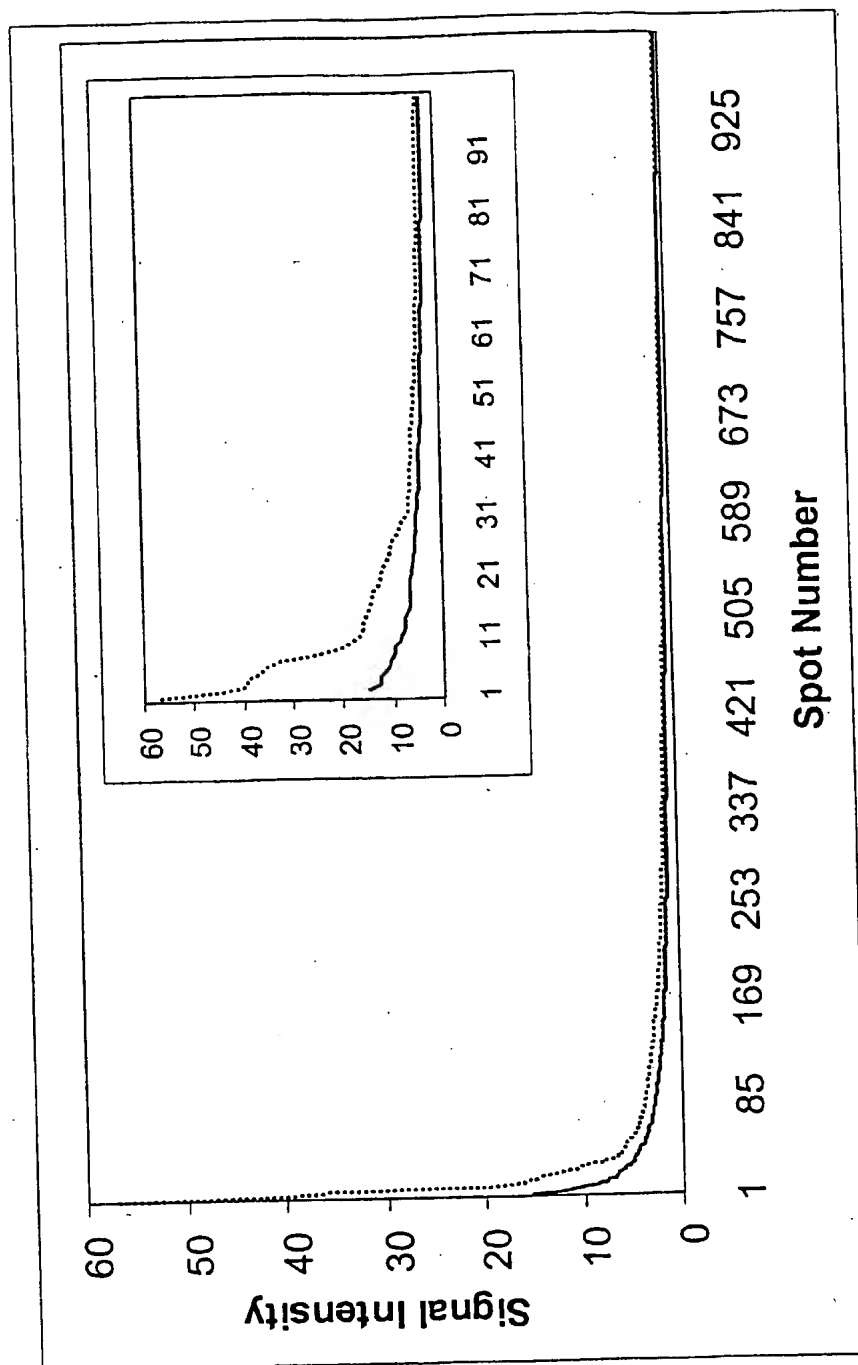


Fig. 8

9/10

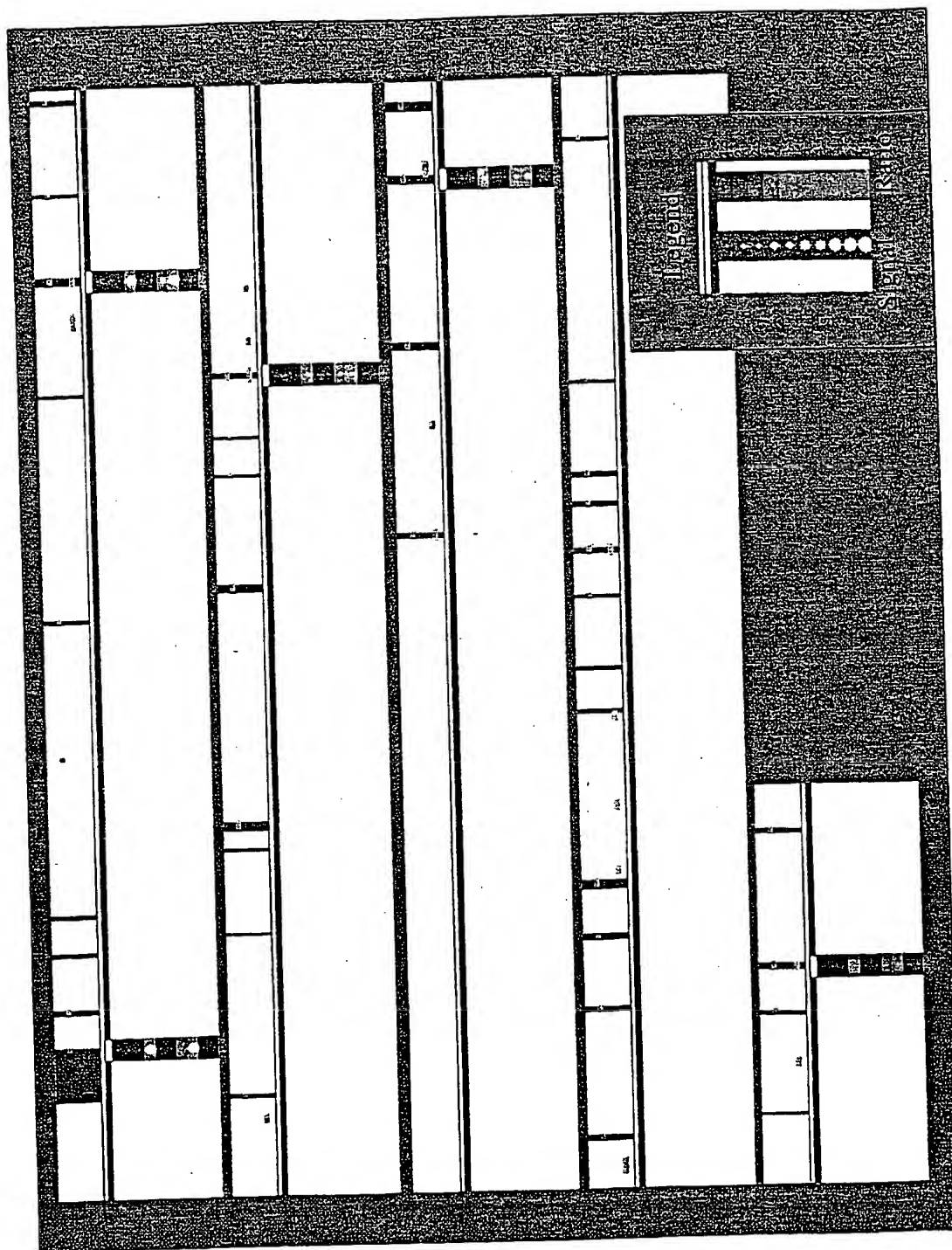


Fig. 9

10/10

Fig. 10

